```
TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
                             TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
                             TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA
This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:
          a294.pep
                             MRITCAPMSL LSAAVWSIRA VRTSSNRFPA AFRRYSAFRP TIFPKPAGTP
                             WHRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
                     51
                    101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
                             FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMPFVVG LLFASGIVMA
                   151
                             ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
                             SKYIHTVVFT HMLLIVFLAK AMFYISW*
                      94.9% identity in 277 aa overlap
m294/a294
                                                                      20
                                                                                         30
                                                                                                            40
                                                                                                                               50
                                                   10
                                   MRITCAPMSLLSAAVWSIRVVRTSSNRFPAAFRRYSAFQPTIFPKPADTPWHRVRRFKSN
          m294.pep
                                   MRITCAPMSLLSAAVWSIRAVRTSSNRFPAAFRRYSAFRPTIFPKPAGTPWHRVRRFKSN
          a294
                                                                                         30
                                                                                                            40
                                                   10
                                                  70
                                                                      80
                                                                                         90
                                                                                                          100
                                   RRMRGGKPLKKPYRPRGGGCRCRRAWTALSHNIAERARESPRRCGKRYADIGGDSDTIRI
          m294.pep
                                   RRTRGGKPLKKTYRPRRAECRCRRARTALSHNIAERARESPRRYGKRYADIGDDSDTIRI
          a294
                                                                      80
                                                                                         90
                                                                                                          100
                                                                                                                             110
                                                                                                                                                120
                                                   70
                                                                                                                             170
                                                                                                          1.60
                                                                    140
                                                                                       150
                                                 130
                                   RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSREARREVEKAMSYR
          m294.pep
                                    14414: 14414: 14414: 14444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 1445: 1444: 1444: 1444: 1444: 1444: 1444: 1444: 144
                                   RVFRLEYRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSCEARREVEKAMSYR
          a294
                                                                                                          160
                                                                                                                             170
                                                 130
                                                                    140
                                                                                                          220
                                                                                                                             230
                                                 190
                                                                    200
                                                                                       210
                                   AVRVMPFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK
          m294.pep
                                    AVRVMPFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK
          a294
                                                                    200
                                                                                                          220
                                                                                                                             230
                                                                                                                                                240
                                                 190
                                                                    260
                                                 250
                                   MARSTLTVGWSKYIHAVVFTHMLLIVFLAKAMFYISWX
          m294.pep
                                    MARSTLTVGWSKYIHTVVFTHMLLIVFLAKAMFYISWX
          a294
                                                                                       270
                                                 250
                                                                    260
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1229>:
 g295.seq
                 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
                 gttgccacgc cgccagcagt ttttccgcct cgtcttcgcc ccgataaacg
         101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa
         151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
         201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc
                 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
         251
                 acggatcagg cggcggactt tcagataacc gttcagcgat ttttccgaca
```

601 ctcgcgtatc aagggctggg cggcacgcgt ttctccgacc gaaacggcgt 651 gtatccaaac cgcgccggta acgggattcg gatgcggctt gccgaaacgc 701 tcgtccctat gcgcccggta tgccgggca cttccggagc gtttgtccaa

701 tcgtccctat gcgcccggta tgccggggca cttccggagc gtttgtccad 751 ataacgccgt atccatatcg gcgcaagcag ccacaataca tcataaagcc 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacggttc

851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

```
g295.pep
         MLGMARHDGO QGIAAILLPR RQQFFRLVFA PINARAAAHG NRPASDAFFK
         LPRQRFHVFR RHQVVFGIAA HLHGCRAQFR QPRRIRLRLR QTARQRSGCG
     51
         TDOAADFQIT VQRFFRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA
    101
         VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ
    151
        LAYOGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
    201
         ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1231>:
m295.seq
         ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
         GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
     51
         CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTTCAAA
    101
         CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGTATGATG TCGTATTTGG
    151
         TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
         GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG
    251
         ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
    301
         GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGCGCGCCC GCATTCCCTC
    351
         ATCAGGTTGG GCCAGATTTC GGTTTCCATC AAAATGCCGA ACATCGGGCG
    401
         GTGTTCGCGC AAAAACTGCC GTACCCACGT TTTTTTGTCA TACGGAAGAT
    451
         AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTTC CCGCCCCGTC
    501
         GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAAAC GCCGCCGCAA
    551
         CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
    601
         GTATCCAAAC CGCGCCGGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
    651
         TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTTCCGGAGC GTTTGTCCAA
    701
         ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
    751
         ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC TGAACGGTTC
         AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:
m295.pep
         MLGMARHDDQ QRIAAILLPR RQQFFRLVFT PINARAAAHG NRPASDAFFK
         LPRORFHLFR RYDVVFGIAA HLHGCRAQFR QPRRIRLCLR QTPRORSGGR
     51
         TDQAADFQIT VQRFFRQPRI RQKQRHTRAP AFPHQVGPDF GFHQNAEHRA
    101
         VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PPRRGHLRHQ QRRIGKTPPQ
    151
         LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
    201
         ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTVQTAFRQR NQIS*
           93.9% identity in 294 aa overlap
m295/q295
                             20
                                      30
                                               40
            \verb|MLGMARHDDQQRIAAILLPRRQQFFRLVFTPINARAAAHGNRPASDAFFKLPRQRFHLFR|
m295.pep
            {\tt MLGMARHDGQQGIAAILLPRRQQFFRLVFAPINARAAAHGNRPASDAFFKLPRQRFHVFR}
q295
                                               40
                                                        50
                             20
                                      30
                   10
                                      90
                                              100
                                                       110
                                                                 120
                   70
                             80
            RYDVVFGIAAHLHGCRAQFRQPRRIRLCLRQTPRQRSGGRTDQAADFQITVQRFFRQPRI
m295.pep
            RHQVVFGIAAHLHGCRAQFRQPRRIRLRLRQTARQRSGCGTDQAADFQITVQRFFRQPRI
g295
                                                       110
                                                                 120
                   70
                             80
                                      90
                                              100
                                     150
                                                       170
                            140
                                              160
            RQKQRHTRAPAFPHQVGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF
m295.pep
            ROKORHTRSPAFLHQIGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF
g295
                                     150
                                              160
                   130
                            140
                                                                 240
                            200
                                     210
                                              220
                                                       230
            PPRRGHLRHQQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI
m295.pep
            PSRRGHLRHQQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRMRLAETLVPMRPV
q295
                            200
                                     210
                                              220
                  190
                                              280
                            260
                                     270
                   250
            CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQISX
m295.pep
            CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVRTVRTAFRQRNQIS
g295
                   250
                            260
                                     270
                                              280
                                                       290
```

a295

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1233>:
    a295.seq
             ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
             GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
          51
             CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
         101
             CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
         151
             TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
         201
             GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
         251
             ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
             GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
         351
             ATCAGATTGG GCCAGATTTC GGTTTCCATC AAAATGCCGA ACATCGGGCG
         401
             GTGTTCGCGC AAAAACTGCC GTACCCACGT TTTTTTGTCA TACGGAAGAT
         451
             501
             GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGGAAAAC GCTGCCGCAA
             CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCCGACC GAAACGGCGT
         601
             GTATCCAAAC CGCGCCGGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
         651
             TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCCGGAGC GTTTGTCCAA
         701
             ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
         751
             ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
         801
             GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:
     a295.pep
              MLGMARHDDQ QGIAAILLPR RQQFFRLVFT PINARAAAHG NLPVSDAFFK
              LPRORFHLFR RHOVVFGIAA HLHGCRAOFR OPRRIRLRLC OTARORSGGR
          51
              TDQAADFQIT V*RFFRQPRI RQKQRHTRAP AFLHQIGPDF GFHQNAEHRA
              VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPQ
              LAYORLGGTR FPDRNGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
              ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
         251
m295/a295 93.2% identity in 294 aa overlap
                                                   40
                                         30
                {\tt MLGMARHDDQQRIAAILLPRRQQFFRLVFTPINARAAAHGNRPASDAFFKLPRQRFHLFR}
     m295.pep
                 {\tt MLGMARHDDQQGIAAILLPRRQQFFRLVFTPINARAAAHGNLPVSDAFFKLPRQRFHLFR}
     a295
                                                   40
                                 20
                                         . 30
                        10
                                                  100
                                                           110
                                                                   120
                                         90
                        70
                                 80
                 RYDVVFGIAAHLHGCRAQFRQPRRIRLCLRQTPRQRSGGRTDQAADFQITVQRFFRQPRI
     m295.pep
                 RHQVVFGIAAHLHGCRAQFRQPRRIRLRLCQTARQRSGGRTDQAADFQITVXRFFRQPRI
     a295
                                                                    120
                                          90
                                                  100
                                                           110
                                 80
                        70
                                         150
                                                  160
                                                           170
                                                                    180
                                140
                       130
                 RQKQRHTRAPAFPHQVGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF
     m295.pep
                 RQKQRHTRAPAFLHQIGPDFGFHQNAEHRAVFAQKLPYPRFFVIRKIAALCIRKQNLRGF
     a295
                                                           170
                       130
                                140
                                         150
                                                  160
                                         210
                                                  220
                                                           230
                                                                    240
                       190
                                200
                 PPRRGHLRHQQRRIGKTPPQLAYQGLGGTRFSDRNGVYPNRAGNGIRIRLAETLVPMRPI
     m295.pep
                 PSRRGHLRHQQRRIGKTLPQLAYQRLGGTRFPDRNGVYPNRAGNGIRIRLAETLAPMRPI
     a295
                                                           230
                                                                    240
                                         210
                                                  220
                       190
                                200
                                                  280
                                                           290
                                         270
                                260
                 CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQISX
     m295.pep
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1235>: g297.seq

260

CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVRTVRTAFRQRNQISX

270

280

290

¹ ATGGCTGTCT TCCCACTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC

```
686
```

```
51 GCTTGCCGTT TCGATTATTC TGGTGtcgGC GGCATACATT GCttcgacag
     aggggaccga gcgcgtcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
101
     CTGTCtTGGg gcggcaacgg CGTtcagacg gcaTATTGGG TGCAGGAGGC
151
     GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
201
     CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
251
     TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
     CGGCAGTGCG CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCGAGCGCA
351
     aTCtGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
 401
     GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
 451
     GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
501
     AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
     GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
 601
     GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
     CAACCCATCA GGCGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
701
     GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
751
     CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
801
     GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
851
     GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
     CCAACGGTGT GGAAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1001
1051 CAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTCG GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
     CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1151
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA
```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

```
g297.pep
         MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
          LSWGGNGVQT AYWVQEAVQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
     101 LRHLRADQSV HVLVGGDGSA REVQFFTDED GERNLVALEK KGGIWRRSAS
     151 DADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
         EGDAVRLLYD SLYFHGQQVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
         GNYYDEDGRV LQEKGGFNIE PLVYTRISSP FGYRMHPILH TWRLHTGIDY
     301 AAPQGTPVRA SADGVITFKG RKGGYGNAVM IRHANGVETL YAHLSAFSQA
         QGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
     351
          DKAAFAAQKQ KADALLARLR GIPVTVSQSD *
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1237>: m297.seq

```
ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
     GCTTGCCGTT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG
 51
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAACAAAA TCTGCCGCCG
     CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
     GGTGCAGCCG GGCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
     CGCGGGACGA GATTGCCCGA ATCACGGAAA AATATGGCGG CGAAGCCGAT
     TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
301
     CGGCGGCGC CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCGAGCGCA
351
401 ATCTGGTCGC TTTGGAAAAG AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
     GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
451
     GTCGGCGCG GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
     GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
     GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
651
     CAAGGCATCA GGCGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
701
     GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
751
     CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
     GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
851
     GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
901
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
     GAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTCG GTTCGACCGG
     GCGTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1101
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCGGAATT GACGCAGGCG
     GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
     GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA
```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>: m297.pep

- MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERVR PQRVEQNLPP 51 LSWGGSGVQT AYWVQEAVQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
- LRHLRADQSV HVLVGGDGGA REVQFFTDED GERNLVALEK KGGIWRRSAS 101 EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK 151

201 251 301 351 401	EGDAVRLMYD SLYFHGQQVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG GNYYDEDGKV LQEKGGFNIE PLVYTRISSP FGYRMHPILH TWRLHTGIDY AAPQGTPVRA SADGVITFKG RKGGYGNAVM IRHANGVETL YAHLSAFSQA EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA DKAAFAAQKQ KADALLARLR GIPVTVSQSD *
m297/g297	97.9% identity in 430 aa overlap
m297.pep	10 20 30 40 50 60 MAVFPLSAKHRKYALRALAVSIILVSAAYIASTERTERVRPQRVEQNLPPLSWGGSGVQT
m297.pep g297	70 80 90 100 110 120 AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA
m297.pep g297	130 140 150 160 170 180 REVQFFTDEDGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV
m297.pep g297	190 200 210 220 230 240 EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQVAAGDILAAEVVKGGTRHQAFY
m297.pep	250 260 270 280 290 300 YRSDKEGGGGGNYYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
m297.pep g297	310 320 330 340 350 360 AAPQGTPVRASADGVITFKGRKGGYGNAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
m297.pep	370 380 390 400 410 420 GFVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR
m297.pep g297	430 GIPVTVSQSDX IIIIIIIIII GIPVTVSQSDX 430

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1239>:

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ATGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC

1 ATGGCTGTCT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAACAAAA ACTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG TGTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCA GGCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA AATTGCCCGA ATAACGGAAA AATATGGCG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCGGCGC CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCGAGCGCA
401 ATCTGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCCC GGTTCGCTGG CGCGGCGGA AGTGCCCGTC GAAATTCGCG
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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG

601	GAAGGCGATG	CCGTGCGCCT	GATTTACGAC	AGCCTGTATT	TCCACGGGCA	
651				GGAAGTCGTT		
701				ACAAGGAAGG		
751				TTGCAGGAAA		
801				TTCTTCGCCG		
851				TGCACACGGG		
901				TCCGCCGACG		
951				CGCGGTGATG		
1001				TGAGCGCGTT		
1051	GAAGGCAATG					
1101	GCGTTCGACG					
1151				CACCCGAATT		
1201	GACAAGGCGG					
1251				GCAATCGGAT		
1201						
This correspond	s to the amin	o acid seque	ence <seo ii<="" td=""><td>D 1240: ORF</td><td>7 297 a></td><td></td></seo>	D 1240: ORF	7 297 a>	
		o doza seque		- 1 - 10, 010	257.00.	
a297.pep	MARKED TO A KILL	D1/(VAT DAT AU	CTTTUCABUT	a carbarana	DODUEOUT DD	
1	MAVFPLSAKH					
51	LSWGGSGVQT					
101	LRHLRADQSV					
151	EADMKVLPTL					
201	EGDAVRLIYD					
251	GNYYDEDGRV					
301	AAPQGTPVRA					
351	EGNVRGGEVI				ALPTPELTQA	•
401	DKAAFAAQKQ	KADALLARLR	GIPVIVSQSD	*		
m297/a297 99	.3% identity	in 430 aa ov	erlap			
		10	20 30	0 40	50	60
m297.pep	MAVFPLSA	KHRKYALRAL	AVSIILVSAAY	IASTERTERVRI	PORVEQNLPPLSW	GGSGVQT
	1 1 1 1 1 1 1	11111111111				111111
a297						
a297		KHRKYALRAL		IASTERTERVRI	PORVEQKLPPLSW 50	
a297		KHRKYALRAL	AVSIILVSAAY	IASTERTERVRI	PQRVEQKLPPLSW	GGSGVQT
a297		KHRKYALRALI 10 2	AVSIILVSAAY	IASTERTERVRI) 40	PQRVEQKLPPLSW	GGSGVQT
	MAVFPLSA	KHRKYALRALI 10 2 70 8	AVSIILVSAAY: 20 30 30 90	IASTERTERVRI 0 40 0 100	PQRVEQKLPPLSW 50	GGSGVQT 60 120
a297 m297.pep	MAVFPLSA AYWVQEAV	KHRKYALRALI 10 2 70 8 QPGDSLADVLI	AVSIILVSAAY 20 30 30 90 ARSGMARDEIAI	IASTERTERVRI) 40) 100 RITEKYGGEADI	PQRVEQKLPPLSW 50 110	GGSGVQT 60 120 VGGDGGA
	MAVFPLSA AYWVQEAV	KHRKYALRAL 10 2 70 6 QPGDSLADVL 	AVSIILVSAAY 20 30 30 90 ARSGMARDEIAI	IASTERTERVRI) 40) 100 RITEKYGGEADI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL	GGSGVQT 60 120 VGGDGGA
m297.pep	MAVFPLSA AYWVQEAV	KHRKYALRALI 10 : 70 : (QPGDSLADVL) (QPGDSLADVL)	AVSIILVSAAY 20 30 30 90 ARSGMARDEIAI	IASTERTERVRI) 40) 100 RITEKYGGEADI 	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL	GGSGVQT 60 120 VGGDGGA
m297.pep	MAVFPLSA AYWVQEAV	KHRKYALRALI 10 : 70 : (QPGDSLADVL) (QPGDSLADVL)	AVSIILVSAAY 20 30 30 90 ARSGMARDEIAH ARSGMARDEIAH 30 90	IASTERTERVRI) 40) 100 RITEKYGGEADI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL 	GGSGVQT 60 120 VGGDGGA
m297.pep	MAVFPLSA AYWVQEAV AYWVQEAV	TO STORY TO	AVSIILVSAAY 20 30 30 90 ARSGMARDEIAH ARSGMARDEIAH 30 90	IASTERTERVRI 100 100 RITEKYGGEADI IIIIIIIIIII RITEKYGGEADI 100 160	PORVEOKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170	GGSGVQT 60 120 VGGDGGA VGGDGGA 120
m297.pep	MAVFPLSA AYWVQEAV AYWVQEAV	TO STORY TO	AVSIILVSAAY 20 30 30 90 ARSGMARDEIAH ARSGMARDEIAH 30 90	IASTERTERVRI 100 100 RITEKYGGEADI IIIIIIIIIII RITEKYGGEADI 100 160	PORVEOKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110	GGSGVQT 60 120 VGGDGGA VGGDGGA 120
m297.pep a297	MAVFPLSA AYWVQEAV AYWVQEAV 1 REVQFFTD	CHRKYALRALI 70 E COPGDSLADVLI COPGDSLADVLI 70 E 30 14	AVSIILVSAAY 20 30 ARSGMARDEIAH 	IASTERTERVRI) 40) 100 RITEKYGGEADI	PORVEOKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV
m297.pep a297	MAVFPLSA AYWVQEAV AYWVQEAV	CHRKYALRALI 70 E COPGDSLADVLI COPGDSLADVLI 70 E 30 14 EDGERNLVALI	AVSIILVSAAY: 20 30 BO 90 ARSGMARDEIAH ARSGMARDEIAH BO 90 40 150 EKKGGIWRRSAS	ASTERTERVRI 0	PORVEOKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV
m297.pep a297 m297.pep	MAVFPLSA AYWVQEAV IIIIIIII AYWVQEAV REVQFFTE IIIIIII	AKHRKYALRALI 10 2 70 8 70PGDSLADVLI 111111111 70PGDSLADVLI 70 8 30 14 EDGERNLVALI 11111111	AVSIILVSAAY: 20 30 BO 90 ARSGMARDEIAH ARSGMARDEIAH BO 90 40 150 EKKGGIWRRSAS	ASTERTERVRI 40	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV
m297.pep a297 m297.pep	MAVFPLSA AYWVQEAV AYWVQEAV 1 REVQFFTD	AKHRKYALRALI 10	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI 40	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV
m297.pep a297 m297.pep	MAVFPLSA AYWVQEAV AYWVQEAV 1 REVQFFTD	AKHRKYALRALI 10	AVSIILVSAAY 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS 	ASTERTERVRI 40	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV
m297.pep a297 m297.pep	MAVFPLSA AYWVQEAV AYWVQEAV 1 REVQFFTD REVQFFTD	AKHRKYALRALI 10	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS 40 150 00 210 LKEGDAVRLMYI	ASTERTERVRI 0	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL 170 230 AGDILAAEVVKGG	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV ARAEVPV 180 240 TRHQAFY
m297.pep a297 m297.pep a297	MAVFPLSA AYWVQEAV AYWVQEAV 1 REVQFFTD REVQFFTD	AKHRKYALRALI 10 70 ROPGDSLADVLI 111111111 ROPGDSLADVLI 70 30 14 EDGERNLVALI 11111111 EDGERNLVALI 30 14 90 20 EFFAGRFSLDGI	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI 0	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL 230 AGDILAAEVVKGG	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV ARAEVPV 180 240 TRHQAFY
m297.pep a297 m297.pep a297	MAVFPLSA AYWVQEAV AYWVQEAV 1 REVQFFTD REVQFFTD	AKHRKYALRALI 10 70 ROPGDSLADVLI 111111111 ROPGDSLADVLI 70 30 14 EDGERNLVALI 11111111 EDGERNLVALI 30 14 90 20 EFFAGRFSLDGI	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI 0	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL 170 230 AGDILAAEVVKGG	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV ARAEVPV 180 240 TRHQAFY
m297.pep a297 m297.pep a297	MAVFPLSA AYWVQEAV AYWVQEAV 1 REVQFFTD REVQFFTD 1 EIRESLSG	AKHRKYALRALI 10 70 R R R R R R R R R R R R R R R R R R	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI 0	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL 230 AGDILAAEVVKGG	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV ARAEVPV 180 240 TRHQAFY
m297.pep a297 m297.pep a297	AYWVQEAV AYWVQEAV 1 REVQFFTD REVQFFTD 1 EIRESLSG	AKHRKYALRALI 10 70 R R R R R R R R R R R R R R R R R R	AVSIILVSAAY: 20 30 BO 90 ARSGMARDEIAH ARSGMARDEIAH BO 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI A0	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL AGDILAAEVVKGG	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV ARAEVPV 180 240 TRHQAFY TRHQAFY
m297.pep a297 m297.pep a297 m297.pep a297	AYWVQEAV AYWVQEAV 1 REVQFFTD REVQFFTD 1 EIRESLSG	AKHRKYALRALI 10 70 R R R R R R R R R R R R R R R R R R	AVSIILVSAAY: 20 30 30 30 90 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI A0	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL AGDILAAEVVKGG 230 290	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV ARAEVPV 180 TRHQAFY TRHQAFY 240 300
m297.pep a297 m297.pep a297 m297.pep	AYWVQEAV AYWVQEAV 1 REVQFFTD REVQFFTD 1 EIRESLSG	AKHRKYALRALI 10 70 R R R R R R R R R R R R R R R R R R	AVSIILVSAAY: 20 30 30 30 90 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI A0	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL 1110 170 RSVVVKTSARGSL 111111111111111111111111111111111111	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV ARAEVPV 180 TRHQAFY TRHQAFY 240 300
m297.pep a297 m297.pep a297 m297.pep a297	AYWVQEAV AYWVQEAV REVQFFTD REVQFFTD 1 EIRESLSG EIRESCSG	### ACT 10 20 20 20 20 20 20 20	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL AGDILAAEVVKGG 230 290 FGYRMHPILHTWR	120 VGGDGGA VGGDGGA VGGDGGA 20 180 ARAEVPV ARAEVPV TRHQAFY TRHQAFY 240 300 LHTGIDY
m297.pep a297 m297.pep a297 m297.pep a297	AYWVQEAV AYWVQEAV REVQFFTD REVQFFTD 1 EIRESLSG EIRESCSG	### ACT 10 20 20 20 20 20 20 20	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL AGDILAAEVVKGG 230 290 FGYRMHPILHTWR	120 VGGDGGA VGGDGGA VGGDGGA 20 180 ARAEVPV ARAEVPV TRHQAFY TRHQAFY 240 300 LHTGIDY
m297.pep a297 m297.pep a297 m297.pep a297	AYWVQEAV AYWVQEAV REVQFFTE REVQFFTE 1 EIRESLSG EIRESLSG	AKHRKYALRALI 10 70 QPGDSLADVLI 1 QPGDSLADVLI 70 30 14 EDGERNLVALI 1 EDGERNLVALI 30 14 ETFAGRFSLDGI 1 ETFAGRFSLDGI 90 20 GGGGNYDEDGI 1 EGGGNYYDEDGI	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL AGDILAAEVVKGG 230 290 FGYRMHPILHTWR	120 VGGDGGA VGGDGGA VGGDGGA 20 180 ARAEVPV ARAEVPV TRHQAFY TRHQAFY 240 300 LHTGIDY
m297.pep a297 m297.pep a297 m297.pep a297	AYWVQEAV AYWVQEAV REVQFFTE REVQFFTE 1 EIRESLSG EIRESLSG YRSDKEGG	### ACT 10 20 20 20 20 20 20 20	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL AGDILAAEVVKGG 230 290 FGYRMHPILHTWR FGYRMHPILHTWR 290	GGSGVQT 60 120 VGGDGGA VGGDGGA 120 180 ARAEVPV ARAEVPV 180 TRHQAFY TRHQAFY 240 300 LHTGIDY LHTGIDY 300
m297.pep a297 m297.pep a297 m297.pep a297 m297.pep	AYWVQEAV AYWVQEAV REVQFFTD REVQFFTD EIRESLSG EIRESLSG YRSDKEGG YRSDKEGG	### ACT 10 20 20 20 20 20 20 20	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL 1110 170 RSVVVKTSARGSL 1111	120 VGGDGGA VGGDGGA VGGDGGA 20 180 ARAEVPV ARAEVPV TRHQAFY TRHQAFY 240 300 LHTGIDY LHTGIDY 300
m297.pep a297 m297.pep a297 m297.pep a297	AYWVQEAV AYWVQEAV REVQFFTE REVQFFTE EIRESLSG EIRESLSG YRSDKEGG YRSDKEGG	AKHRKYALRALI 10 70 ROPGDSLADVLI 111111111 ROPGDSLADVLI 70 30 30 14 EDGERNLVALI 11111111 EDGERNLVALI 30 14 ETFAGRFSLDGI 111111111 ETFAGRFSLDGI 11111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 11111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 11111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 11111111 ETFAGRFSLDGI 11111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 11111111 ETFAGRFSLDGI 11111111 ETFAGRFSLDGI 1111111 ETFAGRFSLDGI 1111	AVSIILVSAAY: 20 30 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL AGDILAAEVVKGG 230 290 FGYRMHPILHTWR 290 350 CAHLSAFSQAEGN	120 VGGDGGA VGGDGGA VGGDGGA 20 180 ARAEVPV ARAEVPV TRHQAFY TRHQAFY 240 300 LHTGIDY LHTGIDY 300 VRGGEVI
m297.pep a297 m297.pep a297 m297.pep a297 m297.pep	AYWVQEAV IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	### ACT 10 20 20 20 20 20 20 20	AVSIILVSAAY: 20 30 30 30 90 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL 170 230 AGDILAAEVVKGG 230 290 FGYRMHPILHTWR 290 350 PGYRMHPILHTWR 290 350 PGYRHLSAFSQAEGN	120 VGGDGGA VGGDGGA VGGDGGA 20 180 ARAEVPV ARAEVPV TRHQAFY TRHQAFY 240 300 LHTGIDY LHTGIDY 300 VRGGEVI
m297.pep a297 m297.pep a297 m297.pep a297 m297.pep	AYWVQEAV AYWVQEAV REVQFFTE REVQFFTE EIRESLSG EIRESLSG AAPQGTPV AAPQGTPV	AKHRKYALRALI 10 70 ROPEDSLADVLI 111111111 ROPEDSLADVLI 70 ROPEDSLADVLI 70 ROPEDSLADVLI 1011111111 ROPEDSLADVLI 10200000000000000000000000000000000000	AVSIILVSAAY: 20 30 30 30 90 ARSGMARDEIAH ARSGMARDEIAH 30 90 40 150 EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS EKKGGIWRRSAS	ASTERTERVRI	PQRVEQKLPPLSW 50 110 LRHLRADQSVHVL LRHLRADQSVHVL 110 170 RSVVVKTSARGSL RSVVVKTSARGSL AGDILAAEVVKGG 230 290 FGYRMHPILHTWR 290 350 CAHLSAFSQAEGN	120 VGGDGGA VGGDGGA VGGDGGA 20 180 ARAEVPV ARAEVPV TRHQAFY TRHQAFY 240 300 LHTGIDY LHTGIDY 300 VRGGEVI

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370
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                               390
                430
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m297.pep
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a297
                430
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1241>: g298.seq

```
ATGAAAACT TTCTTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
 51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
    ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcccccac ggCTCAAGAC GGCGGTTCGG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGGCCGGC
301 GGAACAGAAT GGAAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
    CAAAGTCTTT TTCGCCGGAG ATTCGCTGAT GCAGGGCGTT GCGCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTCC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GCGTCGACCG
    CATCCTTGAA GCCGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAACTGCTTT CGGAACACTT GAAAGGCAAA ATCATCCTGA TTCCCACCGC
801 GCAAACACTG AGCGGCGGGA AAGGCCGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAACC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
    GAAGGACAAA AACTGCTGGC GGAAAAAATA ATGGAAAAAA TCGTTTTTGA
    ACCGAGTACG CAACCATCAA GTACACAGCC ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>: g298.pep

```
MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51 SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPPAG
101 GTEWKQGTEA AAVRSGDKVF FAGDSLMQGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRILE AAHTHRVQVV WLGIPYMKKV KLDGQMRYLD
251 KLLSEHLKGK IILIPTAQTL SGGKGRYTDS VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1243>: m298.seq

```
ATGAAAAACT TTCTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
 51 TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCGG
    CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCGGCG ACTCGCTGAT GCAGGGCGTT GCCCCCTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTCC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAACTGCTTT CGGAACATTT GAAAGGCAAA ATCATCCTGA TTCCCACCAC
801 GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA
```

```
This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:
m298.pep
        MKNFLSLFSS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
        SGAALQENAY ALSDGIKAFL SGETPPTAQD GGSADMPSEA AASEAVPQTG
     51
        ETEWKODTEA AAVRSGDKVF FVGDSLMQGV APFVQKSLKQ QYGIESVNLS
    101
        KOSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
    151
        KFASDEWAQE YLKRVDRILE AAHTHRVQVV WLGIPYMKKA KLDGQMRYLD
        KLLSEHLKGK IILIPTTHTL SGGKDRYTDS VNVNGKPVRY RSKDGIHFTA
    251
        EGOKLLAAKI MEKIVFEPST QPSSTQP*
          94.8% identity in 327 aa overlap
m298/g298
                 10
                          20
                                  30
           MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
m298.pep
           MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
g298
                                          40
                                                   50
                 10
                          20
                                  30
                          80
                                  90
                                          100
                                                  110
           ALSDGIKAFLSGETPPTAQDGGSADMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF
m298.pep
           ALSDGIKTFLSGETPPTAQDGGSADMPPEAAASEAAPPAGGTEWKQGTEAAAVRSGDKVF
g298
                                  90
                                         100
                                                  110
                                                          120
                 70
                          80
                130
                         140
                                 150
                                          160
                                                  170
                                                          180
           FVGDSLMQGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV
m298.pep
           FAGDSLMQGVAPFVQKSLKQQYGIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV
g298
                                         160
                                                  170
                         140
                                 150
                130
                                                  230
                                 210
                                          220
                 190
                         200
           LAVFLGPNDPWDFPVGKLYLKFASDEWAQEYLKRVDRILEAAHTHRVQVVWLGIPYMKKA
m298.pep
           LAVFLGPNDPWDFPVGKRYLKFASDEWAQEYLKRVDRILEAAHTHRVQVVWLGIPYMKKV
g298
                                          220
                                                  230
                190
                         200
                                 210
                                                  290
                                                          300
                 250
                         260
                                 270
                                          280
           KLDGQMRYLDKLLSEHLKGKIILIPTTHTLSGGKDRYTDSVNVNGKPVRYRSKDGIHFTA
m298.pep
           KLDGQMRYLDKLLSEHLKGKIILIPTAQTLSGGKGRYTDSVNVNGKPVRYRSKDGIHFTA
g298
                                                  290
                         260
                                          280
                250
                         320
                310
           EGOKLLAAKIMEKIVFEPSTQPSSTQPX
m298.pep
           EGQKLLAEKIMEKIVFEPSTQPSSTQPX
g298
                         320
                310
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1245>:

a298.s	seq					
	1	ATGAAAAACT	TTCTTTCCCT	TTTCGCCTCC	ATACTGATGT	CTGCCCTGAT
	51	TGCCGTGTGG	TTCAGCCAAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
1	L 01	ACCACCGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
1	151	AGCGGTGCGG	CATTGCAAGA	AAACGCCTAC	GCCCTTTCAG	ACGGCATCAA
2	201	AGCCTTCCTG	TCCGGCGAAA	CGCCGCCGAC	GGCTCAAGAC	GGCGGTTCGG
2	251	CAGATATGCC	GTCTGAAGCC	GCCGCACCCG	AAACCGCCCC	TCAAACTGGC
3	301	GAAACAGAAT	GGAAACAAAA	CACCGAAGCC	GCCGCCGTCC	GAACAGGGGA
3	351	CAAAGTCTTT	TTCGCCGGCG	ACTCGCTGAT	GCAGGGCGTT	GCACCCTTCG
4	101	TGCAAAAAAG	CCTGAAACAG	CAATACGGCA	TCGAATCCGT	CAACCTCAGC
4	151	AAACAAAGCA	CGGGGCTGTC	CTACCCCTCA	TTCTTCGACT	GGCCGAAAAC
Ę	501	GATTGAAGAA	ACCCTGAAAA	AACATCCCGA	AATCAGCGTG	CTCGCCGTCT
ŗ	551	TCCTCGGTCC	GAACGACCCG	TGGGATTTCC	CCGTTGGCAA	ACGCTACCTC
6	501	AAATTCGCTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GCGTCGACCG
6	551	CATCCTTGAA	GCCGCACACA	CGCACTACGT	CCAAGTCGTC	TGGCTCGGCA
7	701		GAAAAAAGCC			

```
AAACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCCTGA TTCCCACCGC
         801
             GCACACCCTG AGCGGCGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
             ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
         851
             GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
         901
            ACCAAGTACG CAACCATCAA GTACACAGCC ATGA
         951
This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:
    a298.pep
             MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
         51
             SGAALQENAY ALSDGIKAFL SGETPPTAQD GGSADMPSEA AAPETAPOTG
             ETEWKONTEA AAVRTGDKVF FAGDSLMQGV APFVQKSLKQ QYGIESVNLS
         101
             KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
        201 KFASDEWAQE YLKRVDRILE AAHTHYVQVV WLGIPYMKKA KLDGQMRYLD
             KLLSEYLKGK IILIPTAHTL SGGKDRYTDS VNVNGKPVRY RSKDGIHFTA
             EGOKLLAAKI MEKIVFEPST QPSSTQP*
          96.3% identity in 327 aa overlap
m298/a298
                                        30
                                                40
                                                         50
                                                                  60
    m298.pep
               MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALOENAY
                MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
    a298
                      10
                               20
                                       30
                                                40
                                                         50
                      70
                               80
                                       90
                                               100
                                                        110
                                                                 120
    m298.pep
               ALSDGIKAFLSGETPPTAQDGGSADMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF
               a298
               ALSDGIKAFLSGETPPTAQDGGSADMPSEAAAPETAPQTGETEWKONTEAAAVRTGDKVF
                      70
                               80
                                       90
                                               100
                     130
                              140
                                      150
                                               160
                                                        170
                                                                 180
               FVGDSLMQGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV
    m298.pep
               FAGDSLMQGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV
    a298
                     130
                              140
                                      150
                                               160
                                                        170
                     190
                              200
                                      210
                                               220
                                                        230
                                                                240
               LAVFLGPNDPWDFPVGKLYLKFASDEWAQEYLKRVDRILEAAHTHRVQVVWLGIPYMKKA
    m298.pep
               LAVFLGPNDPWDFPVGKRYLKFASDEWAQEYLKRVDRILEAAHTHYVQVVWLGIPYMKKA
    a298
                     190
                              200
                                      210
                                               220
                                                        230
                                                                240
                     250
                              260
                                      270
                                               280
                                                        290
                                                                300
               KLDGQMRYLDKLLSEHLKGKIILIPTTHTLSGGKDRYTDSVNVNGKPVRYRSKDGIHFTA
    m298.pep
               KLDGQMRYLDKLLSEYLKGKIILIPTAHTLSGGKDRYTDSVNVNGKPVRYRSKDGIHFTA
    a298
                     250
                              260
                                      270
                                               280
                                                        290
                     310
                              320
    m298.pep
               EGOKLLAAKIMEKIVFEPSTOPSSTOPX
               a298
               EGQKLLAAKIMEKIVFEPSTQPSSTQPX
                     310
                              320
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1247>: g299.seq

```
ATGAACCCCA AACACTTCAT CGCATTTCC GCCCTGTTCG CCGCCACGCA

51 GGCAGAAGCC CTGCCCGTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT

101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC

151 AACGCCGCCG CCTCGCCTTG GATGAAAAAA CTCCGATCCG TCGCACAAGG

201 CAGCGGCGAG GCCTTCCGCA TCCTGCAAAT CGGCGACTCG CATACCGCCG

251 GCGACTTCTT TACCGACGCC CTGCCAAAC GCCTGCAAAA AACATGGGGC

301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT

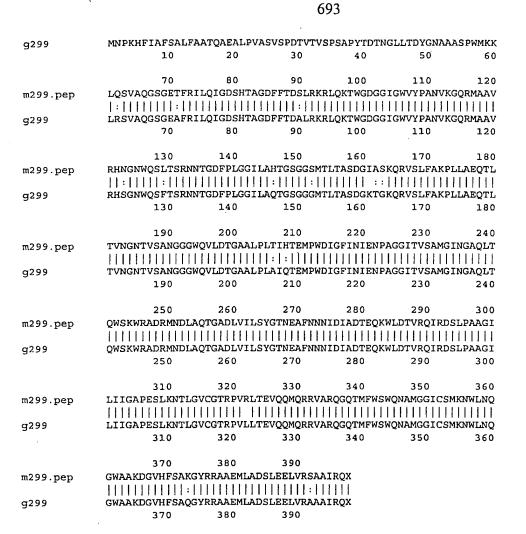
351 GGCGGCCGTC CGTCACAGCG GCAACTGGCA AAGCTTCACC AGCAGGAACA

401 ATACCGGAGA TTTCCCGCTC GGCGGCATCC TCGCCCAAAC CGGCAGCGGC

451 GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCCGCCA AACAGCGCGT
```

```
501 TTCCCTGTTT GCCAAACCGC TGCTCGCCGA ACAAACCCTG ACCGTCAACG
      551 GCAACACCGT CTCCGCCAAC GGCGGCGGCT GGCAGGTACT GGATACGGGC
     601 GCGGCACTGC CCCTGGCCAT ACAGACCGAA ATGCCGTGGG ACATCGGCTT
     651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
          TCAACGGCGC ACAATTGACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
     751 AACGACCTTG CCCAAACCGG CGCCGATTTG GTTATCCTTT CCTACGGCAC
     801 CAACGAAGCC TTCAACAACA ACATCGACAT TGCCGATACC GAACAAAAAT
     851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCCGC CGCCGGCATC
     901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
     951 CACGCGCCCC GTCCTCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCG
    1001 CCCGTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC AATGGGCGGC
    1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCCG CCAAAGACGG
    1101 CGTACACTTC TCCGCCCAAG GCTACCGGCG CGCGGCGGAA ATGCTTGCCG
    1151 ACAGCCTCGA AGAACTCGTC CGCGCCGCCG CAATCAGGCA ATAA
This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:
          MNPKHFIAFS ALFAATQAEA LPVASVSPDT VTVSPSAPYT DTNGLLTDYG
       1
          NAAASPWMKK LRSVAQGSGE AFRILQIGDS HTAGDFFTDA LRKRLQKTWG
      51
     101 DGGIGWVYPA NVKGQRMAAV RHSGNWQSFT SRNNTGDFPL GGILAQTGSG
     151 GGMTLTASDG KTGKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
     201 AALPLAIQTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
     251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRO IRDSLPAAGI
     301 LIIGAPESLK NTLGVCGTRP VLLTEVQQMQ RRVARQGQTM FWSWQNAMGG
          ICSMKNWLNQ GWAAKDGVHF SAQGYRRAAE MLADSLEELV RAAAIRO*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1249>:
m299.seq
         ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCG CCGCCACGCA
       1
          GGCAGAAGCC CTACCTGTCG CCTCCGTCAG CCTCGACACC GTTACCGTTT
      51
     101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
     151 AACGCCTCCG CCTCGCCTTG GATGAAAAA CTCCAATCCG TCGCACAAGG
     201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG
     251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTGCAAAA AACTTGGGGC
          GACGGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
         GGCGGCCGTC CGGCACAACG GTAACTGGCA AAGCCTCACC AGCAGGAACA
     401 ACACCGGAGA CTTCCCGCTC GGCGGCATCC TCGCCCACAC CGGCAGCGGC
         GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
     501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCCTG ACCGTCAACG
     551
         GCAACACCGT CTCCGCCAAC GGCGGCGGCT GGCAGGTACT GGATACGGGC
         GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
     651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
     701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
     751 AACGACCTCG CCCAAACCGG CGCCGATTTG GTTATCCTTT CCTACGGCAC
     801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGACACC GAACAAAAT
     851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCTGC CGCCGGCATC
         CTCATCATCG GCGCACCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
    951 CACACGCCCC GTCCGCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCG
    1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC CATGGGCGGC
    1051 ATATGCAGCA TGAAAAACTG GCTCAACCAA GGATGGGCCG CCAAAGACGG
    1101 CGTACACTTC TCCGCCAAAG GCTACCGGCG CGCGGCGGAA ATGCTCGCCG
    1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA
This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:
m299.pep
         MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
         NASASPWMKK LQSVAQGSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
     51
    101 DGGIGWVYPA NVKGQRMAAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
    151 GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
    201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
    251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRO IRDSLPAAGI
    301 LIIGAPESLK NTLGVCGTRP VRLTEVQQMQ RRVARQGQTM FWSWQNAMGG
    351 ICSMKNWLNQ GWAAKDGVHF SAKGYRRAAE MLADSLEELV RSAAIRQ*
m299/g299
           95.5% identity in 397 aa overlap
                    10
                              20
                                                 40
                                                           50
            MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDTNGLLTDYGNASASPWMKK
m299.pep
```

WO 99/57280 PC



The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1251>:

a299.seq ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCG CCGCCACGCA GGCAGAAGCC CTACCTGTCG CCTCAGTCAG CCTCGACACC GTTACCGTTT 51 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC 101 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAGG 151 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG 201 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAAA AACTTGGGGC 251 GACGGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT 301 351 GGCGGCCGTC CGGCACAACG GTAACTGGCA AAGCCTCACC AGCAGGAACA ACACCGGAGA CTTCCCGCTC GGCGGCATCC TCGCCCACAC CGGCAGCGGC 401 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT 451 501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCCTG ACCGTCAACG GCAACACCGT CTCCGCCAAC GGCGGCGGCT GGCAGGTACT GGATACGGGC 551 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT 601 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA 651 TCAACGCCC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG 701 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC 751 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT 801 851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCCGGCATC 901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG 951 CACACGCCCC GTCCGCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG 1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC GTTTGCAGCA TGAAAAACTG GCTCAACCAC GGATGGGCCG CCAAAGACGG 1051 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG 1101 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA 1151

WO 99/57280

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

a299.pep MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG NASASPWMKK LQSVAQGSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG DGGIGWVYPA NVKGQRMAAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWOVLDTG AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI LIIGAPESLK NTLGVCGTRP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG VCSMKNWLNH GWAAKDGVHF SAKGYQRSAE MLADSLEELV RSAAIRQ* m299/a299 98.0% identity in 397 aa overlap MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDTNGLLTDYGNASASPWMKK m299.pep a299 MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDTNGLLTDYGNASASPWMKK m299.pep LQSVAQGSGETFRILQIGDSHTAGDFFTDSLRKRLQKTWGDGGIGWVYPANVKGORMAAV a299 LQSVAQGSGETFRILQIGDSHTAGDFFTDSLRKRLQKTWGDGGIGWVYPANVKGORMAAV RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL m299.pep RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKORVSLFAKPLLAEOTL a299 TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT m299.pep a299 TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAOLT QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVROIRDSLPAAGI m299.pep QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTEQKWLDTVRQIRDSLPAAGI a299 LIIGAPESLKNTLGVCGTRPVRLTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNO m299.pep LIIGAPESLKNTLGVCGTRPVRLTEVOOMORRIAROGOTMFWSWONAMGGVCSMKNWLNH a299 m299.pep GWAAKDGVHFSAKGYRRAAEMLADSLEELVRSAAIROX a299 GWAAKDGVHFSAKGYQRSAEMLADSLEELVRSAAIRQX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1253>: 9302.sea

. seq					
1	ATGCACTCAA	TATATTTTTT	TAAGGAGAAG	CAGATGAGTC	AAACCGACGC
51	GCGTCGTAGC	GGACGATTTT	TACGCACAGT	CGAATGGCTG	GGCAATATGT
101	TGCCGCACCC	GGTTACGCTT	TTTATTATTT	TCATTGTGTT	ATTGCTGATT
151	GCCTCTGCCG	TCGGTGCGTA	TTTCGGACTA	TCCGTCCCCG	ATCCGCGTCC
201	TGTTGGGGCG	AAAGGACGTG	CCGATGACGG	TTTGATTCAC	GTTGTCAGCC
251	TGCTCGATGC	CGACGGTTTG	ATCAAAATCC	TGACGCATAC	CGTTAAAAAT
301	TTCACCGGTT	TCGCGCCGTT	GGGAACGGTG	TTGGTTTCTT	TATTGGGCGT

WO 99/57280 PCT/US99/09346

```
GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAATG CGCTTATTGC
          TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
          ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
          GTCCGCCGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
         CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
         GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
     651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTTTATGG
     701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
     751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
     801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
     851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
     901 AGCATCGTCC CTGCCGACGG TATTTTGCGT CATCCTGAAA CAGGATTGGT
     951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTTGTTGT
    1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
    1051 GAACGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
    1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTTTAATT
    1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
    1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTTA TTTTAATTTG
    1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
    1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
    1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
    1401 GCCGATGATG AGTTATTTCG GGCTGATTAT GGCGACGGTA ATCAAATACA
    1451 AAAAAGATGC GGGCGTAGGC ACGCTGATTT CTATGATGTT GCCGTATTCC
    1501 GCTTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATTT GGGTATTTGT
    1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:
g302.pep
         MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
         ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
         FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFTG
     151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
     201 GTIDPLLAGI TQQAAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
         IVEPOLGPYO SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
          SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
          EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGAVFLK
     401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPQ
     451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
     501 AFFLIAWIAL FCIWVFVLGL PVGPGTPTFY PVP*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1255>:
m302.seq
         ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
       1
         GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
         TGCCGCATCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
         GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
         TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
         TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
         TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
         GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAATG CGCTTATTGC
         TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
     451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
     501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
     551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
     601 AGCACATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCGT
     651 AGGCCCTGAA GCCAACTGGT TTTTTATGGT AGCCAGTACG TTTGTGATTG
     701 CTTTGATTGG TTATTTTGTT ACTGAAAAAA TCGTCGAACC GCAATTGGGC
         CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCATTCCAA
     801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
     851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGGA GCATCGTCCC TGCCGACGGT
     901 ATTTTGCGTC ATCCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTTTAAA
     951 ATCGATTGTT GTTTTTATTT TCTTGTTGTT TGCACTGyCG GGCmTTGTTT
```

1001 ATGGMCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

PCT/US99/09346 WO 99/57280

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696
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```
1051 ATGGCCGAAT CGATGAGTAC TCTGGSGCTT TmTTTGswCA kcATCTTTTT
    1101 TGCCGCACAG TTTGTCGCAT TTTTTAATTG GACGAATATT GGGCAATATA
    1151 TTGCCGTTAA AGGGGCGACG TTCTTAAAAG AAGTCGGCTT GGGCGGCAGC
    1201 GTGTTGTTTA TCGGTTTTAT TTTAATTTGT GCTTTTATCA ATCTGATGAT
    1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TGCGCCGATT TTCGTCCCTA
    1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
    1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCGG
    1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GGCGTGGGTA
    1451 CGCTGATTTC TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
    1501 ATTGCCTTAT TCTGCATTTG GGTATTTGTT TTGGGCCTGC CCGTCGGTCC
    1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A
This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:
m302.pep
      1 MHSIYFFKEK QMSQTDTQRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
         ASAVGAYFGL SVPDPRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
      51
     101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFTG
     151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
     201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPQLG
```

251 PYOSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFVALSAL LAWSIVPADG 301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA

351 MAESMSTLXL XLXXIFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS 401 VLFIGFILIC AFINLMIGSA SAQWAVTAPI FVPMLMLAGY APEVIQAAYR

451 IGDSVTNIIT PMMSYFGLIM ATVIKYKKDA GVGTLISMML PYSAFFLIAW

501 IALFCIWVFV LGLPVGPGAP TFYPAP*

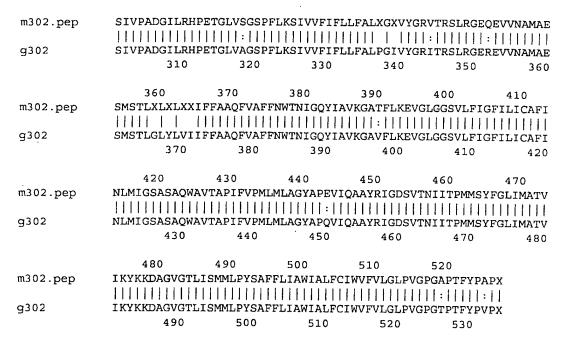
Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from N. gonorrhoeae:

m302/q302

m302.pep g302	10 MHSIYFFKEKQMS MHSIYFFKEKQMS				111111111111111111111111111111111111111	
m302.pep g302	70 SVPDPRPVGAKGF SVPDPRPVGAKGF 70	1111111::111	: :		1111111111	111111
m302.pep g302	130 EKSGLISALMRLI EKSGLISALMRLI 130			111111111111111111111111111111111111111	11111111111	
m302.pep g302	190 AGLAAAFAGVSGO AGLAAAFAGVSGO 190					:
m302.pep g302	240 ALIGYFVTEKIVE ALIGYFVTEKIVE 250 300		ійнини		111111111	



The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1257>:

```
ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
   1
      GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
  51
      TGCCGCACCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
 101
      GCCTCTGCCG CCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
 151
      TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTCAC GTTGTCAGCC
 201
      TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
 251
 301
      TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
 351
      GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAATG CGCTTATTGC
      TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
 401
      ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
 451
 501
      GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
      CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
 551
      GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
 601
      CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTTTATGG
 651
      TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
.701
      ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
 751
      AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
 801
 851
      TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
      AGCATCGTCC CTGCCGACGG TATTTTGCGT CATCCTGAAA CAGGATTGGT
 901
      TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTTGT
 951
      TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1001
      GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1051
      TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTTTAATT
1101
      GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1151
      GAAGTCGGCT TGGGCGGCAG CGTGTTGTTT ATCGGTTTTA TTTTAATTTG
1201
1251
      TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301
      CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCGAA
1351
     GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401
     GCCGATGATG AGTTATTTCG GGCTGATTAT GGCGACGGTG ATCAAATACA
     AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
      GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTTGT
1501
      TTTGGGCCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1551
1601
```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

a302.pep

- 1 MHSIYFFKEK QMSQTDTQRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI 51 ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
- 101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFTG

151 201 251 301 351 401 451 501	ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL GTIDPLLAGI TQQAQQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS AFFLIAWIAL FCIWVFVLGL PVGPGAPTFY PAP*
m302/a302 96	.1% identity in 533 aa overlap
m302.pep	MHSIYFFKEKQMSQTDTQRDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL
a302	
m302.pep	70 80 90 100 110 120 SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGIA
a302	
	130 140 150 160 170 180
m302.pep	EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL
a302	EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL 130 140 150 160 170 180
200	190 200 210 220 230
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAAVVGPEANWFFMVASTFVI
a302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAAQIIHPDYVVGPEANWFFMVASTFVI 190 200 210 220 230 240
m302.pep	240 250 260 270 280 290 ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW
a302	
	300 310 320 330 340 350
m302.pep	SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
a302	SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE 310 320 330 340 350 360
m302.pep	360 370 380 390 400 410 SMSTLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI
a302	
4502	370 380 390 400 410 420
m302.pep	420 430 440 450 460 470 NLMIGSASAQWAVTAPIFVPMLMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
a302	
	480 490 500 510 520
m302.pep	IKYKKDAGVGTLISMMLPYSAFFLIAWIALFCIWVFVLGLPVGPGAPTFYPAPX
a302	IKYKKDAGVGTLISMMLPYSAFFLIAWIALFCIWVFVLGLPVGPGAPTFYPAPX 490 500 510 520 530

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1259>:

MHSIYFFKEKQMSQTDTQRDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL	151 201 251 301 351 401 451 501	ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL GTIDPLLAGI TQQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS AFFLIAWIAL FCIWVFVLGL PVGPGAPTFY PAP*
MHSIYFFKEKQMSQTDTQRDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL	m302/a302 96	•
MHSIYFFKEKQMSQTDTORDGRFLRTVEWLGNMLPHPVILFIIFIVLLLIASAAGAYFGL	m302.pep	MHSIYFFKEKQMSQTDTQRDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL
M302.pep SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGTA		
M302.pep SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGTA		70 80 90 100 110 120
SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA	m302.pep	SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGIA
M302.pep	a302	SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA
### ##################################		
130	m302.pep	
m302.pep AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAAVVGPEANWFFMVASTFVI a302 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	a302	
m302.pep AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAAVVGPEANWFFMVASTFVI a302 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		190 200 210 220 230
AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAAQIIHPDYVVGPEANWFFMVASTFVI 190 200 210 220 230 240 240 250 260 270 280 290 M302.pep ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW	m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAAVVGPEANWFFMVASTFVI
m302.pep ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW 1 1 1 1 1 1 1 1 1 1	a302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAAQIIHPDYVVGPEANWFFMVASTFVI
### a302 ####################################	222	250
300 310 320 330 340 350 m302.pep SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE		
m302.pep SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE a302 SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE 310 320 330 340 350 360 m302.pep 360 370 380 390 400 410 m302.pep SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI	a302	A A A A A A A A A A A A A A A A A A A
m302.pep SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE		300 310 320 330 340 350
a302 SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE 310 320 330 340 350 360 360 370 380 390 400 410 m302.pep SMSTLXLXXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI	m302.pep	SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
360 370 380 390 400 410 m302.pep SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI	a302	SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE
m302.pep SMSTLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI		300
a302 SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI 370 380 390 400 410 420	m302.pep	SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI
370 380 390 400 410 420	a302	
		000
420 430 440 450 460 470 m302.pep NLMIGSASAQWAVTAPIFVPMLMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV	m302 nen	
a302 NLMIGSASAQWAVTAPIFVPMLMLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV 430 440 450 460 470 480	a302	400 440 480
480 490 500 510 520		
m302.pep IKYKKDAGVGTLISMMLPYSAFFLIAWIALFCIWVFVLGLPVGPGAPTFYPAPX	m302.pep	<pre>IKYKKDAGVGTLISMMLPYSAFFLIAWIALFCIWVFVLGLPVGPGAPTFYPAPX </pre>
a302 IKYKKDAGVGTLISMMLPYSAFFLIAWIALFCIWVFVLGLPVGPGAPTFYPAPX 490 500 510 520 530	a302	IKYKKDAGVGTLISMMLPYSAFFLIAWIALFCIWVFVLGLPVGPGAPTFYPAPX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1259>:

```
g305.seq
          ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
         TTTTACCGAA TTTTTACCGA TTTCCAGCAC CGGACATTTG ATTGTGTTCG
          GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
     151
          CAGCTCGGTG CGGTTTTGGC GGTAGTGTTT GAATACCGGC AGCGTTTCAG
          CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
     251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
     301 GACAAACAAA TCAAAGAGTA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
     351 GCTGGTTTTG GGCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
     401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCG
     451 TTGATGATCG GTGTTGCCCA AGTGTTTGCA CTGGTTCCGG GTACGTCCCG
     501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
     551 CGGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTTGCAGCA
     601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
     651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTTCC GGTTTGGTAG
     701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAAACTA TATCCCGTTT
     751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
     801 GGGCTGGATA AGTTGGGAAT GA
This corresponds to the amino acid sequence <SEO ID 1260; ORF 305.ng>:
g305.pep
          MDFLIVLKAL MMGLVEGFTE FLPISSTGHL IVFGNLIGFH SNHKVFEIAI
          QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAIAF IPAAVMGLLF
      51
     101 DKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAEPKIA DVDALRPIDA
          LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
          TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
          AYYRIVFGIV IIILWLSGWI SWE*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1261>:
m305.seq
           (partial)
          Atggattttc tgattgtcct gaaagccctg atgatgggct tggtagaagg
          TTTTACCGAA TTTTTACCGA TTTCCAGCAC CGGACATTTG ATTGTGTTCG
      51
     101
          GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
     151 CAGCTCGGTG CAGTTTTGGC GGTAGTGTTT GAATACCGGC AACGTTTCAG
     201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
          TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
     301 GGCAWACAAA TCAAAGAGYA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
     351 GCTGGTTYTG GrCGGTTTTT YTATTTTGTG GGTGGAGAAA CGCCAAAGCC
     401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
     451 TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCCGG GTACGTCCCG
     501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
     551 CTGCGACAGA ATTCTCGTTT TTCTTGGCTG TGCCGATGAT GGTTGCCGCA
     601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
     651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTTCA GGCTTGGTAG
     701 CGGTAAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...
This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:
m305.pep
           (partial)
       1 MDFLIVLKAL MMGLVEGFTE FLPISSTGHL IVFGNLIGFH SNHKVFEIAI
      51 QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLAIAF IPAAVMGLLF
     101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAEPKIA DVDALRPIDA
         LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
     151
         TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng)
from N. gonorrhoeae:
g305/m305
                     10
                               20
                                        30
            {\tt MDFLIVLKALMMGLVEGFTEFLPISSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF}
g305.pep
             m305
            MDFLIVLKALMMGLVEGFTEFLPISSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
                    10
                              20
                                        30
                                                  40
                                                            50
```

	70 80 90 100 110 120
g305.pep	EYRQRFSNVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL
J	
m305	EYRQRFSNVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL
	70 80 90 100 110 120
	130 140 150 160 170 180
g305.pep	GGFFILWVEKRQSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTVMGGMLWGI
m305	XGFXILWVEKRQSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI
	130 140 150 160 170 180
	190 200 210 220 230 240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR
	190 200 210 220 230 240
	250 260 270
	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX
m305	FVSG
The following	partial DNA sequence was identified in N. meningitidis <seq 1263="" id="">:</seq>
a305.seq	
1	ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51	
101	GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151	
201	
251	
301	
351	GCTGGTTTTG GGCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401	GAGCAGAGCC TAAAATTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451	TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCCAG GTACGTCCCG
501	TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551	CGGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTTGCAGCA
601	ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651	CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTTCA GGCTTGGTGG
701	CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 801	GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
601	AGGCTGGATA AGTTGGGAAT GA
This correspond	ds to the amino acid sequence <seq 1264;="" 305.a="" id="" orf="">:</seq>
	as to the annuo acid sequence SEQ ID 1204; ORF 303.a>:
a305.pep	MDELTULVAL MACLUROTURE DI DECORROLE TURON TORIN
1 51	MDFLIVLKAL MMGLVEGFTE FLPISSTGHL IVFGNLIDFH SNHKVFEITI
101	QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAIAF IPAAVMGLLF
151	GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAEPKIV DVDALRPIDA LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201	TAYDVLKHYR FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251	AYYRIVFGIA IIILWLSGWI SWE*
202	THE TAXABLE OF TAXABLE OF THE TAXABLE OF T
m305/a305 96	5.3% identity in 243 aa overlap
1112 02/ u 202 7(10 00 20 10
m305.pep	10 20 30 40 50 60
mooo.pep	MDFLIVLKALMMGLVEGFTEFLPISSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
a305	
4505	10 00 00 10
	10 20 30 40 50 60
	70 80 90 100 110 120
m305.pep	EYRQRFSNVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL
a305	EYRQRFSNVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL
	STUBIBLUE BOANAMINATI

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRQS	RAEPKIADVDA	LRPIDALMIC	SVAQVFALVPG	TSRSGSTIM	GGMLWGI
	11 1111111				11111111	
a305	GGFFILWVEKRQS			SVAQVFALVPG	TSRSGSTIM	GMLWGI
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAV	/PMMVAATAYE	VLKHYRFFTI	HDVGLILIGF	'IAAFVSGLVA	AVKALLR
			1111111111	1111111111	: 11111111	
a305	ERKTATEFSFFLAV	/PMMVAATAYD	VLKHYRFFTI	HDVGLILIGF	VAAFVSGLVA	AVKALLR
	190	200	210	220	230	240
m305.pep	FVSG					
mooo.pop	111	*				
a305	FVSKKNYIPFAYYE	RIVEGIATIII	WLSGWISWEX	•		
	250	260	270	•		
	200	_ 30	0			
	*					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1265>:

```
ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTCTT
 51
    CTTCGGTTTG ATACTGGCAA CGGTCATTAT TGCCGGTATT TTGCTTTATC
101 TGAACCAGGG CGGTCAAAAT GCGTTCAAAA TCCCGGCTCC GTCGAAGCAG
151 CCTGCAGAAA CGGAAATCCT GAAACTGAAA AACCAGCCTA AGGAAGACAT
201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGTTGCGA
251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
301 GCCGACAAAG CCGACGAGGT TGAAGAAAAG GCGGGCGAGC CGGAACGGGA
351 AGAGCCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACT GAAGAGCGTG
401 AACAAACCGT CAGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
    AAAAAAGCGG TAAAACCGTC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA
    AGAGAAAAG GCGGCGAAAG AAAAAGTTGC ACCCAAACCG ACCCCGGAAC
    AAATCCTCAA CAGCCGCAGT ATCGAAAAAG CGCGTAGTGC CGCTGCCAAA
    GAAGTGCAGA AAATGAAAAA CTTTGGGCAA GGCGGAAGCC AACGCATTAT
    CTGCAAATGG GCGCGTATGC CGAACCCCGG AGCGCGGAAG GGCAGCGTGC
    CAAACTGGCA ATCTTGGGCA TATCTTCCGA AGTGGTCGGC TATCAGGCGG
701
751
    GACATAAAAC GCTTTACCGC GTGCAAAGCG GCAATATGTC CGCCGATGCG
801
    GTGA
```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```
1 MFMNKFSQSG KGLSGFFFGL ILATVIIAGI LLYLNQGGQN AFKIPAPSKQ
```

- 51 PAETEILKLK NQPKEDIQPE PADQNALSEP DVAKEAEQSD AEKAADKQPV
- 101 ADKADEVEEK AGEPEREEPD GQAVRKKALT EEREQTVREK AQKKDAETVK
- 151 KKAVKPSKET EKKASKEEKK AAKEKVAPKP TPEQILNSRS IEKARSAAAK
- 201 EVQKMKNFGQ GGSQRIICKW ARMPNPGARK GSVPNWQSWA YLPKWSAIRR
- 251 DIKRFTACKA AICPPMR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```
..GGTTTGTTCT TCGGTTTGAT ACTGGCGACG GTCATTATTG CCGGTATTTT
 1
       GTTTTATCTG AACCAGAGCG GTCAAAATGC GTTCAAAATC CCGGCTTCGT
 51
101
       CGAAGCAGCC TGCAGAAACG GAAATCCTGA AACCGMAWAA CCAGCVTAAG
       GAAGACATCC AACCTGAWCC GGCCGATCAA AACGCCTTGT CCGAACCGGA
151
       TGCTGCGACA GAGGCAGAGC AGTCGGATGC GGAAAAWGCT GCCGACAAGC
201
251
       AGCCCGTTGC CGATAAAGCC GACGAGGTTG AAGAAAAGGC GGGCGAGCCG
       GAACGGGAAG AGCCGGACGG ACAGGCAGTG CGTAAGAAAG CGCTGACGGA
301
351
       AGAGCGTGAA CAAACCGTCA GGGAAAAAGC GCAGAAGAAA GATGCCGAAA
       CGGTTAAAAW ACAAGCGGTA AAACCGTCTA AAGAAACAGA GAAAAAAGCT
401
       TCAAAAGAAG AGAAAAAGGC GGCGAAGGAA AAAGTTGCAC CCAAACCAAC
451
501
       CCCGGAACAA ATCCTCAACA GCGGCAGCAT CGAAAAAGCG CGCAGTGCCG
       CCGCCAAAGA AGTGCAGAAA ATGAAAACGC CGACAAGGCG GAAGCAACGC
551
```

```
ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
                CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
          651
                GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
          701
          751
                ATGCGGTGA
This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:
     m306.pep
               (partial)
               ..GLFFGLILAT VIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPXNQXK
            1
                EDIQPXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
           51
                EREEPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
          101
                SKEEKKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
          151
                IICKWARMPT VRARKGSVPN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
          201
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 306 shows 88.9% identity over a 253 as overlap with a predicted ORF (ORF 306.ng)
from N. gonorrhoeae:
     m306/q306
                                      10
                                               20
                                                        30
     m306.pep
                              GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
                              9306
                 MFMNKFSQSGKGLSGFFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK
                         10
                                  20
                                           30
                                                    40
                                                              50
                                                                       60
                            60
                                      70
                                               80
                                                        90
                                                                 100
                 {\tt NOXKEDIQPXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEPD}
     m306.pep
                 g306
                 NQPKEDIQPEPADQNALSEPDVAKEAEQSDAEKAADKQPVADKADEVEEKAGEPEREEPD
                        70
                                  80
                                           90
                                                   100
                  110
                           120
                                     130
                                              140
                                                       150
                                                                160
     m306.pep
                 GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
                 GQAVRKKALTEEREQTVREKAQKKDAETVKKKAVKPSKETEKKASKEEKKAAKEKVAPKP
     g306
                       130
                                 140
                                          150
                                                   160
                                                            170
                  170
                           180
                                    190
                                              200
                                                        210
                 TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSVPNWQSWA
     m306.pep
                 g306
                 TPEQILNSRSIEKARSAAAKEVQKMKNFGQGGSQRIICKWARMPNPGARKGSVPNWQSWA
                       190
                                 200
                                          210
                                                   220
                                                            230
                  230
                            240
                                     250
                 YLPRWSVIRRDIKRFTGCKAAICLPMRX
     m306.pep
                 YLPKWSAIRRDIKRFTACKAAICPPMRX
    q306
                       250
                                260
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1269>:
    a306.seq
             ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT
             CTTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC
             TGAACCAGAG CGGTCAAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
         101
         151
             CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
             CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
         201
         251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
             GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA
         301
             AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG
         351
         401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
         451 AAACAAGCGG TAAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA
```

501 AGAGAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCCGGAAC 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

```
601
              GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
         651
              CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
              ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTCGGTTAT CAGGCGGGAC
              ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
         751
         801
This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:
     a306.pep
              MFMNKFSQSG KGLSGFFFGL ILATVIIAGI LFYLNOSGON AFKIPVPSKO
          51
              PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
         101
              ADKADEVEEK ADEPEREKSD GQAVRKKALT EEREQTVGEK AQKKDAETVK
              KQAVKPSKET EKKASKEEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
              EVOKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
         201
              IKRFTGCKAA ICLPMR*
          93.7% identity in 252 aa overlap
m306/a306
                                    10
                                             20
                                                      30
                                                               40
     m306.pep
                             GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
                             a306
                MFMNKFSQSGKGLSGFFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                        10
                                20
                                         30
                                                  40
                                                           50
                                    70
                                             80
                                                      90
                                                              100
                NQXKEDIQPXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEPD
     m306.pep
                NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
     a306
                       70
                                80
                                         90
                                                 100
                                                          110
                                                                   120
                 110
                          120
                                   130
                                            140
                                                     150
                                                              160
                GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
     m306.pep
                GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAEKEKVAPKP
     a306
                      130
                               140
                                        150
                                                 160
                                                          170
                                                                   180
                 170
                          180
                                   190
                                            200
                                                     210
                                                             220
                TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
    m306.pep
                TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
     a306
                      190
                               200
                                        210
                                                 220
                                                          230
                 230
                          240
    m306.pep
                LPRWSVIRRDIKRFTGCKAAICLPMRX
                a306
                LPRWSVIRRDIKRFTGCKAAICLPMRX
                      250
                               260
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1271>:
    q307.seq
```

```
atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
  1
 51
     cgcagcctgc ggcggtcaaa aagacagcgc gcccgcagcc tctgccgccq
101
     ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
     accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
151
     ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtqc
201
    gcccgaatct ggcattggcg gagggcgagt tggacatcaa cgtcttccaa
     cacaaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
     cgaagcette caagtgeega cegegeettt gggaetgtat cegggeaaac
     tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
     gacccgtcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
451
501
     gatcaaactc aaagacggca tcaatccgct gaccqcatcc aaagccqaca
     tcgcggaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
551
     ctgccgcgca gccgccga cgtggatttt gccgtcgtca acggcaacta
601
     cgccataagc agcggcatga agctgaccga agccctgttc caagagccga
```

```
701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaaqacagc
               caatggctta aagacgtaac cgaggcctat aactccgacg cgttcaaagc
           801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
           851
               aaggcgcagc caaataa
This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:
      g307.pep
                MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSADNG AAKKEIVFGT
            51
                TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFO
           101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLKSLEEV KDGSTVSAPN
           151 DPSNFARALV MLNELGWIKL KDGINPLTAS KADIAENLKN IKIVELEAAQ
           201 LPRSRADVDF AVVNGNYAIS SGMKLTEALF QEPSFAYVNW SAVKTADKDS
               QWLKDVTEAY NSDAFKAYAH KRFEGYKYPA AWNEGAAK*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1273>:
      m307.seg
                (partial)
                ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
                  CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCCTGCC GCATGGAATG
            51
           101
                  AAGGCGCAGC CAAATAA
This corresponds to the amino acid sequence <SEO ID 1274; ORF 307>:
               (partial)
     m307.pep
                ...QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA AWNEGAAK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng)
from N. gonorrhoeae:
     m307/g307
                                                        10
                                                                            30
     m307.pep
                                                QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                                SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKYPA
     g307
                         230
                                   240
                                             250
                                                       260
                                                                           280
                         39
     m307.pep
                  AWNEGAAKX
                  q307
                  AWNEGAAKX
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1275>:
     a307.seq
            1
               ATGAAAACCT TCTTCAAAAC CCTTTCCGCC GCCGCACTCG CGCTCATCCT
           51 CGCCGCCTGC GGCGGTCAAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG
          101
               CCGCCGCCGA CAACGGCGCG GCGAAAAAAG NAATCGTCTT CGGCACGACC
               GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
          151
          201
               GAAAAAAGGC TACACCGTCA AACTGGTCGA GTTTACCGAC TATGTGCGCC
               CGAATCTGGC ATTGGCTGAG GGCGAGTNGG ACATCAACGT CTTCCAACAC
          251
               AAACCCTATC TTGACGACTT CAAAAAAGAA CACAATCTGG ACATCACCGA
          301
              AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCCG GGCAAGCTGA
          351
          401 AATCGCTGGA AGAAGTCAAA GACGGCAGCA CCGTATCCGC GCCCAACGAC
          451 CCGTCCAACT TCGCCCGCGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT
          501 CAAACTCAAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG
          551 CCGAAAACCT GAAAAACATC AAAATCGTCG AGCTTGAAGC CGCGCAACTG
          601 CCGCGTAGCC GCGCCGACGT GGATTTTGNC GTCGTCAACG GCAANTACGC
          651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
          701 TTGCCTATGT CAACTGGTCT GCCGTCAAAA CCGCCGACAA AGACAGCCAA
          751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
          801 CGCGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGGAATGAAG
          851 GCGCAGCCAA ATAA
This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:
     a307.pep
```

MKTFFKTLSA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVFGTT

```
51 VGDFGDMVKE QIQPELEKKG YTVKLVEFTD YVRPNLALAE GEXDINVFOH
                KPYLDDFKKE HNLDITEVFQ VPTAPLGLYP GKLKSLEEVK DGSTVSAPND
                PSNFARVLVM LDELGWIKLK XGINPLTASK ADIAENLKNI KIVELEAAQL
                PRSRADVDFX VVNGXYAISS GMKLTEALFQ EPSFAYVNWS AVKTADKDSO
           251
                WLKDVTEAYN SDAFKAYAHK RFEGYKSPAA WNEGAAK*
m307/a307 100.0% identity in 38 aa overlap
      m307.pep
                                                 QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                                 {\tt SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA}
      a307
                           230
                                     240
                                              250
                                                        260
                                                                   270
                          39
                  AWNEGAAKX
      m307.pep
                   11111111
      a307
                  AWNEGAAKX
                280
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1277>:
     g308.seq
               ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
               TCCGTGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
               TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
          101
          151
               GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAACT
               TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
               AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
          251
               TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
          301
          351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCCTGT TCGATGCGGA
          401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
          451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
          501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
               TGGGCGGCGT GGTGTTTCCC CCTGTTCCTG CGATGTACCG CAAGCCGCAG
          601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
               CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA
This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:
     g308.pep
               MLNRVFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RRMMVRRLII
           51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
          101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
          151 ADVVLKERRR LVLMVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
          201 TADDIVAHSI AHTLSLFGID TPDLAEWOGM AD*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1279>:
     m308.seq
                (partial)
              ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
           51 TCCGCGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
          101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
          151
               GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAACT
               TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
              AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
              TTGGCGGACT TCGTGCATCC GATCGCCAAT ATCGGGGCGT GCATTGCCAG
          351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
          401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
          451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
          501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GWAACGGAAA
               TGGGCGGCGT GGTGTTTCCC CCTGTTCCTG CGATGTACCG CAAACCGCAG
              ACGGCGGACG ACATAGTGGC GCACAGTGTT GCACACGCLT TGTCGCTGTT
          651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCArGGAATG gcG...
This corresponds to the amino acid sequence <SEO ID 1280; ORF 308>:
     m308.pep
                (partial)
```

```
1 MLNRVFYRIL GVADNLYPRL SDFCFFTIIA GLPLQAVLWE RRMMVRRLII
              GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
           51
              LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
              ADVVLKERRR LVLMVRETPL NLAHLDNMKR XTEMGGVVFP PVPAMYRKPQ
              TADDIVAHSV AHALSLFGID TPDSAEWQGM A..
 Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng)
from N. gonorrhoeae:
     m308/g308
                        10
                                 20
                                          30
                                                   40
                                                            50
                                                                     60
                 MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLIIGISGASGFQY
     m308.pep
                 MLNRVFYRILGVADNLYPCLSDFCFFTIIAGLPLQAVLWERRMMVRRLIIGISGASGFQY
     g308
                                 20
                                          30
                                                   40
                                                            50
                        70
                                 80
                                          90
                                                  100
                                                           110
                                                                    120
                 GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF
     m308.pep
                 GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF
     g308
                        70
                                 80
                                          90
                                                  100
                                                           110
                                                                    120
                       130
                                140
                                         150
                                                  160
                                                           170
                                                                    180
                 {\tt KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR}
     m308.pep
                 KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
     q308
                       130
                                140
                                         150
                                                  160
                                                           170
                                                                    180
                       190
                                200
                                         210
                                                  220
                                                           230
     m308.pep
                XTEMGGVVFPPVPAMYRKPQTADDIVAHSVAHALSLFGIDTPDSAEWQGMA
                  g308
                VTEMGGVVFPPVPAMYRKPQTADDIVAHSIAHTLSLFGIDTPDLAEWQGMADX
                       190
                                200
                                         210
                                                  220
                                                           230
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1281>:
    a308.seq
               ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
            1
              TCCGTATTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
          51
         101
              TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
              GGCATCAGTG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGANCT
         151
              TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
         201
              AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
         251
              TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
         301
              CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
         351
              CGCTTGCCTC GGTCGTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
         401
         451
              GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
              AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
         501
         551
              TGGGCGGCGT GGTGTTTCCC CCTGTTCCTG CGATGTACCG CAAACCGCAG
              ACGGCGGACG ACATAGTGGC GCACAGTGTT GCACACGCTT TGTCGCTGTT
         601
              CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA
         651
This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:
    a308.pep
              MLNRIFYRIL GVADNLYPYL SDFCFFTIIA GLPLQAVLWE RRMMVRRLII
           1
              GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
          51
              LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVVH GFGDNLLTRA
         101
         151
              ADVVLKERRR LVLMVRETPL NLAHLDNMXR VTEMGGVVFP PVPAMYRKPQ
```

TADDIVAHSV AHALSLFGID TPDSAEWQGM AD*

```
m308/a308 95.7% identity in 231 aa overlap
```

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVAD	NLYPRLSDFO	FFTIIAGLP	LQAVLWERRMN	VRRLIIGIS	GASGFQY
	1111:111111111	1111 11111	111111111	11111111111	111111111	1111111
a308	MLNRIFYRILGVAD	NLYPYLSDFO	FFTIIAGLP	LQAVLWERRM	VRRLIIGIS	GASGFQY
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVE	THLVVSKGAE	MARASETAY	ARDEVYALADE	VHPIGNIGA	CIASGTF
	11111 111111:1	111111111	1111111		111111111	111111
a308	GVKALXLLRAQDIE	THLVVSKGAE	MARASETXY	ARDXVYALADX	VHPIGNIGA	CIASGTF
	70	80	90	100	110	120
	. 130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRT	LASVAHGFGD	NLLTRAADV	VLKERRRLVLM	VRETPLNLA	HLDNMKR
	[1111:1111		14 1 1 1 1 1 1 1 1 1 1 1 1 1	11111111	11111
a308	KTDGMLVAPCSMRT	LASVVHGFGD	NLLTRAADV	JLKERRRLVLM	VRETPLNLA	HLDNMXR
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPPVPA	MYRKPQTADD	IVAHSVAHAI	SLFGIDTPDS	AEWQGMA	
				[1] [[[[[[[[[[[[[[[[[[111111	
a308	VTEMGGVVFPPVPA	MYRKPQTADD	IVAHSVAHAI	LSLFGIDTPDS	AEWQGMADX	
	190	200	210	220	230	

The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 1283>:

```
1 ATGTTAAAȚC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
 51 TCCGTGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAACT
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCCTGT TCGATGCGGA
    CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551
    TGGGCGGCGT GGTGTTTCCC CCTGTTCCTG CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>: g308-1.pep

```
1 MLNRVFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RRMMVRRLII
51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
```

- 151 ADVVLKERRR LVLMVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
- 201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1285>: m308-1.seq

```
1 ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
 51 TCCGCGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAACT
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
    TGGGCGGCGT GGTGTTTCCC CCTGTTCCTG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTT GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

¹ MLNRVFYRIL GVADNLYPRL SDFCFFTIIA GLPLQAVLWE RRMMVRRLII

```
GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
     51
         LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
    101
         ADVVLKERRR LVLMVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPQ
    151
         TADDIVAHSV AHALSLFGID TPDSAEWQGM AD*
    201
                97.0% identity in 232 aa overlap
m308-1/g308-1
                   10
                            20
                                    30
                                             40
                                                      50
                                                               60
m308-1.pep
           MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLIIGISGASGFQY
            g308-1
           MLNRVFYRILGVADNLYPCLSDFCFFTIIAGLPLQAVLWERRMMVRRLIIGISGASGFQY
                  10
                           20
                                    30
                                             40
                   70
                           80
                                    90
                                            100
                                                     110
           GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF
m308-1.pep
            GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF
q308-1
                  70
                           80
                                    90
                                            100
                                                     110
                  130
                          140
                                   150
                                            160
                                                     170
                                                              180
m308-1.pep
           KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
            KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
g308-1
                 130
                          140
                                            160
                                                     170
                 190
                          200
                                   210
                                            220
           VTEMGGVVFPPVPAMYRKPQTADDIVAHSVAHALSLFGIDTPDSAEWQGMADX
m308-1.pep
           VTEMGGVVFPPVPAMYRKPQTADDIVAHSIAHTLSLFGIDTPDLAEWQGMADX
g308-1
                 190
                          200
                                   210
                                            220
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1287>:
a308-1.seq
      1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
        TCCGTATTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
        TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
    101
        GGCATCAGTG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGANCT
    151
    201
        TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
        AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
    251
        TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
    301
    351
        CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
        CGCTTGCCTC GGTCGTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
        GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
    451
        AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
        TGGGCGGCGT GGTGTTTCCC CCTGTTCCTG CGATGTACCG CAAACCGCAG
    551
        ACGGCGGACG ACATAGTGGC GCACAGTGTT GCACACGCTT TGTCGCTGTT
        CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA
This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:
a308-1.pep
      1 MLNRIFYRIL GVADNLYPYL SDFCFFTIIA GLPLQAVLWE RRMMVRRLII
        GISGASGFOY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
     51
    101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVVH GFGDNLLTRA
        ADVVLKERRR LVLMVRETPL NLAHLDNMXR VTEMGGVVFP PVPAMYRKPO
    151
        TADDIVAHSV AHALSLFGID TPDSAEWQGM AD*
    201
a308-1/m308-1
              96.1% identity in 232 aa overlap
                           20
                                    30
                                             40
a308-1
           MLNRIFYRILGVADNLYPYLSDFCFFTIIAGLPLQAVLWERRMMVRRLIIGISGASGFQY
           m308-1
           MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLIIGISGASGFQY
                  10
                           20
                                    30
                                             40
                                                     50
                                                              60
                  70
                           80
                                    90
                                            100
                                                    110
                                                             120
a308-1
           GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF
           m308 - 1
           GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF
                  70
                           80
                                    90
                                                    110
                                            100
                                                             120
                          140
                                   150
                                            160
           KTDGMLVAPCSMRTLASVVHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR
a308-1
```

```
KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
m308-1
                                            160
                                                     170
                           140
                                    150
                  190
                           200
                                    210
                                            220
                                                     230
           VTEMGGVVFPPVPAMYRKPQTADDIVAHSVAHALSLFGIDTPDSAEWQGMADX
a308-1
            VTEMGGVVFPPVPAMYRKPQTADDIVAHSVAHALSLFGIDTPDSAEWQGMADX
m308-1
                           200
                                    210
                                            220
                                                     230
                 190
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1289>:
     g311.seg
               atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
            1
               gctqtcqcct gttgcggcac ttgcgtgccg gcgcgctttg gggtgtttgq
           51
               gtttggaaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
               aaattgggcg gcattctgat tgaaacagtc agggcgggcg gtaaaacggt
          201
               tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
               acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
               qccqatqccq ccqtattgct ggaaacattg cttgcggaac tgggcgcqqt
          351
               gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
          401
               aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
               gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
          451
          501
               gcacttggaa acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
          551
              gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
              gaacgttttt tgctgttgga aggcgggaac agccggctca agtgggcgtg
          601
          651
              ggtggaaaac ggcacgttcg caaccgtggg cagcgcgccg taccgcgatt
          701
              tgtcgccttt gggcgcggag tgggcggaaa aggcggatgg aaatgtccgc
               atcqtcqqtt gcgccgtgtg cggagaatcc aaaaaggcac aagtqaaqqa
               acagetegee egaaaaateg agtggetgee gtetteegea eaggetttgg
          851
              gcatacqcaa ccactaccgc caccccgaag aacacggttc cgaccgttgq
          901
              ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
              cagttgcggc acggcggtaa cggttgacgc gctcaccgat gacggacatt
          951
              atctcqqcqq aaccatcatq cccqqcttcc acctgatgaa agaatcqctc
         1001
         1051
              gccqtccqaa ccqccaacct caaccqcccc gccgqcaaac gttacccttt
               cccqaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
         1151
               qcqctcqat aatqatqatq cacqqccqtt tqaaaqaaaa aaacqqcqcq
              ggcaagcctg tcgatgtcat cattaccggc ggcggcgcgg cgaaagtcgc
              cqaaqccctq ccgcctgcat ttttggcgga aaataccgtg cqcqtqqcqq
               acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
               gaatcggaac acgcttaa
This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:
     g311.pep
              MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
              KLGGILIETV RAGGKTVAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
               ADAAVLLETL LAELGAVLEQ YAEEGFAPFL NEYETANRDH GKAVLLLRDG
          101
          151
               ETVCEGTVKG VDGRGVLHLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
          201
              ERFLLLEGGN SRLKWAWVEN GTFATVGSAP YRDLSPLGAE WAEKADGNVR
              IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
          251
              FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
          351
              AVRTANLNRP AGKRYPFPTT TGNAVASGMM DAVCGSIMMM HGRLKEKNGA
              GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
          401
          451
              ESEHA*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1291>:
     m311.seq
              (partial)
              ATGTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
              GCTGTCGCCT GTTGCGGCAG TGGCGTGTCG GCGCGCCTTG TCGCGTTTAG
          101 GTTTGGATGT GCArATTAAG TGGCCCAATG ATTTGGTTGT CGGACGCGAC
              AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
          201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAN GAAGTAGAAA
          251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
          301 GCCGATGCCG CCGTGCTGCT nnnnnnnnn nnnnnnnnn nnnnGGAAAT
          351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CGTGnCGAAG CGGCGGGATT
```

CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGQCG

```
TGGGTGGAAA ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCGCGA
              TTTGTCGCCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
              GCATCGTCGG TTGCGCTGTG TGCGGAGAAT TCAAAAAGGC ACAAGTGCAG
              GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
         651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
         701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCGTC
         751 GTCGTCAGTT GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACGG
         801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTTCCACCTG ATGAAAGAAT
         851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
         901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
         951 GGTTTGCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
        1001 GGGCGGCAA GCCTGTCGAT GTCATCATTA CCGGCGGCGG CGCGCCAAAA
        1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTTG GCGGAAAATA CCGTGCGCGT
        1101 GGCGGACAAC CTCGTCATTT ACGGGTTGTT GAACATGATT GCCGCCGAAG
        1151
             GCAGGGAATA TGAACAT....
This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:
     m311.pep
               (partial)
             MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
          51 KLGGILIETV RTGGKTVAVV GIGINFVLPX EVENAASVQS LFQTASRRGN
         101 ADAAVLLXXX XXXXXEISLR SDXRPVSVXK RRDSERFLLL DGGNSRLKWA
         151 WVENGTFATV GSAPYRDLSP LGAEWAEKAD GNVRIVGCAV CGEFKKAQVO
         201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
         251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
         301 PFPTTTGNAV ASGMMDAVCG SVMMMHGRLK EKTGAGKPVD VIITGGGAAK
         351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AAEGREYEH....
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 311 shows 78.5% identity over a 455 as overlap with a predicted ORF (ORF 311.ng)
from N. gonorrhoeae:
    m311/g311
                                 20
                        10
                                          30
                                                   40
                                                            50
                MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV
    m311.pep
                g311
                MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETOIKWPNDLVVGRDKLGGILIETV
                        10
                                 20
                                          30
                                                   40
                                                            50
                        70
                                 80
                                          90
                                                  100
                                                           110
                RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADAAVLLXXX-----
    m311.pep
                RAGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADAAVLLETLLAELGAVLEO
    g311
                        70
                                80
                                          90
                                                  100
                   -----XXXX
    m311.pep
                YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
    q311
                      130
                               140
                                         150
                                                 160
                                                           170
                   120
                            130
                                     140
                                              150
                                                       160
    m311.pep
                XEISLRSDXRPVSVXKRRDSERFLLLDGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE
                 GEISLRPDNRSVSVPKRPDSERFLLLEGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE
    q311
                      190
                               200
                                         210
                                                  220
                                                           230
                                                                    240
                            190
                                     200
                                              210
                WAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
    m311.pep
                WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
    g311
```

250

260

270

280

```
250
                                        260
                                                  270
                                                           280
                                                                     290
                  WFNALGSRRFSRNACVVVSCGTAVTVDALTDDGHYLGGTIMPGFHLMKESLAVRTANLNR
     m311.pep
                  WFNALGSRRFSRNACVVVSCGTAVTVDALTDDGHYLGGTIMPGFHLMKESLAVRTANLNR
     q311
                300
                          310
                                   320
                                             330
                                                      340
                                                                350
                     300
                              310
                                        320
                                                 330
                                                           340
                                                                     350
                  HAGKRYPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKPVDVIITGGGAAKVAEA
     m311.pep
                   PAGKRYPFPTTTGNAVASGMMDAVCGSIMMMHGRLKEKNGAGKPVDVIITGGGAAKVAEA
     g311
                360
                          370
                                   380
                                             390
                                                      400
                                                                410
                     360
                              370
                                        380
                                                 389
                  LPPAFLAENTVRVADNLVIYGLLNMIAAEGREYEH
     m311.pep
                  LPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
     g311
                420
                         430
                                   440
                                            450
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1293>:
              ATGTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
            1
              GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
           51
          101
              GTTTGAAAAC GCAAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
          151
              AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGCG GCAAAACGGT
              TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCCAAG GAAGTGGAAA
              ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
          301
              GCCGATGCCG CCGTGTTGCT GGAAACGCTG TTGGCGGAAC TTGATGCGGT
              GTTGTTGCAA TATGCGCGGG ACGGATTTGC GCCTTTTGTG GCGGAATATC
          351
              AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
          401
          451
              GAAACCGTGT TCGAAGGCAC GGTTAAAGGC GTGGACGGAC AAGGCGTTCT
              GCACTTGGAA ACGGCAGAGG GCAAACAGAC GGTCGTCAGC GGCGAAATCA
         501
              GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAAGCG GCGGGATTCG
         551
          601
              GAACGTTTTC TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
          651
              GGTGGAAAAC GGCACGTTCG CAACCGTCGG TAGCGCGCCG TACCGCGATT
              TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
         701
         751
              ATCGTCGGTT GCGCCGTGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
              ACAGCTCGCC CGAAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
         801
         851
              GCATACGCAA CCACTACCGC CACCCCGAAG AACACGGTTC CGACCGCTGG
              TTCAACGCCT TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
         901
         951
              CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCGAT GACGGACATT
        1001
              ATCTCGGGGG AACCATCATG CCCGGTTTCC ACCTGATGAA AGAATCGCTC
         1051
              GCCGTCCGAA CCGCCAACCT CAACCGGCAC GCCGGTAAGC GTTATCCTTT
        1101
              CCCGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
              GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCGGGGCG
        1151
              GGCAAGCCTG TCGATGTCAT CATTACCGGC GGCGGCGCGG CAAAAGTTGC
        1201
              CGAAGCCCTG CCGCCTGCAT TTTTGGCGGA AAATACCGTG CGCGTGGCGG
        1251
             ACAACCTCGT CATTCACGGG CTGCTGAACC TGATTGCCGC CGAAGGCGGG
        1301
        1351
              GAATCGGAAC ATACTTAA
This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:
     a311.pep
              MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
           1
          51
              KLGGILIETV RTGGKTVAVV GIGINFVLPK EVENAASVQS LFOTASRRGN
         101
              ADAAVLLETL LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
              ETVFEGTVKG VDGQGVLHLE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
         151
              ERFLLLDGGN SRLKWAWVEN GTFATVGSAP YRDLSPLGAE WAEKVDGNVR
         201
         251
              IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
         301
              FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
              AVRTANLNRH AGKRYPFPTT TGNAVASGMM DAVCGSVMMM HGRLKEKTGA
         351
         401
              GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
         451
              ESEHT*
```

	·
m311.pep	10 20 30 40 50 60 MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV
a311	
	70 80 90 100 110
m311.pep	RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADAAVLLXXXXXXX
a311	RTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADAAVLLETLLAELDAVLLQ 70 80 90 100 110 120
m311.pep	
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVDGQGVLHLETAEGKQTVVS
	130 140 150 160 170 180
m311.pep	120 130 140 150 160 170 -EISLRSDXRPVSVXKRRDSERFLLLDGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE
a311	
asıı	GEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAWVENGTFATVGSAPYRDLSPLGAE 190 200 210 220 230 240
m311.pep	180 190 200 210 220 230 WAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
a311	:
	250 260 270 280 290
211	240 250 260 270 280 290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDDGHYLGGTIMPGFHLMKESLAVRTANLNR
a311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDDGHYLGGTIMPGFHLMKESLAVRTANLNR 300 310 320 330 340 350
	300 310 320 330 340 350
m311.pep	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKPVDVIITGGGAAKVAEA
a311	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKPVDVIITGGGAAKVAEA
	330 400 410
m311.pep	360 370 380 389 LPPAFLAENTVRVADNLVIYGLLNMIAAEGREYEH
a311	
	420 430 440 450

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1295>: g311-1.seq

```
1 ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
 51 CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCT GATGTTCAGT TTCGGCTGGG CGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA CTTGCGTGCC GGCGCGCTTT
501 GGGGTGTTTG GGTTTGGAAA CGCAAATCAA GTGGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGCAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGCGGAA
    CTGGGCGCGG TGTTGGAACA ATATGCGGAA GAAGGGTTCG CGCCATTTTT
```

```
801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
     TGCGCGACGG CGAAACCGTG TGCGAAGGCA CGGTTAAAGG CGTGGACGGA
     CGAGGCGTTC TGCACTTGGA AACGGCAGaa qqCGAACAGa cqqtcGtcaq
     cggcGaaaTC AGccTGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001
      gGccggatTC GgaacgttTT tTGCTgttgg aaggcgggaa cagccggctc
     aAGTGGgcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGCgCC
     GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
     GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
     CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
     AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCTT TCCCGACCAC AACGGGCAAC GCCGTCGCAA GCGGCATGAT
1551 GGACGCGGTT TGCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
     GCGAAAGTCG CCGAAGCCCT GCCGCCTGCA TTTTTGGCGG AAAATACCGT
     GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
     CCGAAGGCGG GGAATCGGAA CACGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>: g311-1.pep

```
1 MTVLKPSHWR VLAELADGLP QHVSQLAREA DMKPQQLNGF WQQMPAHIRG
51 LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLRDGETV CEGTVKGVDG
301 RGVLHLETAE GEQTVVSGEI SLRPDNRSVS VPKRPDSERF LLLEGGNSRL
351 KWAWVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSSAQAL GIRNHYRHPE EHGSDRWFNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDDGH YLGGTIMPGF HLMKESLAVR TANLNRPAGK
501 RYPFPTTTGN AVASGMMDAV CGSIMMMHGR LKEKNGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1297>: m311-1.seq

```
1 ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
     CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
 101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
 151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
     TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
 251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
 301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
 351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
     GCGAGTGTCT GATGTTCAGT TTTGGCTGGG TGTTTGACCG GCCGCAGTAT
 451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGTC GGCGCGCCTT
 501 GTCGCGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTTGGTTG
     TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
 601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTTG TCCTGCCCAA
 651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
 701 GGCGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
 751 CTGGACGCGG TGTTGTTGCA ATATGCGCGG GACGGATTTG CGCCTTTTGT
 801 GGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
 851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
 901
     CAAGGCGTTT TGCACTTGGA AACGGCAGAG GGCAAACAGA CGGTCGTCAG
 951 CGGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GGCGGGATTC GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTC GCAACCGTCG GTAGCGCGCC
     GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1101
     GAAATGTCCG CATCGTCGGT TGCGCTGTGT GCGGAGAATT CAAAAAGGCA
1201
     CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
     ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
     CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1301
1351
     TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
     TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451
     AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
     CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551
     GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCCTGCA TTTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTTGAAC ATGATTGCCG
```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <seq 1298;="" 311<="" id="" orf="" th=""><th>-1>:</th></seq>	-1>:
m311-1.pep	

m311-1.pep					
1 M	ITVLKLSHWR VLAELAI	DGLP QHVSQI	LARMA DMKP	QQLNGF WQQI	MPAHIRG
	LRQHDGYWR LVRPLA				
	RIAPDKAHK TICVTH				
151 E	LGSLSPVAA VACRRAI	LSRL GLDVQ	KMBN DTAA	SRDKLG GIL:	IETVRTG
	KTVAVVGIG INFVLP				
251 <u>I</u>	DAVLLQYAR DGFAPF	AEY QAANRI	OHGKA VLLLI	RDGETV FEG	rvkgvdg
	GVLHLETAE GKQTVVS				
351 K	WAWVENGTF ATVGSA	YRD LSPLGA	AEWAE KADGN	VRIVG CAVO	CGEFKKA
401 Q	VQEQLARKI EWLPSS	AQAL GIRNH	KHPE EHGSI	DRWFNA LGSI	RRFSRNA
451 <u>C</u>	VVVSCGTAV TVDALTI	DDGH YLGGTI	MPGF HLMKE	SLAVR TANI	LNRHAGK
	KVAEALPPA FLAENTV				LITGGGA
331 A	KVACALPPA FLACKIV	KAN DMPAT	GLLN MIAAR	GREIE HI'	
m311-1/g311	-1 93.9% ident	ity in 591	aa overla	n	
, y		,		·P	
	10	20	30	40	50 60
m311-1.pep	MTVLKLSHWRVLAEI	ADGLPQHVSQ	LARMADMKPO	QLNGFWQOME	PAHIRGLLRQHDGYWR
g311-1	MTVLKPSHWRVLAEL	ADGLPQHVSQ	LAREADMKPQ	QLNGFWQQMF	AHIRGLLRQHDGYWR
	10	20	30	40	50 60
	70	80	90	100	110 120
m311-1.pep	LVRPLAVFDAEGLRE	LGERSGFQTA	LKHECASSND	EILELARIAF	DKAHKTICVTHLQSK
		1111111111	111111111	111111111	
g311-1	LVRPLAVFDAEGLRD				DKAHKTICVTHLQSK
	70	80	90	100	110 120
	. 120	1.40	150	1.60	150
m211 1 man	130	140	150	160	170 180
m311-1.pep	GRGRQGRKWSHRLGE	CLMFSFGWVF	DKLÖIFTG2T	SPVAAVACRR	ALSRLGLDVQIKWPN
g311-1			1111111111		: ::
9311-1	130	140	150	160	
	130	140	150	160	170 180
	190	200	210	220	230 240
m311-1.pep	DLVVGRDKLGGILIE				
ozi i.pop		111.111111	111111111	!!!!!!!!!	I I I I I I I I I I I I I I I I I I I
q311-1	DLVVGRDKLGGILIE	TVRAGGKTVA	VVGTGTNEVT.	PKENENDVCN	051 FOTA CDDCNADA
3011 1	190	200	210	220	230 240
				220	230 240
	250	260	270	280	290 300
m311-1.pep	AVLLETLLVELDAVL	LQYARDGFAP	FVAEYQAANR	DHGKAVLLLR	DGETVFEGTVKGVDG
	11111111:11 111	111::111	1: 11::111	11111111	FF1 FF 1 1 1 7 2 1 1 1 1 1
g311-1	AVLLETLLAELGAVL	EQYAEEGFAP:	FLNEYETANR	DHGKAVLLLR	DGETVCEGTVKGVDG
	250	260	270	280	290 300
	310	320	330	340	350 360
m311-1.pep	QGVLHLETAEGKQTV	VSGEISLRSDI	ORPVSVPKRRI	DSERFLLLDG	GNSRLKWAWVENGTF
-211 1	:		:		ішшин
g311-1	RGVLHLETAEGEQTV				
	310	320	330	340	350 360
	370	380	390	400	410 420
m311-1.pep	ATVGSAPYRDLSPLGA				410 420
			LILLILLE	I IIIIIIII	LARRIEWLPSSAQAL
g311-1	ATVGSAPYRDLSPLGA	AEMAEKADON!	ITTUCCAUCCE		ABKIENI DOCAGAI
J 4	370	380	390	400	410 420
					410 420
	430	440	450	460	470 480
m311-1.pep	GIRNHYRHPEEHGSDE	RWFNALGSRRE			DDGHYLGGTTMPGF
			1111111111	1111111111	
g311-1	GIRNHYRHPEEHGSDE	RWFNALGSRRE	SRNACVVVS	GTAVTVDALT	DDGHYLGGTIMPGF
	430	440	450	460	470 480
	490	500	510	520	530 540
m311-1.pep	HLMKESLAVRTANLNF	RHAGKRYPFPT	TTGNAVASGN	IMDAVCGSVMN	MHGRLKEKTGAGKP
~211 1	1111111111111111		1111111111	1111111:11	11111111:1111
g311-1	HLMKESLAVRTANLNF				
	490	500	510	520	530 540
	550	560	570	580	500
	330	555	370	200	590

```
VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMIAAEGREYEHIX
m311-1.pep
             q311-1
             VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
                   550
                             560
                                      570
                                                580
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1299>:
a311-1.seq
         ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
       1
      51 CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
         CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
         CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
     151
         TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
     201
         CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
     301
         GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
         GCAAAGTAAG GGCAGGGGCC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
     351
         GCGAGTGTCT GATGTTCAGT TTTGGCTGGG TGTTTGACCG GCCGCAGTAT
     451
         GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGCC GGCGCGCCTT
         GTCGCGTTTG GGTTTGAAAA CGCAAATCAA GTGGCCAAAC GATTTGGTCG
     501
         TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
     551
         GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
     651
         GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
         GGCGGGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
     701
     751
         CTTGATGCGG TGTTGTTGCA ATATGCGCGG GACGGATTTG CGCCTTTTGT
         GGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
     801
         TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
     851
         CAAGGCGTTC TGCACTTGGA AACGGCAGAG GGCAAACAGA CGGTCGTCAG
     901
         CGGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
    1001
         GGCGGGATTC GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
    1051
         AAGTGGGCGT GGGTGGAAAA CGGCACGTTC GCAACCGTCG GTAGCGCGCC
         GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
    1101
         GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATT CAAAAAGGCA
    1151
         CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
    1201
    1251
         ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
    1301
         CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
         TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
    1351
         TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
    1451
         AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
         CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
         GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
    1551
    1601
         AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
    1651 GCAAAAGTTG CCGAAGCCCT GCCGCCTGCA TTTTTGGCGG AAAATACCGT
    1701 GCGCGTGGCG GACAACCTCG TCATTCACGG GCTGCTGAAC CTGATTGCCG
    1751 CCGAAGGCGG GGAATCGGAA CATACTTAA
This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:
a311-1.pep
      1 MTVLKPSHWR VLAELADGLP QHVSQLARMA DMKPQQLNGF WQQMPAHIRG
     51 LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
     101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDRPQY
         ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGRDKLG GILIETVRTG
    201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
         LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVDG
    301
         QGVLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
         KWAWVENGTF ATVGSAPYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
     351
         QVQEQLARKI EWLPSSAQAL GIRNHYRHPE EHGSDRWFNA LGSRRFSRNA
     401
         CVVVSCGTAV TVDALTDDGH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
         RYPFPTTTGN AVASGMMDAV CGSVMMMHGR LKEKTGAGKP VDVIITGGGA
     501
     551
         AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*
a311-1/m311-1
                98.5% identity in 591 aa overlap
                              20
                                       30
                                                40
a311-1.pep
            MTVLKPSHWRVLAELADGLPQHVSQLARMADMKPQQLNGFWQQMPAHIRGLLRQHDGYWR
            m311-1
            MTVLKLSHWRVLAELADGLPQHVSQLARMADMKPQQLNGFWQQMPAHIRGLLRQHDGYWR
                             20
                    10
                                       30
                                                40
                                                          50
                                                                    60
                    70
                             80
                                       90
                                               100
                                                         110
                                                                  120
a311-1.pep
            LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLOSK
            m311-1
            LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLOSK
```

80

90

100

a311-1.pep	130 140 150 160 170 180 GRGRQGRKWSHRLGECLMFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLKTQIKWPN
a311-1.pep m311-1	190 200 210 220 230 240 DLVVGRDKLGGILIETVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA
a311-1.pep m311-1	250 260 270 280 290 300 AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVDG
a311-1.pep m311-1	310 320 330 340 350 360 QGVLHLETAEGKQTVVSGEISLRSDDRPVSVPKRDSERFLLLDGGNSRLKWAWVENGTF
a311-1.pep	370 380 390 400 410 420 ATVGSAPYRDLSPLGAEWAEKVDGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL
a311-1.pep m311-1	430 440 450 460 470 480 GIRNHYRHPEEHGSDRWFNALGSRRFSRNACVVVSCGTAVTVDALTDDGHYLGGTIMPGF
a311-1.pep	490 500 510 520 530 540 HLMKESLAVRTANLNRHAGKRYPFPTTTGNAVASGMMDAVCGSVMMMHGRLKEKTGAGKP
a311-1.pep	550 560 570 580 590 VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHTX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1301>: g312.seq

atgaGtatCc aatCcGgcga AATTTtagaa accqtCAAAA TGGTTGCCGA 51 ccggaATttt gAtgtccgCA CCATTAccat cggcaTTgaT ttgcacqact 101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc 151 accaeggteg geaaagactT GGTGGCAacg Gegaaacace tTTccgcCAA 201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc 251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact 301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC 351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT 401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG 551 CCAAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAATCC GTTTATGGCG 601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT 651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAATTCG GACGCGGTCA 701 GCCTGACCGA GGTCGCCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC 751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC 801 GTTCGGCATT CTCGATTTGT CGCTGGCACC GACCCCCGCC GTCGGCGACT 851 CGGTGGCGC CATTCTTGAA GAAATGGGCT TGAGCGTCTG CGGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
          951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGC TTTATCCCCG
               TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAGGCAGG CGTGTTGACG
         1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
         1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCC GGCATCATCG
         1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
         1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
         1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
         1301 TGTTCGTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
         1351 AACTGA
This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:
     q312.pep
               MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
               TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAOT
               LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
               IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
               GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
               RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
          301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
          351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
          401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVOSMK
          451
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1303>:
     m312.seq
              ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
              CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
               GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
          101
              ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
              ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
              AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAACT
              TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
              CGCGTTGGTG CAAAAAGGGA TGTCGCCTTC GGATGAGGTG TTAATCCGCT
              CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
              ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
          451
              CGAAACCGTC AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
              CTAAAATTGT CGTGTTCTGC AACGCGGTGG AAGACAACCC GTTTwTGGCG
          601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
          651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
              CCGAAGTTGC GGAAGTAGTG AAGAAAACTG CTTTCAAAAT TACCCGCGTG
              GGCGAACTCA TCGGCCGCGA AGCCTCAAAA ATGCTGAATA TCCCGTTTGG
               TATTCTCGAC TTGTCGCCGA CCCCGCCCGT CGGCGACTCA GTGGCACGCA
               TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
              GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
              CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
         1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
         1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
         1101 CGGCGACACG CCCGCGCACA CCATTTCCGG CATCATTGCC GACGAAGCCG
         1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
         1201 ACCGGTAAAA CCGTCGGCGA CACGGTCGAG TTCGGCGGCT TGTTGGGCTA
         1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTC GTGCGAAGTA TTCGTCAACC
               GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA
This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:
     m312.pep
              MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
              TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAOIAAATH ADSYVSVAOT
              LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCXSIN
              IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
          201 GAFHGSGDAV INVGVSGPGV VKAALENSDA TTLTEVAEVV KKTAFKITRV
          251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
         301 ALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
              EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
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TGKTVGDTVE FGGLLGYAPV MPVKEGSCEV FVNRGGRIPA PVQSMKN*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from N. gonorrhoeae:

m312/g312

			-			
	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMV					
g312	MSIQSGEILETVKM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIVNO					
1112.pcp	:					
g312	AKHLSAKYGVPIVNO					
J-	70	80	90	100	110	120
				•		
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLIRSI					
	11111111111111					. ,
g312	QKGMSPSDEVLIRSV					-
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFCNAVED					LTEVAE
msiz.pop				111111111		
g312	FGCAKIVVFCNAVED					
3	190		210	220	230	240
	240 250	260	270	280	290	
m312.pep	240 250 VVKKTAFKITRVGEL					SVCGTH
	VVKKTAFKITRVGEL	IGREASKMLNIP	FGILDLS	PTPPVGDSV	ARILEEMGL	
m312.pep g312	VVKKTAFKITRVGEL VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP	FGILDLS FGILDLSLA	PTPPVGDSV.	ARILEEMGL ARILEEMGL	 SVCGTH
	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP	FGILDLS	PTPPVGDSV	ARILEEMGL	
	VVKKTAFKITRVGEL VVKKTAFKITRVGEL 250	IGREASKMLNIP	PFGILDLS PFGILDLSLA 270	PTPPVGDSV. APTPAVGDSV. 280	ARILEEMGL ARILEEMGL 290	 SVCGTH
g312	VVKKTAFKITRVGEL VVKKTAFKITRVGEL 250 300 310	IGREASKMLNIP IGREASKMLNIP 260 320	PFGILDLS PFGILDLSLA 270	PTPPVGDSV. APTPAVGDSV. 280	ARILEEMGL ARILEEMGL 290	 SVCGTH 300
	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL	FGILDLS PFGILDLSLA 270 330 SGAFIPVSE	PTPPVGDSV. PTPAVGDSV. 280 340 CDEGMIXAAE.	ARILEEMGL ARILEEMGL 290 350 AGVLTLDKL	SVCGTH 300
g312 m312.pep	VVKKTAFKITRVGEL VVKKTAFKITRVGEL 250 300 310	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL	FGILDLS FGILDLSLA 270 330 .SGAFIPVSE	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE.	ARILEEMGL ARILEEMGL 290 350 AGVLTLDKL	SVCGTH 300 EAMTAV
g312	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL	FGILDLS FGILDLSLA 270 330 .SGAFIPVSE	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE.	ARILEEMGL ARILEEMGL 290 350 AGVLTLDKL	SVCGTH 300 EAMTAV
g312 m312.pep	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL	FGILDLS FGILDLSLA 270 330 .SGAFIPVSE 	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE.	ARILEEMGL: ARILEEMGL: 290 350 AGVLTLDKL:	SVCGTH 300 EAMTAV EAMTAV
g312 m312.pep	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400	ARILEEMGLE	SVCGTH 300 EAMTAV EAMTAV 360
g312 m312.pep	VVKKTAFKITRVGEL	IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 TAVRIIPVT	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	SVCGTH 300 EAMTAV EAMTAV 360
g312 m312.pep g312 m312.pep	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 CTAVRIIPVTC	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	SVCGTH 300 EAMTAV EAMTAV 360 FGGLLG
g312 m312.pep g312	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 TAVRIIPVTC	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	EAMTAV 360 FGGLLG FGGLLG FGGLLG
g312 m312.pep g312 m312.pep	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 CTAVRIIPVTC	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	SVCGTH 300 EAMTAV EAMTAV 360 FGGLLG
g312 m312.pep g312 m312.pep	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 TAVRIIPVTC	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	EAMTAV 360 FGGLLG FGGLLG FGGLLG
g312 m312.pep g312 m312.pep g312	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA AHTISGIIADEA 380	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT AIGMINSKT	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 TAVRIIPVTC	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	EAMTAV 360 FGGLLG FGGLLG FGGLLG
g312 m312.pep g312 m312.pep	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA AHTISGIIADEA 380 440 VNRGGRIPAPVQ	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT AIGMINSKT	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 TAVRIIPVTC	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	EAMTAV 360 FGGLLG FGGLLG FGGLLG
g312 m312.pep g312 m312.pep g312	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA 380 AHTISGIIADEA 380 VNRGGRIPAPVQ	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT AIGMINSKT 390 SMKNX	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 TAVRIIPVTC	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	EAMTAV 360 FGGLLG FGGLLG FGGLLG
g312 m312.pep g312 m312.pep g312	VVKKTAFKITRVGEL	IGREASKMLNIP IGREASKMLNIP 260 320 GGMMASSAVGGL GGMMASSAVGGL 320 380 AHTISGIIADEA 380 AHTISGIIADEA 380 VNRGGRIPAPVQ	FGILDLS FGILDLSLA 270 330 SGAFIPVSE SGAFIPVSE 330 390 AIGMINSKT AIGMINSKT 390 SMKNX	PTPPVGDSV. APTPAVGDSV. 280 340 CDEGMIXAAE. CDEGMIAAAE. 340 400 TAVRIIPVTC	ARILEEMGLE ARILEEMGLE 290 350 AGVLTLDKLE AGVLTLDKLE 350 410 GKTVGDTVE	EAMTAV 360 FGGLLG FGGLLG FGGLLG

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>: a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGGTTGCCGA
51	CCAGAATTTC	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAAATATC	TGTCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAACT

	·
301	
351	CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401	CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451	ATCGGCAGTA CGCGCCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501	
551	CCAAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAACCC GTTTATGGCG
601	GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651	ALL MANUEL COLUMN TO COLUM
701	
751	
801	
851	
901	
951	
1001	The state of the s
1051	TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCGGTCG GCTTGGATAT
1101	
1151	CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201	
1251	
1301	TGTTCGTCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351	AACTGA
This correspond	ds to the amino acid sequence <seq 1306;="" 312.a="" id="" orf="">:</seq>
a312.pep	, , , , , , , , , , , , , , , , , , , ,
i	MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51	TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101	LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151	IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201	GAFHGSGEAD AVINVGVSGP GVVKAALENS DATTLTEVAE VVKKTAFKIT
251	RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301	GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GITADEAATC MINSKETTAVD
351	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N*
351 401	LDK <u>LEAMTAV CSVGLDMIAV</u> PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
351 401 451	LDK <u>LEAMTAV CSVGLDMIAV</u> PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N*
351 401 451	LDK <u>LEAMTAV CSVGLDMIAV</u> PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap
351 401 451 m312/a312 96	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60
351 401 451	LDK <u>LEAMTAV CSVGLDMIAV</u> PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNONIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep	LDK <u>LEAMTAV CSVGLDMIAV</u> PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep	LDK <u>LEAMTAV CSVGLDMIAV</u> PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep	LDK_LEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312	LDK_LEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR 1IPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312	LDK_EAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312	LDKLEAMTAV CSVGLDMIAV IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK 1.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLIG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312 m312.pep a312	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLIG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312 m312.pep	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 3.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312 m312.pep a312 m312.pep a312	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 5.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
351 401 451 m312/a312 96 m312.pep a312 m312.pep a312 m312.pep a312	LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK N* 3.7% identity in 451 aa overlap 10 20 30 40 50 60 MSIQSGEILETVKMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT

			•				
		250	260	270	280	290	300
			310 32			350)
m31	2.pep	GTTAALALLND	AVKKGGMMASSA	VGGLSGAFIP	/SEDEGMIXAAI	EAGVLTLDKI	LEAMTAV
	_					111111111	
a31	.2	GTTAALALLND	AVKKGGMMASSA	VGGLSGAFIP	/SEDEGMIAAAI	EAGVLTLDKI	LEAMTAV
		310	320	330	340	350	360
_	_		370 38			410)
m31	.2.pep	CSVGLDMIAVPO	SDTPAHTISGII	ADEAAIGMINS	SKTTAVRIIPVI	GKTVGDTVE	FGGLLG
	_		1111111111	111111111	1111111111	[]:[][][]	11111
a31	. 2	CSVGLDMIAVPO	DTPAHTISGII	ADEAAIGMINS	KTTAVRIIPVI	CGKTVGDSVE	FGGLLG
		370	380	390	400	410	420
			30 44				
m31	2.pep	YAPVMPVKEGSO	EVFVNRGGRIP	APVQSMKNX			
				11111111			
a31	2	YAPVMPVKEGSC	EVFVNRGGRIP	APVQSMKNX			
		430	440	450			
			•				
The follo	wing partia	al DNA seque	nce was ident	tified in N. e	onorrhoeae	<seo id<="" td=""><td>1307></td></seo>	1307>
g313.seq	01	•			,	OLQ ID	15072.
1		ice egegeacet	a constrono	. aatooooo	7	4-	
51	tttaccca	ac cacaaaaa	a eggaceggge	aatteegge	g cyaccaatg	С	
101	cccacgca	igc ggcaaaaaa	a aggeggeege	getgaeget	c trgggcgate	3	
		gg tttggttgc					
151	ctcggttt	at ccgacagcg	c aatcgccgcc	gtcgcactcg	g ccgcgctggi	t	
201	cgggcata	itg tggccggtg	t ttttcggatt	: taagggcgg	c aaaggcgtg	3	
251		tt gggcgtgct					
301		ga tttggcttg					
351	tgccgcgc	tg gtcgccaca	a ccgccgcccc	: ccttgccgca	a ctgttttta	ā	
401	tgccgcat	ac ttcttggat	ttcgcaaccc	tcgcaatcgc	catattqqt	7	
451	ttgctccg	cc ataagagca	a catcctcaac	ctqattaaac	qcaaaqaaa	י נ	
501		gc gaaaaacgci			, , <u>,</u>	,	
This corre		the amino acid		SEO ID 130	Q. ODE 212	na>.	
g313.pep	osponas to	the alline act	soquence \		o, OKI 313.	.ng/.	
	MUDDDWAG	CC NUCLEUR D					
1	TOT ODGET	SG NPGATNVLRS	GKKKAAALTL	LGDAAKGLVA	VLLARVLQE	,	
51	LGLSDSAI.	AA VALAALVGH	WPVFFGFKGG	KGVATALGVI	LALSP <u>ATAL</u>	<u> </u>	
101		<u>AF GF</u> KVSS <u>LAAI</u>		<u>LFFMPHTSWI</u>	FATLAIAIL	<u>7</u>	
151		LN LIKGKESKI					
The follow	wing partia	l DNA sequer	ice was ident	ified in N. m	eningitidis <	SEO ID 1	309>.
m313.seq	•	•				4 1	505.
1	ATGGACGA	CC CGCGCACCTA	CGGATCGGGC	AATCCGGGG	СААССААТСТ	n	
. 51		GC GGCAAAAAA					
101	CCGCCAAA	GG TTTAGTTGC		CACCCCTCCT	TIGGGCGAIG	, ,	
151	CTCCCTTT	AT CCGACAGCGC	· AATCCCCCCC	CACGCG1GC1	TCAAGAACCG	; -	
201							
251		TG TGGCCGGTGT					
	CAACGGCA.	TT GGGCGTGCTT	CIGGCACTCT	CTCCCGCAAC	TGCCTTGGTC	,	
301	TGCGCGTTC	GA TTTGGCTTGI	TATGGCATTC	GGCTTCAAGG	TGTCCTCCCT	1	
351	TGCCGCAT	TA ACCGCCACAA	TCGCCGCACC	GGTCGCCGCA	TCCTTCTTTA	L	
401	TGCCGCAC	GT CTCGTGGGTT	TGGGCGACCG	TCGCCATTGC	TTTGCTGGTG	;	
451	TTGTTCCG	CC ACAAAAGTAA	TATCGTCAAG	CTGCTCGAAG	GCAGAGAAAG	ļ	
501	CAAAATCG	GC GGCAGCCGCT	GA				
This corre	sponds to t	the amino acid	sequence <	SEO ID 1316). OPE 212~	»·	
m313.pep	oponus to t	willio uolu	. soquonoo <		, OKI 313/	•	
	MDDDDDDVCC	בר אווארווארווא אים	CUUUNAAT	*	717 7 3		
1	TOTOPOTT	SG NPGATNVLRS	GARRAAALTL	LGDAAKGLVA	VLLARVLQEP		
51	LGLSDSA17	AA VALAALVGHM	wPVFFGFKGG	KGVATALGVL	LALSPATALV		
101		AF GFKVSSLAAL		SFFMPHVSWV	WATVAIALLV		
		K LLEGRESKIG					
Computer	analysis of	f this amino ac	id sequence	gave the foll	lowing resul	ts:	

Computer analysis of this amino acid sequence gave the following results:

WO 99/57280 721 Homology with a predicted ORF from N. gonorrhoeae ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from N. gonorrhoeae: m313/g313 10 20 30 40 60 MDDPRTYGSGNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA m313.pep MDDPRTYGSGNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPLGLSDSAIAA q313 10 20 30 40 50 60 70 90 100 110 120 VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMAFGFKVSSLAAL m313.pep VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMAFGFKVSSLAAL g313 70 80 90 100 110 120 130 140 150 160 170 m313.pep TATIAAPVAASFFMPHVSWVWATVAIALLVLFRHKSNIVKLLEGRESKIGGSRX VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLIKGKESKIGEKRX g313 130 140 150 160 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1311>: a313.seq ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT 51 TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG 101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT 151 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG 251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCACAAC TGCCTTGGTC TGCGCGTTGA TTTGGCTTGT GATGGCATTC GGCTTCAAGG TGTCCTCCCT 301 TGCCGCATTA ACCGCCACAA TCGCCGCCC CCTTGCCGCA CTGTTTTTTA 351 TGCCGCATAC TTCTTGGATT TTCGCAACCC TCGCAATCGC CATATTGGTG 401 TTGCTCCGCC ATAAGAGCAA CATCCTCAAC CTGATTAAAG GCAAAGAAAG 451 CAAAATCGGC GAAAAACGCT GA

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

501

MDDPRTYGSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP

- LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPTTALV 51
- CALIWLVMAF GFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
- 151 LLRHKSNILN LIKGKESKIG EKR*

m313/a313 90.8% identity in 173 aa overlan

.,	P				
10	20	30	40	50	60
MDDPRTYGSGNPGA	TNVLRSGKKK	AAALTLLGDA	AAKGLVAVLLA	RVLQEPLGLS	SDSAIAA
111111111111111	111111111				111111
MDDPRTYGSGNPGA	TNVLRSGKKK	AAALTLLGDA	AKGLVAVLLA	RVLQEPLGLS	DSAIAA
10	20	30	40	50	60
m.o.					
· •				110	120
VALAALVGHMWPVF	FGFKGGKGVA	TALGVLLALS	SPATALVCALI	WLVMAFGFKV	SSLAAL
111111111111	111111111				
VALAALVGHMWPVF	FGFKGGKGVA	TALGVLLALS	SPTTALVCALI	WLVMAFGFKV	SSLAAL
70	80	90	100	110	120
130	140	150	160	170	
11111111111	11:11::11:	111:111:11		: :	
TATIAAPLAALFFM	PHTSWIFATL	AIAILVLLRH	KSNILNLIKG:	KESKIGEKRX	
130	140	150	160	170	
	MDDPRTYGSGNPGA	MDDPRTYGSGNPGATNVLRSGKKK	MDDPRTYGSGNPGATNVLRSGKKAAALTLLGDA	MDDPRTYGSGNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLA	MDDPRTYGSGNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPLGLS

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The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 1313>:
     g401.seg
               atgaaattac aacaattggc tgaagaaaaa atcggcgttc tgattgtgtt
            1
           51 cacgetgett gtagteagtg teggtetgtt gattgaagtt gtgecettgg
          101 cctttaccaa ggcggcaaca cagccggcgc cgggcgtgaa gccttacaat
          151 gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
          201 ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcgttacg
          251 gtcattactc tgttgccgga gagtcggttt acgaccatcc gttccaatgg
          301 ggttccaaac gtaccggtcc tgatttggca cgtgtgggcg gccgctattc
          351 cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
          401 agtocaatat googgoatto cogtggottg cacgoaataa agtogatgto
          451 gatgcaaccg ttgccaacat gaaggetttg cgtaaagtag gtacteetta
          501 cagtgatgag gaaattgcga aagcgcctga ggctttggca aacaaatccg
          551 agctggatgc tgtagtcgcc tatctgcaag gattgggtct ggctttgaaa
          601 aacgtaaggt aa
This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:
     9401.pep
         1 MKLQQLAEEK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
        51 ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
       101 GSKRTGPDLA RVGGRYSDEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
       151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
       201 NVR*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1315>:
     m401.seq
               ATGAAATTAC AACAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
               CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
           51
               CCTTTACCAA GGCGGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAAT
          101
          151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
          201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TGCGGAAACC GAGCGTTACG
          251 GTCATTACTC TGTTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
          301 GGTTCCAAAC GTACCGGTCC TGATTTGGCA CGTGTGGGCG GTCGCTATTC
          351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
          401 AGTCCAATAT GCCGGCATTC CCGTGGCTTG CACGCAATAA AGTCGATGTC
              GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
              CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
              AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
              AACGTAAGGT AA
This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:
     m401.pep
              MKLQQLAEEK IGVLIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
           1
           51 ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
          101
              GSKRTGPDLA RVGGRYSDEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
          151
              DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLOGLGLALK
              NVR*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng)
from N. gonorrhoeae:
     m401/g401
                                             30
                 MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
     m401.pep
                  g401
                 MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
                         10
                                   20
                                             30
                                                       40
                                                                 50
                         70
                                   80
                                             90
                                                      100
                                                                          120
    m401.pep
                 IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSDEW
```

9401			HYSVAGESVY	DHPEOWGSKR	TGPDLARVCC	TRY CDEW
2	70	80	90	100	110	120
	130	140	150	160	170	180
m401.pep	111111111111	1111111111		1111111111	111111111	11111
g401	HRIHLLNPRDVVPE 130	SNMPAFPWLA 140	RNKVDVDATV 150	ANMKALRKVG 160	TPYSDEELAK 170	APEALA 180
	190	200			- · ·	100
m401.pep	NKSELDAVVAYLQG	LGLALKNVRX				
g401	NKSELDAVVAYLQG					
The following r	partial DNA sequence		ified in N n	naninaiti dia	<ceo id<="" td=""><td>1017</td></ceo>	1017
a401.seq					•	131/>:
1 51	ATGAAATTAC AACAAT CACGCTGCTT GTAGTC	TGGC TGAAG	AAAAA ATCG	GCGTTC TGA	TTGTGTT	
101	CCTTTACCAA GGCGGC	AACA CAGCC	GGCGT CGGG	CGTGAA GCC	TTACAAT	
151 201	GCCCTGCAGG TTGCCG CTGCCACTCG CAAATG	GACG CGATA	TTTAC ATCC	GTGAGG GCT	STTACAA	
251	GTCATTACTC TGTTGC	CGGA GAGTC	GGTTT ACGA	CCATCC GTT	CCAATGG	
301	GGTTCCAAAC GTACCG	GTCC TGATT	TGGCA CGTG	TGGGCG GTC	GCTATTC	
351 401	CGACGAATGG CACCGT. AGTCCAATAT GCCGGC.	ATCC ACCTG ATTC CCGTG	CTGAA TCCC(CGTGAT GTC(STGCCTG	
451	GATGCAACCG TTGCCA	ACAT GAAGG	CTTTG CGTA	AAGTAG GTAG	CTCCTTA	
501	CAGTGATGAG GAAATT					
551 601	AGCTGGATGC TGTAGT AACGTAAGGT AA	UGCC TATCT	GCAAG GATTO	GGTCT GGCT	.'TTGAAA	
This correspond	s to the amino acid s	equence <s< td=""><td>SEO ID 131</td><td>8: ORF 401</td><td>.a>:</td><td></td></s<>	SEO ID 131	8: ORF 401	.a>:	
a401.pep		•		ĺ		
1	MKLQQLAEEK IGVLIV	FTLL VVSVG	LLIEV VPLA	TKAAT QPAS	GVKPYN	
51 101	ALQVAGRDIY IREGCYNGSKRTGPDLA RVGGRYS	NCHS QMIRP SDEW HRIHLI	ERAET ERYGE LNPRD VVPES	HYSVAG ESVY SNMPAF PWI.	DHPFQW	
151	DATVANMKAL RKVGTP	YSDE EIAKAI	PEALA NKSEI	LDAVVA YLQG	LGLALK	
201	NVR*				1	
m401/a401 99	.5% identity in 203 a	•	2.0			
m401.pep	10 MKLQQLAEEKIGVLI	20 [VFTLLVVSV0	30 Slutevvplar	40 TTKAATOPAPG	50 אער ז מער ז מער.	60
_ _				111111111111111111111111111111111111111		11111
a401	MKLQQLAEEKIGVLI 10	VFTLLVVSVO 20	GLLIEVVPLAF	TKAATQPASG	VKPYNALQVA	AGRDIY
			30	40	50	60
m401.pep	70 IREGCYNCHSQMIRE	80 FRAETERYGH	90 IYSVAGESVYD	100 HPFQWGSKRT	110 GPDLARVGGR	120 RYSDEW
a401		HHIIIIIII	11111111111	11111111111	1111111111	11111
4101	70	80	90	100	110	120
m401.pep	130	140	150	160 .	170	180
m401.pep	HRIHLLNPRDVVPES			NMKALRKVGT	PYSDEEIAKA !!!!!!!!!	PEALA
a401	HRIHLLNPRDVVPES 130	NMPAFPWLAR 140	NKVDVDATVA 150	NMKALRKVGT 160	PYSDEEIAKA 170	PEALA 180
	190	200				
m401.pep	NKSELDAVVAYLQGL					
a401						
	190	200				

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1319>:
9402.seq
          ATGGATATGG TGAACACTAA Accgaatact aqtqtgatta atatqctttc
       1
          tttccttacc ggatTATTGA GCTTGGGTat aqaaqtCtTq tGGGTAAGGA
          TGttttcgTT CGCagcAcag tccqtqcctc aqqCATTTTC atttattctt
     151 gcctGttttc tgACCGgtat cgccgtcggc gCgTATTTTG GCAAACGGAT
     201 TTGCCGCAGC CGCTTTGTTG ATATTCCCtT TATCGGGCAG TgcttcttgT
     251 GGGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTTGACG
     301 GGTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
     351 CGtcGTCAGG GGGTTGATTT TCCCACTTGT ACACCATGtg GGTACGGATG
     401 GCAACAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTTGCC
     451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
     501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTTCT GCTGCtgtcc
     551 cTTTGTTTTg tacaCTGtTC CAAAAAGTC TCCGACTGAA TGCAGTGTCG
     601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCCTAC TGCCGGATTC
          TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
          ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
          GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
         CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
     851 GCATTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
     901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
     951 CCGTAGCCTT ATCGCGGACG agccgcAAAT CGCACCGCTT TTGCAGGACA
    1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
    1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
    1101 TGCCTATTCC ACTAACCTGT TGAGTGCGGA ATTTTTAAAA CAGGTGCAAA
    1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
    1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
    1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCcct AATAAAGAAC
          TGCTCaagca aCGCCTTTcc cgGTTGATTT GGCCGGAAAG CGGCAGgcac
    1351 gtATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGtctctCG
          TATGCTGATT CGGATGACGG AACCTTCGGC TGGGGCGGAA GTCATTACTG
    1401
    1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA
This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:
g402.pep
       1
          MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAFSFIL
          ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
      51
          GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
          GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
          VAVSLMFGIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVVYG
          ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRIFVVGL STGSWARVLS
     301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
     351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
     401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
         VFDSSTVDAA AQKVVSRMLI RMTEPSAGAE VITDDNMIVE YKYGRGI*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1321>:
m402.seq
         ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCNTTC
         TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
         TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCTT
         GCCTGTTTTC TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
         TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
         GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTTGACG
     251
         GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
     301
         CGTCGTCASA SGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
         GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAMCGTTGCC
     451
         GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
         GTCCACCCAA CAGATTTACC TGCTCATCTG TwTGATTTCT GCTGCTGTCC
    551 CTTTGTTTTG TACACTGTTC CAAAAAAGTC TCCGACTGAA TGCAGTGTCG
    601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCYTAC TGCCGGATTC
```

```
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
 701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
 751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
 801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
 851 GCATTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
 901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
 951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA
```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>: m402.pep

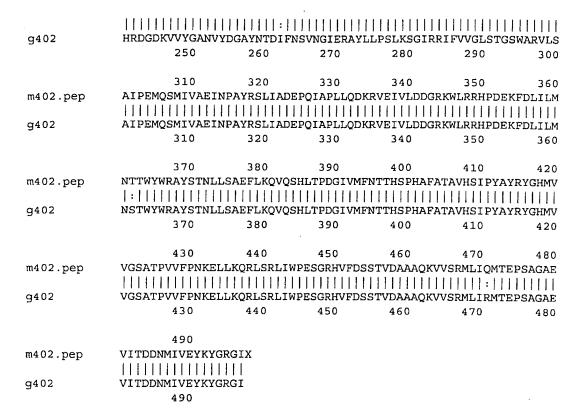
- 1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL
 51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
 101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
 151 GSALGPVLIG FVILDFLSTQ QIYLLICXIS AAVPLFCTLF QKSLRLNAVS
 201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVVYG
 251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFVVGL STGSWARVLS
 301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
 351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
 401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
- 451 VFDSSTVDAA AQKVVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*
 Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae:*

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIY	MXSFLSGLLS	LGIEVLWVRM	IFSFAAQSVPQ	AFSFTLACFI	TGIAVG
		:		111111111		
g402		MLSFLTGLLS	LGIEVLWVRM	IFSFAAQSVPQ	AFSFILACFI	TGIAVG
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVD	IPFIGOCFLW.	AGIADFLILG	AAWLLTGFSG	FVHHAGIFI	rLSAVVX
			1111111111	111111111		
g402	AYFGKRICRSRFVD			AAWLLTGFSG	FVHHAGIFI7	rlsavvr
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTDG	NKSGRQVSNV	YFAXVAGSAL	GPVLIGFVIL	DFLSTQQIYI	LICXIS
			111 111111		1:1111111	
g402	GLIFPLVHHVGTDG		YFANVAGSAL	GPVLIGFVIL	DLLSTQQIYI	LICLIS
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSL	RLNAVSVAVS	LMFGILMFLL	PDSVFQNIAD:	RPDRLIENKE	IGIVAVY
			!			
g402	AAVPLFCTLFQKSL	RLNAVSVAVS:	LMFGILMFLL	PDSVFQNIAG:	RPDRLIENKE	IGIVAVY
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVVYGANVYI	OGAYNTDVFN:	SVNGIERAYL	LPSLKSGIRR:	I FVVGLSTGS	WARVLS



The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1323>:

```
a402.seq
          ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCTTTC
      1
          TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
     51
         TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
     101
         GCCTGTTTTC TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
    151
         TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
     201
          GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTTGACG
     301
          GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
    351
         CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
         GCAACAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTTGCC
    401
         GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
    451
         GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
    501
         CTTTGTTTTG TACACTGTTC CAAAAAAGTC TCCGACTGAA TGCAGTGTCG
    551
         GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCCTAC TGCCGGATTC
         TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
    701
         ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
         GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
    801
         CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
         GCATTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
    851
         GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
    951
         CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
         AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
         CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
         TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTTAAAA CAGGTGCAAA
         GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
         CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
   1201
   1251
         GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCCT AATAAAGAAC
   1301
         TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
   1351
         GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
         TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
   1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA
```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

¹ MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

51 101 151 201 251 301 351 401 451	ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT GFSGFVHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVVYG ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFVVGL STGSWARVLS AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH VFDSSTVDAA AQKVVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*	
m402/a402 99	0.0% identity in 497 aa overlap	
m402.pep	10 20 30 40 50 60 MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPQAFSFTLACFLTGIAVG	;
a402		į
a402	10 20 30 40 50 60	
	70 80 90 100 110 120	
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX	
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR 70 80 90 100 110 120	
m402.pep	130 140 150 160 170 180 XLIFPLVHHVGTDGNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS	
_		
a402	130 140 150 160 170 180	
	190 200 210 220 230 240	
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY	
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY	•
	190 200 210 220 230 240	
m402.pep	250 260 270 280 290 300 HRDGDKVVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKSGIRRIFVVGLSTGSWARVLS	
a402	250 260 270 280 290 300	
	310 320 330 340 350 360	
m402.pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM	i
a402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM	Ī
	310 320 330 340 350 360	
m402.pep	370 380 390 400 410 420 NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV	
a402	370 380 390 400 410 420	
	430 440 450 460 470 480	
m402.pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAAAQKVVSRMLIQMTEPSAGAE	
a402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAAAQKVVSRMLIQMTEPSAGAE	2
	430 440 450 460 470 480	,
m402.pep	490 VITDDNMIVEYKYGRGIX	
	11111111111111111	
a402	VITDDNMIVEYKYGRGIX 490	

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1325>:
g406.seq
```

```
ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
 1
    CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
51
    TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
    GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC AACATAGACA
951 AGGGCAACCT TGA
```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>: g406.pep

```
MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
 51 DMDLQALHGR KVALYIATMG DQGSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
    IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
    AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGQP *
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1327>: m406.seq

```
ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51 CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
    GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
    CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
    TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
    GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
    TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
    CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
    AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCGAC AACATAGACA
901
    AGGACAACCT TGA
```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>: m406.pep

MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK

WO 99/57280

729

```
51 DMDLOALHGR KVALYIATMG DQGSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
```

251 AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN

301 SHEGYGYSDE VVRQHRQGQP *

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. meningitidis menA with menB ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from N. gonorrhoeae: g406/m406

g406.pep	10 MRARLLIPILFSVF	20 ILSACGTLTO	30 SIPSHGGGKRF	40 AVEQELVAAS	50 SARAAVKDMDI	60 LQALHGR
m406	: MQARLLIPILFSVF		 SIPSHGGGKRF		 GARAAVKDMDI	
	10	20	30	40	50	60
g406.pep	70 KVALYIATMGDQGS0	80 SSLTGGRYSI	90 DALIRGEYIN	100 SPAVRTDYTY	110 PRYETTAETT	120 TSGGLTG
m406	KVALYIATMGDQGS					
	70	80 140	90 150	160	110 170	120
g406.pep	130 LTTSLSTLNAPALS		RSSLGLNIGGM			
m406	LTTSLSTLNAPALS			GDYRNETLTT	NPRDTAFLSH	
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANAD					
m406	FLRGIDVVSPANAD	rdvfinidvr 200	GTIRNRTEMH	LYNAETLKAQ 220	TKLEYFAVDR	
	250	260	270	280	290	300
g406.pep		1YALWMGPYK 	CVSKGIKPTEG	LMVDFSDIQP 	YGNHTGNSAF	SVEADN
m406	IKPKTNAFEAAYKEN 250	YALWMGPYK 260	VSKGIKPTEG 270	LMVDFSDIRP 280	YGNHTGNSAF 290	SVEADN 300
	310	320				
g406.pep						
m406	SHEGYGYSDEVVRQF 310	320		•		

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1329>: a406.seq

```
1
    ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
    CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
```

WO 99/57280 PCT/US99/09346

730

```
CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
         501
             GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
             ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
             TGCCGAAACA CTGAAAGCCC AAACAAAACT GGAATATTTC GCAGTAGACA
             GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
         701
         751
            GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
            AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTTCTCC GATATCCAAC
             CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
         901
             AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC GACATAGACA
         951
             AGGGCAACCT TGA
This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:
    a406.pep
             MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
             DMDLOALHGR KVALYIATMG DQGSGSLTGG RYSIDALIRG EYINSPAVRT
          51
        101
             DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
             IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
             IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
             AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
         251
             SHEGYGYSDE AVRRHRQGQP *
         301
                98.8% identity in 320 aa overlap
    m406/a406
                                        30
                                                 40
                                                          50
                                                                   60
                MOARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEOELVAASARAAVKDMDLOALHGR
    m406.pep
                a406
                MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR
                       10
                                20
                                        30
                                                 40
                                                          50
                       70
                                        90
                                80
                                                100
                                                         110
                                                                  120
    m406.pep
                KVALYIATMGDQGSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG
                KVALYIATMGDQGSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG
    a406
                       70
                                80
                                        90
                                                100
                                                                  120
                                                         110
                      130
                               140
                                       150
                                                160
                                                         170
    m406.pep
                LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF
                \verb|LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTTNPRDTAFLSHLVQTVF|
    a406
                                       150
                      130
                               140
                                                160
                                                         170
                                                                  180
                      190
                               200
                                       210
                                                220
                                                         230
                                                                  240
    m406.pep
                FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
                FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
    a406
                      190
                               200
                                       210
                                                220
                                                         230
                                                                  240
                               260
                                       270
                                                280
                                                         290
                                                                  300
    m406.pep
                IKPKTNAFEAAYKENYALWMGPYKVSKGIKPTEGLMVDFSDIRPYGNHTGNSAPSVEADN
                a406
                IKPKTNAFEAAYKENYALWMGPYKVSKGIKPTEGLMVDFSDIQPYGNHMGNSAPSVEADN
                      250
                               260
                                       270
                                                280
                                                         290
                      310
               SHEGYGYSDEVVRQHRQGQPX
    m406.pep
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 1331>: g501.seq

320

SHEGYGYSDEAVRRHRQGQPX

310

a406

¹ atggtcggac ggaccttgac cgcaqatacc qacatatttq ttctqcttqc,

ggcaggcgga gatggcaaga tgcagcatca ctttgacggc agggttgcgt

WO 99/57280

```
togtcaaacg attoggacac caagecgetg totoggtcga ggccgagggt
 101
      caqctqqqtc atqtcqttcg agccgatgga gaagccgtcg aagtattgca
      qqaattqttc cqccaatacc gcgttgctcg gcagctcgca catcataatc
 251
      aggegeagge egittitgee gegitteeaag eegittiett teaatgeett
 301
      aaccactgct teggettege ceaaagtgeg gaegaaegga atcatgattt
      cgacgttggt cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
 351
 401
      tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
      acggaagece aacategggt tttcttcatg eggttegtat acgetgeege
 451
     cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
 501
 551 gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
 601 tttatcgacg tagaagtcga caggggatgc gtaaccggcg atgcggcgga
 651 taatttccgc tttcagttcg tcgtcttgtt tgtcaaattc caacaaggct
701 ttcgggtgga tgccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801 tqccgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851 gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccggt
901 ategeetteg geacaggata eggtaactte etgacegttt tecaagagtt
 951 eggtegeatt geegeageeg aegaeggeag gaataceeag ttegegegeg
1001 atqatqqcqq cqtqqcaggt gcqtccqccq cqgttqqtca cqatqqcqqa
1051 agcacqtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacca
1101 qtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgcacaa
1201 gacggttttt tegecgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttqqqa tttqacqqtt tcqqqqqqqq cttqcaqqat qtaqaqtttq
1301 ccqtccaqqc cqtcqcqtcc ccattcqata tccatcggqc ggccqtaqtq
     tttttcqatg gtcagcgcgt agtgtgccaa ctcggtgatt tcttcgtcgg
     taatqqaqaa geggttgegg tettettegg ggaettegae gttggttace
1451 gatttgeegg etteggettt gteggtgaaa ateattttga tgtgtttega
     acceatggte ttgcgcagga tggcgggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtac gacgttttcg
1601 cccaqaccqt aagaggaggt aacaaagacg acttggttgt agccggattc
     ggtgtcgagg gtgaacatca cacctga
```

731

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

```
q501.pep
1
     MVGRTLTADT DIFVLLAAGG DGKMQHHFDG RVAFVKRFGH QAAVSVEAEG
51
    OLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
    NHCFGFAOSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAOHRVFFM RFVYAAADOV GVFVGFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLFVKF QQGFRVDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGNF LTVFQEFGRI AAADDGRNTQ FARDDGGVAG ASAAVGHDGG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHLALTD FLTDGTTFAQ
401 DGFFAVDGVA AQVAAAFFLG FDGFGAGLQD VEFAVQAVAS PFDIHRAAVV
451 FFDGORVVCO LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
    THGLAODGGF ACFERGFEHI KFVRVDRALY DVFAQTVRGG NKDDLVVAGF
    GVEGEHHT*
551
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1333>: m501.seq

```
atggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51
    ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
    tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgagggt
151 cagttgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggcttt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggy caaccccatt tcatcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451
    acggaagccc aacatcgggt tttcttcatg cggttcgtat acgttqccqc
    cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
501
    gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
551
    tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
    taatttccgc ttttaattcg tcgtcttgtt tgtcaaattc caacaargct
```

```
701
      ttggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
      gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
 751
      tgccgacgtt catcatgact tttacaggtg ctttaggcat attgtctaag
 801
      gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
 851
 901 ategeetteg geacaggata eggtaactte ttgacegttt tteageaatt
 951 cggttgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgccg cggttggtaa cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaagcg gcgcaggttg cggttgccct
1251 cttcttggga tttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa ctcagtaatt tcttcgtcgg
1401 taatggagaa geggttgegg tetteetegg ggacategae gttggttacq
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatggtt ttacgcagga tggcgggctt gcccgytttg agcgtgggtt
1551
     tgaacacatr aaattcgtcc gggttgaccg caccttgtac gacgttttcg
      cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1601
      ggtgtcgagg gtgaacatca cacctga
1651
```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

m501.pep

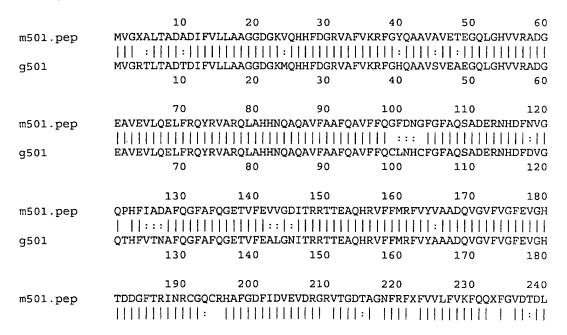
```
MVGXALTADA DIFVLLAAGG DGKVQHHFDG RVAFVKRFGY QAAVAVETEG
 1
    QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
    DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
    TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLFVKF QQXFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301
    IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
    STFHHGFPIR IGHVGNEYVA GFDGIHLGSI FNQAHLALTD FLTDGAAFAX
    YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFAVQAVAS PFDIHRAAVV
    FFDGQCVMRQ LSNFFVGNGE AVAVFLGDID VGYGFTGFCF VGKNHFDVFX
     THGFTQDGGL ARFERGFEHX KFVRVDRTLY DVFAQTVRGG NKDDLIVXGF
    GVEGEHHT*
551
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from N. gonorrhoeae:

m501/g501



			133			
0501	and other transfer	ID COVECUA FOR		an 1 1 number		
g501	1DDGF1R1R	IRCGKRCHAFGDF	1DVEVDRGCVT	GDAADNFRFQF 220		
	1.2	200	210	220	230	240
	25	0 260	270	280	290	300
m501.pep	AVDDKFHTR	QADAFAGQVGEA	ECEFGIADVHH	DFYRCFRHIVXC		TGIDKAG
					11111111	: 111111
g501		QADAFAGQIGEA				AGIDKAG
	. 25	0 260	270	280	290	300
	31	0 320	330	340	350	360
m501.pep		FLTVFQQFGCIA			VGNDGRSTF	UOC STGFDHH
			: : :		11:11 111	111111
g5 0 1	IAFGTGYGN	FLTVFQEFGRIA	AADDGRNTQFAF	RDDGGVAGASAA	VGHDGGSTF	HHGFPIR
	31	0 320	330	340	350	360
	37	0 380	390	400		
m501.pep		AGFDGIHLGSIF		400	410	420
					AVDGEAAQVA	
g501	IGHVGNOYV	AGFDGIHLGSIF	TITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TICTTEACDGEE	1111	ן: :
3 * *	37		390	400	410	420
				100	110	.120
	430		450	460	470	480
m501.pep	FYGFGTGLQI	OVEFAVQAVASPI	FDIHRAAVVFFD	GQCVMRQLSNF	FVGNGEAVA	FLGDID
				11 1: 11::1		1:11:1
g501		OVEFAVQAVASPI	FDIHRAAVVFFD	GQRVVCQLGDF	FVGNGEAVA	FFGDFD
	430	440	450	460	470	480
	490	500	510			
m501.pep			510	520	530	540
msor.pep	VGIGFIGFCI	FVGKNHFDVFXT1 	IGFIQDGGLARF	ERGFEHXKFVR	VDRTLYDVFA	QTVRGG
g501	VGYRFAGFGF	VGENHFDVFRT	:: :	FECERATERIO	:	
300 -	490		510	520	VDKALIDVFA 530	QTVRGG 540
			310	320	330	340
	550)				
m501.pep	NKDDLIVXGF	GVEGEHHT				
g501	NKDDLVVAGE					
	550	1				
following ==	etial DNIA ac-				one ==	
ionowing pa	rtial DNA sequ	uence was ide	intified in N.	meningitidis	<seq id<="" td=""><td>1335>:</td></seq>	1335>:
a501.seq						
1	ATGGTCGGAC	GGGCCTTGAC	CGCAGATGCC	GACATATTT	G TTCTGC	rtgc
51	GGCAGGCGGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGG	C AGGGTT	GCGT
101	TCGTCAAACG					GGGT
151	$C\Delta GTTGGGTC$	Δ TCTCCTTCC	እርርርር እጥርር እ	CNNCCCCMC	~ nnamme	000

The fo

```
CAGTTGGGTC ATGTCGTTCG AGCCGATGGA GAAGCCGTCG AAGTATTGCA
151
    GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAATC
251 AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301 GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
    CAACGTTGGT CAACCCCATT TCATCGCGGA CGCGTTTCAA GGCTTTGCAT
351
401
     TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGCACC
    ACGGAAGCCC AACATCGGGT TTTCTTCATG CGGTTCGTAT ACGTTGCCGC
451
    CGACCAGGTT GGCGTATTCG TTGGATTTGA AGTCGGACAT ACGGACGATG
501
    GTTTTACGCG GATAAACCGA TGCGGCCAAT GTCGCCACGC CTTCGGCGAT
551
601
     TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651
     TAATTTCCGC TTTTAATTCG TCGTCTTGTT TGTCAAATTC CAACAAGGCT
701
    TTGGGGTGGA TACCGATTTG GCGGTTGATG ATAAATTCCA TACGCGCCAA
751
    GCCGATGCCT TCGCTGGGCA GGTTGGCGAA GCTGAATGCG AGTTCGGGAT
801
    TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCCAAA
851
    GCAACATCGG TAATTTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901 ATCGCCTTCG GCACAGGATA CGGTAACTTC TTGACCGTTT TTCAGCAATT
951 CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG
```

340

350

360

1001	ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA	
1051	AGCGCGTTTC ATCACCGGTT CCCAATCTGG GTCGGTCATG TCGGTAACCA	
1101	GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG	
1151	CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTCGCACAA	
1201	GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT	
1251	CTTCCTGGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG	
1301	CCCTCCAACC CCTCCCCTCC CCATTCCAACA TOCATCCAGCAT GTAGAGTTTG	
1351	CCGTCCAAGC CGTCGCGTCC CCATTCGATG TCCATCGGGC GGCCGTAGTG	
1401	TTTTTCGATG GTCAGTGCGT AATGCGCCAA CTCGGTGATT TCTTCGTCGG	
1451	TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC	
	GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA	
1501	GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT	
1551	TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGTAC GACGTTTTCG	
1601	CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTCGT AACCGGATTC	
1651	GGTATCGAGG GTGAACATCA C	
ent :		
	to the amino acid sequence <seq 1336;="" 501.a="" id="" orf="">:</seq>	
a501.pep		
1	MVGRALTADA DIFVLLAAGG DGKVQHHFDG RVAFVKRFGY QAAVAVETEG	
51	QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF	
101	DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT	
151	TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD	
201	FIDVEVDRGR VTGDTAGNFR F*FVVLFVKF QQGFGVDTDL AVDDKFHTRQ	
251	ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQQAGVDEAG	
301	IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHDGG	
351	CAFHUDEDIW VCUVCNOVVA CEDCIULOGI ENOLVIALED EXERCICA	
401	SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ	
451	DGFFAVDRKA AQVAAAFFLG FDGFGTGLQD VEFAVQAVAS PFDVHRAAVV	
	FFDGQCVMRQ LGDFFVGNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*	
501	AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVVTGF	
551	GIEGEHH	
#044 #04 00	****	
m501/a501 90.3	3% identity in 557 aa overlap	
	10 20 30 40 50 60	
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG	
a501	MYCDAL TADADI FINI I A CODONIONI POR DELLA DI CONTROLLA D	
4501	MVGRALTADADIFVLLAAGGDGKVQHHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG 10 20 30 40 50 60	
	10 20 30 40 50 60	
	70 80 90 100 110 120	
m501.pep	EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFDNGFGFAQSADERNHDFNVG	
a501		
4001	70 80 90 100 110 120	
	130 140 150 160 170 180	
m501.pep	QPHFIADAFQGFAFQGETVFEVVGDITRRTTEAQHRVFFMRFVYVAADQVGVFVGFEVGH	
a501		
4001	130 140 150 160 170 180	
	100	
	190 200 210 220 230 240	
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLFVKFQQXFGVDTDL	
a501		
4301	190 200 210 220 230 240	
	230 240	
	250 260 270 280 290 300	
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIGNLYVOOTGIDKAG	
a501	ANDDE FUTPOADA FACOVO PARCEPOLA DALLA DEL CONTROLLO DE LA CONTRA DEL CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DEL CONTRA DE LA CONTRA DEL CONTRA	
a301	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQQAGVDEAG 250 260 270 280 290 300	
	250 260 270 280 290 300	
	310 320 330 340 350 360	
m501.pep	IAFGTGYGNFLTVFQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR	
a501		
#201	TAT STOTEMENT OF VERVE GULAAADNGKNTUFAKUDGGVAGTSAPVGHDGGSAFHHRFPTW	
	310 320 330 340 350 360	

```
370
                         380
                                 390
                                          400
                                                          420
           IGHVGNEYVAGFDGIHLGSIFNQAHLALTDFLTDGAAFAXYGFVAVDGEAAQVAVALFLG
m501.pep
           VGHVGNQYVAGFDGIHLGSIFNQAYLALTDFLTDGAAFAQDGFFAVDRKAAQVAAAFFLG
a501
                         380
                                         400
                                 390
                                                  410
                 430
                         440
                                 450
                                         460
                                                  470
           {\tt FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGQCVMRQLSNFFVGNGEAVAVFLGDID}
m501.pep
           FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGQCVMRQLGDFFVGNGEAVAVFFGDID
a501
                 430
                         440
                                 450
                                                  470
                490
                         500
                                 510
                                         520
           VGYGFTGFCFVGKNHFDVFXTHGFTQDGGLARFERGFEHXKFVRVDRTLYDVFAQTVRGG
m501.pep
           a501
           VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFEHIEFVGIDCALYDVFAQTVGXS
                         500
                                 510
                                         520
                                                 530
                550
                        559
m501.pep
           NKDDLIVXGFGVEGEHHTX
           : [ ] [ ] : [ : [ ] ] : [ ] ] [ ]
a501
           DKDDLVVTGFGIEGEHH
                550
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1337>:

```
1 atgatgaaac cgcacaacct gttccaattc ctcgccgttt gctccctgac
51 cgtcgccgtc gcttccgcac aggcgggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcggca gcttcaacca aaccgtccaa
151 agcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcggcgc agccccgccg ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg cccaaacgca acaacgccgg
451 ctaccaatac atccgcatcg gcttcaaagg cggcaacctc gccgccatgc
501 agcttaa
```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>: 9502.pep

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ 51 SKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT

101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RGNAQTQQRR

151 LPIHPHRLQR RQPRRHAA*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1339>: m502.seq

atgatgaaac cgcacaacct gttccaattc ctcgccgttt gctccctgac 1 51 cgtcgccgtc gcttccgcac aggcgggcgc ggtagacgcg cttaagcaat 101 tcaacaacga tgccgacggt atcagcggca gcttcaccca amccqtccaa wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgacc 151 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgtcg 201 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc 251 301 aagtcgtccc aagaccaggc cataggcgsc agccccgccg ccatcctgtc gaacaaarcc gccctcgaaa gcagctacac gctgaaagag gacggttcgt 351 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgccggcta 401 ccaatacatc cgcatcggct tcaaaggcgg caacctcgcc gccatgcagc 451 501 tyaa

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>: m502.pep

- 1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
- 51 XKKKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
- 101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQQRRL
- 151 PIHPHRLQRR QPRRHAAX

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from N. gonorrhoeae: m502/g502 10 30 20 40 MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVOXKKKTOTAHG m502.pep g502 MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG 10 20 30 40 50 60 70 80 90 100 110 120 TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX m502.pep TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT q502 70 80 90 100 110 120 130 140 150 160 m502.pep ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA q502 ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRROPRRHAA 130 140 150 160 The following partial DNA sequence was identified in N. meningitidis <SEO ID 1341>: a502.seq ATGATGAAAC CGCACAACCT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC 1 51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA 101 AGCAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC 201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTTGGC ACAAGTGACC 251 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC 301 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT 351 CCAACGCAT CGATTATGTG GGCAACGCCC AAACGCAACA ACGCCGGCTA CCAATACATC CGCATCGGCT TCAAAGGCGG CAACCTCGCC GCCATGCAGC 501 TTAA This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>: 1 MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTOTVO SKKKTQTAHG TFKILRPGLF KWEYTSPYKQ TIVGDGQTVW LYDVDLAQVT 51 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV GNAOTOORRL 101 151 PIHPHRLQRR QPRRHAA* m502/a502 95.2% identity in 167 aa overlap 10 20 30 40 50 60 ${\tt MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG}$ m502.pep ${\tt MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG}$ a502 10 20 30 40 50 60 70 80 90 100 110 120 TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX m502.pep

a502	TFKILRPGLFKWE	YTSPYKQTIV	GDGQTVWLYD	VDLAQVTKSS(QDQAIGGSPA	AILSNKT
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGS	SNGIDYVGNA	QTQQRRLPIH	PHRLQRRQPRI	RHAAX	
a502	ALESSYTLKEDGS	SNGIDYVGNA	QTQQRRLPIHI	PHRLQRRQPR	RHAAX	
	130	140	150	160		

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```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1343>:
g502-1.seq
```

```
1 ATGATGAAAc cgcaCaacct gttccaaTTc CTCGCCGTTT GCTCCCTGAC
    CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
 51
    TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
101
151 AGCAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATTTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGCCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
    TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GGCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
    GGCGTGGACG TGTTGAGCAA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>: g502-1.pep

- MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ 1
- 51 SKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
- 101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
- YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
- 201 GVDVLSN*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1345>: m502-1.seq

```
1 ATGATGAAAC CGCACAACCT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTAGACGCG CTTAAGCAAT
    TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
    AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
    TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GGCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GGCGTGGACG TGTTGAGCAA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>: m502-1.pep

- 1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
- 51 SKKKTQTAHG TFKILRPGLF KWEYTKPYRQ TIVGDGQTVW LYDVDLAQVT
- 101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
- YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK 151
- 201 GVDVLSN*

m502-1/q502-1 99.0% identity in 207 aa overlap

m502-1.pep	10 MMKPHNLFQFLAVCS	20 LTVAVASA(30 QAGAVDALKQFI	40 NNDADGISGS	50 FTQTVQSKKI	60 TQTAHG
g502-1	MMKPHNLFQFLAVCS	LTVAVASA	QAGAVDALKQFI	NNDADGISGS	FTQTVQSKK	TQTAHG
	10	20	30	40	50	60
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYT	KPYRQTIVO	GDGQTVWLYDVI	DLAQVTKSSQ	DQAIGGSPA	ILSNKT
	1111111111111111	41111111		111111111	1111111111	111111
g502-1	TFKILRPGLFKWEYT	LPYRQTIVO	GDGQTVWLYDVI	OLAQVTKSSQ	DQAIGGSPA	ILSNKT
-	70	80	90	100	110	120
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNO	SIDYVLATI	PKRNNAGYQYI	RIGFKGGNLA	AMQLKDSFGN	QTSISF
		[14] [4]	111111111111		T11111111	111111
g502-1	ALESSYTLKEDGSSNO	SIDYVRATE	KRNNAGYQYI	RIGFKGGNLA	AMQLKDSFGN	QTSISF
	130	140	150	160	170	180

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200 190 GGLNTNPQLSRGAFKFTPPKGVDVLSNX m502-1.pep

GGLNTNPQLSRGAFKFTPPKGVDVLSNX a502-1 200 190

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1347>: a502-1.seq

- ATGATGAAAC CGCACAACCT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC 1
- CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT 51
- 101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
- 151 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
- 251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTTGGC ACAAGTGACC
- AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC 301
- 351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
- CCAACGCAT CGATTATGTG CTGGCAACGC .CCAAACGCAA CAACGCCGGC 401
- TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GGCGGTTTGA
- 501
- ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
- GGCGTGGACG TGTTGAGCAA CTGA

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>: a502-1.pep

- MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
- SKKKTOTAHG TFKILRPGLF KWEYTSPYKO TIVGDGQTVW LYDVDLAQVT 51
- KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG 101
- YOYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
- 201 GVDVLSN*

98.6% identity in 207 aa overlap a502-1/m502-1

30 ${\tt MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG}$ a502-1.pep ${\tt MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG}$ m502 - 120 30 40 50 100 110 120 70 80 90 TFKILRPGLFKWEYTSPYKQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT a502-1.pep

m502-1 TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT 90 100 110 120 70 80

140 150 160 ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF a502-1.pep

m502-1ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF 130 140 150 160

> 190 200

GGLNTNPOLSRGAFKFTPPKGVDVLSNX a502-1.pep

GGLNTNPQLSRGAFKFTPPKGVDVLSNX m502-1 200 190

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1349>:

q503.seq

- atgtccgcgc cgtcggcatc ggtaatcatt ttgttccatg ccgcttcgat
- 51 ttcqqcatcq agctqttcgg ggaagggcgt gtccaaaatc cattggcgga
- 101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
- 151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
- 201 gcggtag

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

- g503.pep
 - MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSTSNF 1
 - ARAAEMRSFR PLCARNAR* 51

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1351>:

```
m503.seq
                atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat
            51 ttcggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga
           101 tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
               gccagtgcgg cggaaatgcg ttcgctcaga ccgttgtgtg cgaggaatgc
           201
               gcggtag
 This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:
      m503.pep
               MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
               ASAAEMRSLR PLCARNAR*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng)
from N. gonorrhoeae:
     m503/g503
                          10
                                    20
                                              30
                                                       40
                                                                 50
                                                                           60
                  MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLR
     m503.pep
                  MSAPSASVIILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSTSNFARAAEMRSFR
     q503
                          10
                                             30
                                                       40
                                                                 50
                         69
     m503.pep
                  PLCARNAR
                  1111111
     a503
                  PLCARNAR
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1353>:
     a503.seq
               ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCCATG CCGCTTCGAT
           51
              TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
          101 TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
          151 GCCAGTGCGG CGGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC
          201 GCGGTAG
This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:
     a503.pep
               MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
            1
           51
              ASAAEMRSLR PLCARNAR*
           100.0% identity in 68 aa overlap
m503/a503
                          10
                                   20
                                             30
                                                       40
                                                                50
                  MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLR
     m503.pep
                  MSAPPASATILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLR
     a503
                         10
                                   20
                                             30
                                                                50
                        69
     m503.pep
                  PLCARNARX
                  11111111
     a503
                  PLCARNARX
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1355>:
g503-1.seq
     1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
     51 AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
        ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
```

151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTTGTTCC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301 TTTGCCAGAG CGGCGGAAAT GCGTTCGTTC AGACCGTTGT GTGCGAGAAA

351 TGCGCGGTAG

a503-1.pep

m503-1

This corresponds to the amino acid sequence <SEO ID 1356; ORF 214.ng>: g503-1.pep 1 MARSLYREAK TWRIAFLTLS KPLIFRKVSC WPANDASGRS SAVAEERTAT 51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSETSSTSN 101 FARAAEMRSF RPLCARNAR* The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1357>: m503-1.seq 1 ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT AACGTTATCC AAGCCGTTGA TGTTCAAGAA GGTTTCCTGT TGTCCAGCGA 51 101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTTGTTCC ATGCCGCTTC 201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC 251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA 301 351 TGCGCGGTAG This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>: m503-1.pep 1 MARSLYREAN TWCIASLTLS KPLMFKKVSC CPANDASGRS SAVAEERTAT EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN 51 FASAAEMRSL RPLCARNAR* g503-1 / m503-1 89.9% identity in 119 aa overlap 20 30 40 MARSLYREAKTWRIAFLTLSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPSASVI g503-1.pep MARSLYREANTWCIASLTLSKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT m503-120 30 40 70 80 90 100 110 120 g503-1.pep ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSTSNFARAAEMRSFRPLCARNARX ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX m503-170 80 100 110 120 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1359>: a503-1.seq 1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT 51 AACGTTTTCC AAGCCGTTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA 101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTTGTTCC ATGCCGCTTC 201 GATTTCGGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA TGCGCGGTAG 351 This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>: a503-1.pep 1 MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT 51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN FASAAEMRSL RPLCARNAR* a503-1 / m503-1 95.8% identity in 119 aa overlap 20 10 30 40 50 a503-1.pep MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT m503-1MARSLYREANTWCIASLTLSKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT 10 20 30 40 50 60 80 90 100

> ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX

> ILFHAASISASSCSGKGVSKIHWRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX 90

100

110

120

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741
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1361>:
      q504.seq
               atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
             1
           51
               cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
           101 taacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
           151 catcetttga cettgeacgg catcacgatt tatcaggega gttttgeega
           201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
          251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttggaa
          301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
          351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
          401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
          451 atcggccctt ccatcgtgta ccgcatccgt gatgcggcag ggcaggcggt
          501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattatttt
          551 ggctgaccgg cacgcgcagc ggcttgcagc agcaataccg ctggctgcgt
          601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
          651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
          701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
          751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
          801 tacgtccaat atcccgaaag ggcagcagga taagatgcag ggctatttct
          851 acgaaatgct ttacggcgtg atgaacgctg ctttggatga aaccatacqc
          901 cggtacggct tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
          951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
               tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
         1051 atgacccgtt cgccgggtgc gcttttggtc tatctcggct cggtattgtt
         1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
         1151 tattgttttc aaacdgcaaa atccgttttg ctatgtcttc ggcccgcagc
         1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcctgcaacg
         1251
               gctcggcaag gacttgaatc atgactga
This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:
     g504.pep
               MLVQDLPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
               HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQFPLE
               IGKHKYRLEF DQFTSMNVED MSEGAEREKS LKSTLNDVRA VTQEGKKYTN
          101
               IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
          151
          201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAAEN
          251 TLNIFAQKGY LGLDEFITSN IPKGQQDKMQ GYFYEMLYGV MNAALDETIR
          301 RYGLPEWQQD EARNRFLLHS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
          351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFSNKI RFAMSSARSE
          401 RDLQKEFPKH VESLQRLGKD LNHD*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1363>:
     m504.seg..
            1 atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
           51 cgatttttac aatacgggta tgccgcgtga tttcgccagc gatattgaag
          101 tgacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
          151 catcetttga cettgeacgg catcacgatt tatcaggega gttttgeega
          201 cggcggttcg gatttgacat tcaaggcgtg gaatttgggt gatgcttcgc
          251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttggaa
          301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
          351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
          401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
          451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggt
          501 cgaatataaa aactatatgc tgccggtttt gcaggaacag gattattttt
```

551 ggattaccgg cacgcgcagc ggcttgcagc agcaataccg ctggctgcgt 601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga 651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac 701 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat 751 801 tacgtccaat atcccgaaag agcagcagga taagatgcag ggctatttct 851 acgaaatgct ttacggcgtg atgaacgctg ctttggatga aaccatacgc 901 cggtacggct tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct 951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta 1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgtc gggtttgcag

1051 atgacccgtt ccccgggtgc gcttttggtc tatctcggct cggtgctgtt 1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg 1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgcagc 1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg 1251 gctcggcaag gacttgaatc atga

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..

1 ILVQDLPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAEREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLLHS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae:*

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPFEVKLKKF	HIDFYNTGM	PRDFASDIEV'	TDKATGEKLE	RTIRVNHPLT	FLHGITI
	:			11111111		
g504	MLVQDLPFEVKLKKF					
	10	20	30	40	50	60
	50					
504	70	80	90	100	110	120
m504.pep	YQASFADGGSDLTFK	AWNLGDASK	EPVVLKATSI	HÖRRPETGKH	KYRLEFDQFI	SMNVED
~504	VON CENDOCCODI TEM					
g504	YQASFADGGSDLTFK 70	AWNLKDASK 80	90	HQFPLEIGKH 100	IKYRLEFDQFT 110	
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAEREKSLKSTL					
g504	MSEGAEREKSLKSTL					
3	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRSGLQQQ	YRWLRIPLD	KQLKADTFMAI	LREFLKDGEG	RKRLVADATK	GAPAEI
		11111111			<u> </u>	
g504	DYFWLTGTRSGLQQQ					DAPAEI
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIF.	AQKGYLGLD.	EFITSNIPKE(QOKMQGYFY	EMLYGVMNAA	LDETIR
~F.0.4	DECEMBARMENTE	AOVOVI GI D			THE WOLDOWS	
g504	REQFMLAAENTLNIF.	260	270	280 280	EMLYGVMNAA 290	
	250	200	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNR					
					1111111111	IIIIII
g504	RYGLPEWQQDEARNR	FLLHSMDAY'	TGLTEYPAPMI	LOLDGESEV		DCDLLU
3041	310	320	330	340	350	360
					550	200
	. 370	380	390	400	410	420
m504.pep	YLGSVLLVLGTVLMF	YVREKRAWVI				
				111111111		

YLGSVLLVLGTVFMFYVPKKRAWVLFSN-KIRFAMSSARSERDLOKEFPKHVESLORLGK

```
g504
                                  380
                                            390
                                                      400
                 DLNHD
     m504.pep
                 11111
                 DLNHD
     g504
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1365>:
     a504.seq
              ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAACTGAAAA AATTCCATAT
           51
              CGATTTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
              TAACGGATAA GGCAACCGGT GAGAAACTCG AGCGCACCAT CCGCGTGAAC
          101
              CATCCTTTGA CCTTGCACGG CATCACGATT TATCAGGCGA GTTTTGCCGA
          201 CGGCGGTTCG GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
          251 GCGAGCCTGT CGTGTTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
          301 ATTGGCAAAC ACAAATATCG TCTTGAGTTC GATCAGTTTA CTTCTATGAA
              TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAAGC CTGAAATCCA
              CGCTGAACGA TGTCCGCGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT
              ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT
          451
              CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
          501
          551 GGATTACCGG CACGCGCAGC GGCTTGCAGC AGCAATACCG CTGGCTGCGT
          601 ATCCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
          651 GTTTTTGAAA GATGGGGAAG GGCGCAAACG TCTGGTTGCC GACGCAACCA
          701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TGCGGAAAAC
          751 ACGCTGAACA TCTTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
          801 TACGTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
         851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC
          901 CGGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT
          951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
         1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTTGCAG
              ATGACCCGTT CCCCGGGTGC GCTTTTGGTC TATCTCGGCT CGGTGCTGTT
         1051
              GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCGAAAAA CGGGCGTGGG
         1101
              TATTGTTTC AGACGGCAAA ATCCGTTTTG CCATGTCTTC GGCCCGCAGC
         1151
              GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
             GCTCGGCAAG GACTTGAATC ATGACTGA
This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:
     a504.pep
              ILVQDLPFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
           51
              HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
              IGKHKYRLEF DQFTSMNVED MSEGAEREKS LKSTLNDVRA VTQEGKKYTN
              IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
              IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
              TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
              RYGLPEWQQD EARNRFLLHS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
         351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
              ERDLOKEFPK HVESLORLGK DLNHD*
m504/a504 99.8% identity in 425 aa overlap
                                            30
                                                      40
                 ILVQDLPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI
     m504.pep
                 a504
                 ILVQDLPFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI
                                   80
                                            90
                                                     100
                 YQASFADGGSDLTFKAWNLGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
     m504.pep
                 YQASFADGGSDLTFKAWNLGDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
     a504
                         70
                                  80
                                            90
                                                     100
                                                              110
                                  140
                                           150
                                                     1.60
                                                              170
```

MSEGAEREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ

m504.pep

a504	
m504.pep	190 200 210 220 230 240 DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
m504.pep	250 260 270 280 290 300 REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
m504.pep	310 320 330 340 350 360 RYGLPEWQQDEARNRFLLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV [
m504.pep	370 380 390 400 410 420 YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
m504.pep	DINHDX DINHDX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1367>: q505.seq

```
atgtttcgtt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
 1
    catcetgttg accecetge teaaatgeet etceetgetg tegettteet
    qtctqcacac qctqqqaaac cqqctcqqac atctqqcqtt ttacctttta
    aaqqaaqacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
    ccccqacacq cagacggtca aagccgtttt tgcggaaacg qcaaaatqcq
    qtttqqaact tqccccqcg tttttcaaaa aaccqqaaqa catcqaaaca
    atqttcaaag cggtacacgg ctgggaacac gtgcagcagg ctttggacaa
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagc tacgatttgg
401 geggacgeta cateageeag eagetteegt teeacetgae egecatgtae
451 aagccgccga aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cgcccaccgg catacaaggg gtcaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaccac
601 gtcccttctc cgcaggaagg cggcggcgtg tgggcggatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tqaaaaccct gtttttctgc tgcgaacgcc tgcccgacgg acaaggcttc
751 gtgttgcaca tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa
```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>: g505.pep

- 1 MFRLQFRLFP PLRTAMHILL TALLKCLSLL SLSCLHTLGN RLGHLAFYLL 51 KEDRARIVAN MRQAGLNPDT QTVKAVFAET AKCGLELAPA FFKKPEDIET 101 MFKAVHGWEH VQQALDKGEG LLFITPHIGS YDLGGRYISQ QLPFHLTAMY
- 151 KPPKIKAIDK IMQAGRVRGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
- 201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDGOGF 251 VLHIRPVQGE LNGNKAHDAA VFNRNTEYWI RRFPTQYLFM YNRYKTP*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1369>:

```
m505.seq
               (partial)
               GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
            1
           51 GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
          101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
          151 TTAAAGGAAG ACCGCGCGC CATCGTCGCC AATATGCGGC AGGCGGGTTT
          201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTTGCGGAA ACGGCAAAAG
          251
              GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
          301
              ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
          351
               CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
          401
               TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
               TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
          451
               GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
          501
          551 AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
          601 ACGTCCCCTC CCCTCAAGAA GGCGGGGAAG GCGTATGGGT GGATTTCTTC
               GGCAAACCTG CCTATACCAT GACGCTGGCG GCAArATTGG CACACGTCAA
          651
              AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAAG
          751 GTTTCGATTT GCACATCCGC CCCGTCCAAG GGGAATTGAA CGGCGACAAA
          801 GCCCATGATG CCGCCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
          851
              TTTTCCGACG CAtATC....
This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:
     m505.pep (partial)
              MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSCLHTLGN RLGHLAFYLL
              KEDRARIVAN MRQAGLNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
```

101 MFKAVHGWEH VQQALDKHEG LLFITPHIGS YDLGGRYISQ QLPFPLTAMY

151 KPPKIKAIDK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH

201 VPSPQEGGEG VWVDFFGKPA YTMTLAAXLA HVKGVKTLFF CCERLPGGQG

251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTHI...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from N. gonorrhoeae:

m505/g505

		10	20	30	40	50	60
m505.pep	MFRLQ:	FRLFPPLRT	TAMHILLTALL	KCLSLLPLSC	LHTLGNRLGH	LAFYLLKED	NAVIRAS
		11111			111111111		
g505	MFRLQ:	FRLFPPLRI	TAMHILLTALL	KCLSLLSLSC	LHTLGNRLGH	LAFYLLKED	RARIVAN
		10	20	30	40	50	60
		70	80 .	90	100	110	120
m505.pep	MRQAG	LNPDPKTV	CAVFAETAKGG	LELAPAFFRK	PEDIETMFKA	VHGWEHVQQA	LDKHEG
		[[]: [[]]		1111111:1			111 11
g505	MRQAGI	LNPDTQTVE	CAVFAETAKCG	LELAPAFFKK	PEDIETMFKA	VHGWEHVOOA	LDKGEG
		70	80	90	100	110	120
		130	140	150	160	170	180
m505.pep	LLFIT	PHIGSYDLO	GRYISQQLPF	PLTAMYKPPK	IKAIDKIMQA	GRVRGKGKTA	PTSIQG
] [] [] [111111111		11111111	$\Pi: \widetilde{\Pi}$
g505	LLFITE	PHIGSYDLO	GRYISQQLPF	HLTAMYKPPK	IKAIDKIMQA	GRVRGKGKTA	PTGIOG
		130	140	150	160	170	180
		190	200	210	220	230	240
m505.pep	VKQIII	KALRSGEAT	IVLPDHVPSP	QEGGEGVWVD	FFGKPAYTMT:	LAAXLAHVKG	VKTLFF
			1:11111111			111 11111	111111
g505	AKĞİİ	(ALRAGEAT		QEGG-GVWAD	FFGKPAYTMT	LAAKLAHVKG	VKTLFF
		190	200	210	220	230	
						•	
		250	260	270	280	289	
m505.pep	CCERLE	GGQGFDLH?			RNAEYWIRRF		
q505	111111			. , , , , , , , , ,		11:	
9505	240	250 250			RNTEYWIRRF		YKTP
	240	250	260	270	280	290	

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1371>: a505.seq

1 ATGITICGIT TACAATICAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCAA
```

1	ATGTTTCGTT	TACAATTCAG	GCTGTTTCCC	CCTTTGCGAA	CCGCCATGCA
51	CATCCTGTTG	ACCGCCCTGC	TCAAATGCCT	CTCCCTGCTG	CCGCTTTCCT
101	GTCTGCACAC	GCTGGGAAAC	CGGCTCGGAC	ATCTGGCGTT	TTACCTTTTA
151	AAGGAAGACC	GCGCGCGCAT	CGTCGCCAAT	ATGCGTCAGG	CAGGCATGAA
201				TGCGGAAACG	
251	GTTTGGAACT	TGCCCCCGCG	TTTTTCAGAA	AACCGGAAGA	CATAGAAACA
301	ATGTTCAAAG	CGGTACACGG	CTGGGAACAT	GTGCAGCAGG	CTTTGGACAA
351	ACACGAAGGG	CTGCTATTCA	TCACGCCGCA	CATCGGCAGC	TACGATTTGG
401	GCGGACGCTA	CATCAGCCAG	CAGCTTCCGT	TCCCGCTGAC	CGCCATGTAC
451	AAACCGCCGA	AAATCAAAGC	GATAGACAAA	ATCATGCAGG	CGGGCAGGGT
501	TCGCGGCAAA	GGAAAAACCG	CGCCTACCAG	CATACAAGGG	GTCAAACAAA
551	TCATCAAAGC	CCTGCGTTCG	GGCGAAGCAA	CCATCGTCCT	GCCCGACCAC
601				GTATGGGTGG	
651	CAAACCTGCC	TATACCATGA	CGCTGGCGGC	AAAATTGGCA	CACGTCAAAG
701	GCGTGAAAAC	CCTGTTTTTC	TGCTGCGAAC	GCCTGCCTGG	CGGACAAGGT
751	TTCGATTTGC	ACATCCGCCC	CGTCCAAGGG	GAATTGAACG	GCGACAAAGC
801	CCATGATGCC	GCCGTGTTCA	ACCGCAATGC	CGAATATTGG	ATACGCCGTT
851	TTCCGACGCA	GTATCTGTTT	ATGTACAACC	GCTACAAAAT	GCCGTAA

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

```
a505.pep
```

1				PLSCLHTLGN	
51	KEDRARIVAN	MRQAGMNPDP	KTVKAVFAET	AKGGLELAPA	FFRKPEDIET
101	MFKAVHGWEH	VQQALDKHEG	LLFITPHIGS	YDLGGRYISQ	QLPFPLTAMY
151	KPPKIKAIDK	IMQAGRVRGK	GKTAPTSIQG	VKQIIKALRS	GEATIVLPDH
201	VPSPQEGGEG	VWVDFFGKPA.	YTMTLAAKLA	HVKGVKTLFF	CCERLPGGQG
251	FDLHIRPVQG	ELNGDKAHDA	AVFNRNAEYW	IRRFPTQYLF	MYNRYKMP*

m505/a505 99.0% identity in 287 aa overlap

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRT	'AMHILLTALI	LKCLSLLPLS	CLHTLGNRLG	HLAFYLLKEDI	RARIVAN
	1111111111111111	3111111111	[[]]			
a505	MFRLQFRLFPPLRT	AMHILLTALI	LKCLSLLPLSO	CLHTLGNRLG	HLAFYLLKEDE	RARIVAN
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVK	AVFAETAKGO	SLELAPAFFRE	(PEDIETMEK)	AVHGWEHVOOR	LDKHEG
	11111:1111111					
a505	MRQAGMNPDPKTVK					
	70	80	90	100	110	120
						120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLG	GRYTSOOLPE	PITAMYKPPK			
a505	LLFITPHIGSYDLG					
	130	140	150	160	170	180
	200	2.0	100	100	170	100
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEAT					
moosipep	[]]]]]]]]]					111111
a505	VKQIIKALRSGEAT					
4400	190	200	210	220	230	240
	130	200	210	220	230	240
	250	260	270	280		
m505.pep						
mouo.pep	CCERLPGGQGFDLH					
-505						
a505	CCERLPGGQGFDLH					YKMPX
	250	260	270	280	290	

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1373>:

```
m505-1.seg
       1 ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
      51 CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
          GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
     101
         AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
     151
         CCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
     201
          GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
     251
     301
          ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
         ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
     351
         GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
     401
         AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
     451
         TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
     501
     551
         TCATCAAAGC CCTGCGTTCG GGCGAAGCAA CCATCGTCCT GCCCGACCAC
         GTCCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
     601
         CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
     651
         GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
         TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
     751
         CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
         TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA
This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:
m505-1.pep
         MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSCLHTLGN RLGHLAFYLL
       1
         KEDRARIVAN MRQAGLNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
      51
     101 MFKAVHGWEH VQQALDKHEG LLFITPHIGS YDLGGRYISO OLPFPLTAMY
     151 KPPKIKAIDK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
         VPSPQEGGEG VWVDFFGKPA YTMTLAAKLA HVKGVKTLFF CCERLPGGQG
         FDLHIRPVOG ELNGDKAHDA AVFNRNAEYW IRRFPTOYLF MYNRYKMP*
m505-1/g505 94.3% identity in 298 aa overlap
                   10
                            20
                                     30
                                              40
                                                       50
            MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN
m505-1.pep
            a505
            {\tt MFRLQFRLFPPLRTAMHILLTALLKCLSLLSLSCLHTLGNRLGHLAFYLLKEDRARIVAN}
                                     30
                                              40
                                                       50
                                                                60
                   70
                            80
                                     90
                                             100
                                                      110
            MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG
m505-1.pep
            MRQAGLNPDTQTVKAVFAETAKCGLELAPAFFKKPEDIETMFKAVHGWEHVQQALDKGEG
g505
                            80
                   70
                                     90
                                             100
                                                      110
                                                               120
                           140
                  130
                                    150
                                             160
                                                      170
                                                               180
m505-1.pep
            LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIDKIMQAGRVRGKGKTAPTSIQG
            a505
            LLFITPHIGSYDLGGRYISQQLPFHLTAMYKPPKIKAIDKIMQAGRVRGKGKTAPTGIQG
                  130
                           140
                                    150
                                             160
                                                      170
                                                               180
                           200
                  190
                                    210
                                             220
                                                      230
                                                               240
            VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
m505-1.pep
            q505
            VKQIIKALRAGEATIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGVKTLFF
                  190
                           200
                                     210
                                              220
                  250
                           260
                                    270
                                             280
                                                      290
            CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
m505-1.pep
            CCERLPDGQGFVLHIRPVQGELNGNKAHDAAVFNRNTEYWIRRFPTQYLFMYNRYKTPX
q505
          240
                   250
                            260
                                     270
                                              280
                                                      290
m505-1/a505
            99.7% identity in 298 aa overlap
                            20
                                     30
                                              40
           MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN
m505-1.pep
            a505
           MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN
                   10
                            20
                                    30
                                             40
                                                      50
                                                               60
                   70
                            80
                                     90
                                             100
                                                      110
                                                              120
```

m505-1.pep	MRQAGLNPDPKTVK	VFAETAKGG	LELAPAFFRK	PEDIETMFKA	VHGWEHVQQ	ALDKHEG
a505	MRQAGMNPDPKTVKA				~~	
	70	80	90	100	110	120
	130	140	150	160	170	180
m505-1.pep	LLFITPHIGSYDLGG	RYISQQLPF	PLTAMYKPPK	IKAIDKIMQA	GRVRGKGKT	APTSIQG
		111111111		11111111	111111111	
a505	LLFITPHIGSYDLGG	RYISQQLPF	PLTAMYKPPK	IKAIDKIMQA	GRVRGKGKT	APTSIQG
	130	140	150	160	170	180
	190	200	210	220	230	240
m505-1.pep	VKOIIKALRSGEATI					
mJUJ-I.pcp	11111111111111111	111111111	1111111111	11111111111		
a505	VKQIIKALRSGEATI	VI.PDHVPSP	OEGGEGAMAD.	FFCKDAYYMY		1111111 2000 T.FF
4505	190	200	210	220	230	240
	2,0	200	220	220	230	210
	250	260	270	280	290	299
m505-1.pep	CCERLPGGQGFDLHI	RPVQGELNG:	DKAHDAAVFN:	RNAEYWIRRF	PTQYLFMYNF	XXWDX
		11111111	111111111	1111111	1111111111	
a505	CCERLPGGQGFDLHI	RPVQGELNG:	DKAHDAAVFN	RNAEYWIRRF	PTQYLFMYNF	XAWAX
	250	260	270	280	290	

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1375>: 9506.seq

```
ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
     TGTCAAACAA AGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAAGGCG
 101 CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
 151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GGCGAAGTCG GGTTGTTGCT
 201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
 251 CCGTCGGCGC GGCCTTGTCC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
 301 CGGACGATTG ACGGGGATTT GGCGGAAGTT CACACCCAAG CGGTAACGTT
 351 GCGCGTCGGC GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
     GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
     ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
     CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
     TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
 601 CGTCCATTC GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT
 651 GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
 701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAATTTCA CCCAAAAACG
 751 TTCGCCCGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
 801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
 851 TGGTGCAGGG CTTCGGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC
 901 GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG TGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGGCGCGC CGTTGTTCAT
1351 GGTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCCTT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTTGGCG
     GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTTGAATCG
     ACATTTTATT TTCCTTTTGC AAAAACTATG GATGCGATTA TACGCCAAGA
     TTTTCGTTAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>: g506.pep

- 1 MAVFDEVGRI AHGCGGVVKQ SLFLRVVHQV EQGARLAEVV VIVLAVVPVC
- 51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
- 101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
- 151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLDVH

g505

240

250

```
m505.seg
               (partial)
              GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
            1
              GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
           51
          101
              CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
          151
              TTAAAGGAAG ACCGCGCGC CATCGTCGCC AATATGCGGC AGGCGGGTTT
          201
              GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTTGCGGAA ACGGCAAAAG
          251
              GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
              ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
          301
              CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
          351
              TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTTCCCGCT GACCGCCATG
          401
              TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
          451
              GGTTCGCGGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
         501
              AAATCATCAA AGCCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
         551
              ACGTCCCCTC CCCTCAAGAA GGCGGGGAAG GCGTATGGGT GGATTTCTTC
         601
              GGCAAACCTG CCTATACCAT GACGCTGGCG GCAArATTGG CACACGTCAA
         651
              AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GGCGGACAAG
         701
              GTTTCGATTT GCACATCCGC CCCGTCCAAG GGGAATTGAA CGGCGACAAA
         751
              GCCCATGATG CCGCCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
         801
         851
              TTTTCCGACG CAtATC....
This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:
     m505.pep
              (partial)
             MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSCLHTLGN RLGHLAFYLL
           1
             KEDRARIVAN MRQAGLNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
          51
             MFKAVHGWEH VQQALDKHEG LLFITPHIGS YDLGGRYISQ QLPFPLTAMY
             KPPKIKAIDK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
              VPSPQEGGEG VWVDFFGKPA YTMTLAAXLA HVKGVKTLFF CCERLPGGQG
             FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTHI...
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng)
from N. gonorrhoeae:
    m505/g505
                                 20
                                          30
                                                   40
                                                             50
                                                                      60
                MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN
    m505.pep
                MFRLQFRLFPPLRTAMHILLTALLKCLSLLSLSCLHTLGNRLGHLAFYLLKEDRARIVAN
    g505
                        10
                                 20
                                          30
                                                   40
                                                            50
                                                                      60
                        70
                                 80
                                          90
                                                  100
                                                           110
                                                                     120
                MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG
    m505.pep
                MRQAGLNPDTQTVKAVFAETAKCGLELAPAFFKKPEDIETMFKAVHGWEHVQQALDKGEG
    g505
                        70
                                 80
                                          90
                                                  100
                                                           110
                                                                     120
                       130
                                140
                                         150
                                                  160
                                                           170
                LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIDKIMQAGRVRGKGKTAPTSIQG
    m505.pep
                LLFITPHIGSYDLGGRYISQQLPFHLTAMYKPPKIKAIDKIMQAGRVRGKGKTAPTGIQG
    9505
                      130
                                140
                                         150
                                                  160
                                                           170
                                                                    180
                      190
                                200
                                         210
                                                  220
                                                           230
    m505.pep
                VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGVKTLFF
                VKQIIKALRAGEATIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGVKTLFF
    g505
                      190
                                200
                                          210
                                                   220
                                                            230
                                260
                                         270
                CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTHI
    m505.pep
```

CCERLPDGQGFVLHIRPVQGELNGNKAHDAAVFNRNTEYWIRRFPTQYLFMYNRYKTP

270

280

290

260

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1371>:
a505.seq

1 ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
```

1	AIGITICGII	INCANTICAG	GCIGITICCC	CCITIGCGAA	CCGCCATGCA
51	CATCCTGTTG	ACCGCCCTGC	TCAAATGCCT	CTCCCTGCTG	CCGCTTTCCT
101	GTCTGCACAC	GCTGGGAAAC	CGGCTCGGAC	ATCTGGCGTT	TTACCTTTTA
151	AAGGAAGACC	GCGCGCGCAT	CGTCGCCAAT	ATGCGTCAGG	CAGGCATGAA
201	TCCCGACCCC	AAAACGGTCA	AAGCCGTTTT	TGCGGAAACG	GCAAAAGGCG
251	GTTTGGAACT	TGCCCCCGCG	TTTTTCAGAA	AACCGGAAGA	CATAGAAACA
301	ATGTTCAAAG	CGGTACACGG	CTGGGAACAT	GTGCAGCAGG	CTTTGGACAA
351			TCACGCCGCA	CATCGGCAGC	TACGATTTGG
401		CATCAGCCAG		TCCCGCTGAC	
451				ATCATGCAGG	
501				CATACAAGGG	
551				CCATCGTCCT	
601				GTATGGGTGG	
651				AAAATTGGCA	
701	GCGTGAAAAC	CCTGTTTTTC	TGCTGCGAAC	GCCTGCCTGG	CGGACAAGGT
751				GAATTGAACG	
801	CCATGATGCC	GCCGTGTTCA	ACCGCAATGC	CGAATATTGG	ATACGCCGTT
851	TTCCGACGCA	GTATCTGTTT	ATGTACAACC	GCTACAAAAT	GCCGTAA

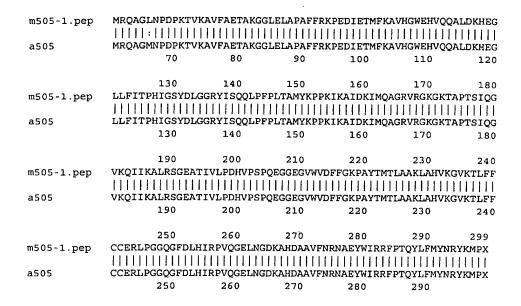
This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>: a505.pep

1	MFRLQFRLFP				
51				AKGGLELAPA	
101	MFKAVHGWEH	VQQALDKHEG	LLFITPHIGS	YDLGGRYISQ	QLPFPLTAMY
151	KPPKIKAIDK				
201				HVKGVKTLFF	
251	FDLHIRPVQG	ELNGDKAHDA	AVFNRNAEYW	IRRFPTQYLF	MYNRYKMP*

m505/a505 99.0% identity in 287 aa overlap

	•		A			
	10	20	30	. 40	50	60
m505.pep	MFRLQFRLFPPLRT	AMHILLTAL	LKCLSLLPLS	CLHTLGNRLG	HLAFYLLKED:	RARIVAN
	111111111111111		111111111111111111111111111111111111111			
a505	MFRLQFRLFPPLRT	AMHILLTAL	LKCLSLLPLS	CLHTLGNRLG	HLAFYLLKED	RARIVAN
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVK	AVFAETAKG	GLELAPAFFR	KPEDIETMFK/	AVHGWEHVOO	ALDKHEG
	111111111111111111111111111111111111111	111111111				
a505	MRQAGMNPDPKTVK	AVFAETAKG	GLELAPAFFRI	KPEDIETMFK/	AVHGWEHVOO	ALDKHEG
	70	80	90	100	110	120
						-20
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLG	GRYISQQLP	FPLTAMYKPPH	KIKAIDKIMQA	GRVRGKGKT	APTSIOG
	11111111111111	ППППП				
a505	LLFITPHIGSYDLG	GRYISQQLPI	FPLTAMYKPPK	KIKAIDKIMO	GRVRGKGKT	APTSIOG
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEAT	IVLPDHVPSI	PQEGGEGVWVE	FFGKPAYTM	LAAXLAHVKO	VKTLFF
				111111111	111 11111	
a505	VKQIIKALRSGEAT	IVLPDHVPSI	PQEGGEGVWVD	FFGKPAYTMI	LAAKLAHVKO	VKTLFF
	190	200	210	220	230	240
	,					
	250	260	270	280		
m505.pep	CCERLPGGQGFDLH	IRPVQGELNO	GDKAHDAAVFN	RNAEYWIRRE	PTHI	
	1111111111111	1111111111			11:	
a505	CCERLPGGQGFDLH	IRPVQGELNO	DKAHDAAVFN	RNAEYWIRRE	PTOYLFMYNE	RYKMPX
	250	260	270	280	290	

```
m505-1.seq
       1 ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
      51 CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
          GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
     151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
     201 CCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
     251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
          ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
     351
          ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
     401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
     451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
     501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
          TCATCAAAGC CCTGCGTTCG GGCGAAGCAA CCATCGTCCT GCCCGACCAC
     601 GTCCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
     651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
         GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
         TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
          CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
         TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA
 This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:
m505-1.pep
         MFRLQFRLFP PLRTAMHILL TALLKCLSLL PLSCLHTLGN RLGHLAFYLL
       1
         KEDRARIVAN MRQAGLNPDP KTVKAVFAET AKGGLELAPA FFRKPEDIET
      51
     101 MFKAVHGWEH VQQALDKHEG LLFITPHIGS YDLGGRYISQ QLPFPLTAMY
         KPPKIKAIDK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
         VPSPQEGGEG VWVDFFGKPA YTMTLAAKLA HVKGVKTLFF CCERLPGGQG
     201
         FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*
m505-1/g505 94.3% identity in 298 aa overlap
                   10
                            20
                                     30
                                              40
                                                       50
                                                                60
            MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN
m505-1.pep
            q505
            MFRLQFRLFPPLRTAMHILLTALLKCLSLLSLSCLHTLGNRLGHLAFYLLKEDRARIVAN
                   10
                            20
                                     30
                                              40
                                                       50
                            80
                                     90
                                             100
                                                      110
                                                               120
            MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG
m505-1.pep
            MRQAGLNPDTQTVKAVFAETAKCGLELAPAFFKKPEDIETMFKAVHGWEHVQQALDKGEG
g505
                   70
                            80
                                     90
                                             100
                                                      110
                                                              120
                  130
                           140
                                    150
                                             160
                                                      170
m505-1.pep
            LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIDKIMQAGRVRGKGKTAPTSIOG
            9505
            LLFITPHIGSYDLGGRYISQQLPFHLTAMYKPPKIKAIDKIMQAGRVRGKGKTAPTGIQG
                  130
                           140
                                    150
                                             160
                                                     170
                                                              180
                  190
                           200
                                    210
                                             220
                                                     230
                                                              240
            VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
m505-1.pep
            VKQIIKALRAGEATIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGVKTLFF
q505
                  190
                           200
                                     210
                                             220
                  250
                           260
                                    270
                                             280
                                                     290
                                                             299
m505-1.pep
           CCERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
            q505
           CCERLPDGQGFVLHIRPVQGELNGNKAHDAAVFNRNTEYWIRRFPTOYLFMYNRYKTPX
          240
                   250
                            260
                                     270
                                             280
                                                      290
m505-1/a505
            99.7% identity in 298 aa overlap
                   10
                            20
                                    30
                                             40
           {\tt MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN}
m505~1.pep
           a505
           MFRLQFRLFPPLRTAMHILLTALLKCLSLLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN
                  10
                            20
                                    30
                                             40
                                                      50
                  70
                            80
                                    90
                                            100
                                                     110
                                                              120
```



The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1375>: g506.seq

```
ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
   1
      TGTCAAACAA AGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAAGGCG
  51
      CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
 101
      CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GGCGAAGTCG GGTTGTTGCT
 151
      GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
      CCGTCGGCGC GGCCTTGTCC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
 301
      CGGACGATTG ACGGGGATTT GGCGGAAGTT CACACCCAAG CGGTAACGTT
 351
      GCGCGTCGGC GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
      GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
 401
      ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
 501
      CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
      TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
 551
      CGTCCATTTC GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT
 601
 651
      GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
     AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAATTTCA CCCAAAAACG
 701
 751
      TTCGCCCGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
 801
     TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
 851
     TGGTGCAGGG CTTCGGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC
     GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
 901
     GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG TGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
     CGAGTTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1251
1301
     CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGGCGCGC CGTTGTTCAT
     GGTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCCTT
     TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTTGGCG
     GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTTGAATCG
1501
     ACATTTATT TTCCTTTTGC AAAAACTATG GATGCGATTA TACGCCAAGA
     TTTTCGTTAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>: g506.pep

- 1 MAVFDEVGRI AHGCGGVVKQ SLFLRVVHQV EQGARLAEVV VIVLAVVPVC
- 51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
- 101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
- 151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLDVH

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201 RPFRELAALD GFVQVALMAF AVVGDDFCSF FVGQVFNPLL AAEMEFHPKT
       251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFGQ QRPEVPVVCG
       301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD
       351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
       401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH
       451 GQMGYGAFGG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
           TFYFPFAKTM DAIIRQDFRY *
 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1377>:
 m506.seq
           ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
        1
          TGCCGAACAA TGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAGGGCG
       51
      101
          CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
      151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GGCGAAtCG9 GGTTGTTGCT
      201 GCCATTGGCC GAAGCTGTYG GGTTCGTAGT GCGGCAGGCT GCCGYAGTTG
      251 CCGTCGGCGC GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
          CGGACGATTG ACGGGAATTT GGCGGAAGTT TACGCCCAAA CGGTAGCGTT
      351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG
      401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
      451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CTCAAACGGA TGATAAGGTA
           CTTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
           GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
           GCGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA
           TGCCTTGTTG GGTGCGGAAA TGGAATTTCA CCCAAAAACG CTCGCCTGCT
           TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
           GCCGGCGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCAGTG
          CTTCGGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC AGAGCGCATA
          TTGGTGCGCG GGTCGCGTTT GACGGCTTTG TTCAGGTCGG GGAACTTACG
      901 CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC ACATCCCAGT
      951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCGCGGAT GTCGCGTTCT
     1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
     1051 CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
    1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
    1151 CTTGTTCCTT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC
    1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
    1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
    1301 ACGCCAAGAT TTTCGCTATT AA
This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:
m506.pep
          MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVC
         RVAVDFQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
     101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGNE VARCEGGLFH
     151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHDLDVH
     201 RPFRKLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
     251 LACFVPEAVG MRTEAVHMAV AGGDAAVAHH DGNLVQCFGQ QRPEVPVVCG
     301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQGKTAD
     351 VAFCIGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
     401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRAVVH
     451 GQMGYRAFGG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
     501 TFYFPFVKTM DATIRQDFRY *
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng)
from N. gonorrhoeae:
m506/q506
                              20
                                        30
                                                  40
            {\tt MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF}
m506.pep
            MAVFDEVGRIAHGCGGVVKQSLFLRVVHQVEQGARLAEVVVIVLAVVPVCRVAVDFQRRF
g506
                    10
                              20
                                        30
                                                  40
```

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEA	VGFVVRQAAXV	AVGAALPVAXX	AVNXATRTID	GNLAEVYAQ?	TVALCVG
					: :: :	
g506	GEVGLLLPLAEA				_	
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIX					
555.1951			1111111111			
g506	VIEOTGLOHFIR					
	130	140	150	160	170	180
						_
m506 non	190 VKRMIRYFFRVC	200	210	220	230	240
m506.pep				VALMAFAVVGI		
g506	VKRMIRHFFGIG					
3300	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLA					
	:		<u> </u>			, , , , , ,
g506	AAEMEFHPKTFAI					•
	250	260	270	280	290	300
	310	320	330	340	350	360
m506.pep	RAHIGARVAFDG					
<i>I I</i>	:[]]:[][:
g506	GTHIGARIAFDG	FVQVGEFARVA(DEEHGRVVADH:	IPVAFFGIEFC	RKTADVAFR	IGCAAL
	310	320	330	340	350	360
	270	200	200	100		
mEAC man	370 ACHGGETGEHLGI	380	390	400	410	420
m506.pep	ACROGE TOERLOS				ITAEGUDEAA	11111
g506	ACHGGETGEHLG	FFADFAENFGAG	SVFGDVVCYGKI	RTERARTFGVH	TAFGDDFAH	EVGEFF
_	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQRAAF					
-506	111111111111111111111111111111111111111					
g506	IQPQILRQQGAAF 430	AGGQAVLIVGI 440	IGRAVVHGQMG: 450	YGAFGGSHRSC 460	SFSQVGQMG 470	GKRLTV
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLI	CNKFLESTFY	PFVKTMDATI	RQDFRY		
		1111111111	11:111111111			
g506	RFGGKRIRNRFLI					
	490	500	510	520		
The following	r nortial DNIA a	aallanaa wa	idontified t	n λ7	المراجع المراجعة	O ID 127
_	g partial DNA s	equence was	identified if	u 14. mening	mais <se< td=""><td>7 ID 13/9</td></se<>	7 ID 13/9
a506.se		TTGATGAAGT	CCCCCCC	CCCCAmmccc	CCCCCC	C TP
		TGCCTGTTTC				
		TGAAATAGTC				
15	1 CGCGTCGCCG					
20	1 GCCATTGGCC	GAAGCTGTTG	GGTTCGTAGT	GCGGCAGGCT	GCCGTAGT	TG

201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG 251 CCGTCGGCGC GTCCTTGTCC GTCGCGCTGG TTGCTGTGAA CAGGGCAACG 301 CGGACGGTTG ACAGGGATTT GGCGGAAGTT CACGCCCAAG CGGTAGCGTT 351 GCGCGTCGGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC 451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT 501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA 551 TGATACGGCA CTTTTTCCGC ATCGGCTTCA GGCATGACTT GGATGTACAT 601 CGTCCATTTC GGAAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT

	•	
651	GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC	
701	AGGTTTTTAA TGCCTTGTTG GGTGCGGAAA TGGAATTTCA CCCAAAAACG	
751	CTCGCCTGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA	
801	TATGGCGGTA GCCGGCGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT	
851	TGGTGCAGTG CTTCGGGCAG CAGCGTCCAG AAGTCCCAGT TGTTTGTGGC	
901	AGAGCGCATA TTGGTGCGCG GGTCGCGTTT GACGGCTTTG TTCAGGTCGG	
951	GGAACTTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC	
1001	ACATCCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCGCGGAT	
1051	GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC	
1101	GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG	
1151	GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA	
1201	ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG	
1251		
1301	CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTCAT	
1351	GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCCTT	
1401	TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTTGGCG	
1451		
1501	ACATTTTATT TCCCTTTTGT AAAAACTATG GATGCGACTA TACGCCAAGA	
1551	TTTTCGCTAT TAA	
This correspond	s to the amino acid sequence <seq 1380;="" 506.a="" id="" orf="">:</seq>	
a506.pep		
1	MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR	
51	RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT	
101	RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH	
151	IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLDVH	
201	RPFRKLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT	
251	LACFVPEAVG MRTEAVHMAV AGGDAAVAHH DGNLVQCFGQ QRPEVPVVCG	
301	RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD	
351	VAFCIGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR	
401	TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRAVVH	
451	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES	
451 501	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY *	
	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES	
501	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY *	
501	GOMGYRAFGG XHRSCSFSQV GOXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRODFRY * 8% identity in 520 aa overlap	
501 m506/a506 94	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * .8% identity in 520 aa overlap 10 20 30 40 50	60
501	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFO	RRF
501 m506/a506 94 m506.pep	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * .8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF
501 m506/a506 94	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF
501 m506/a506 94 m506.pep	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * .8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF
501 m506/a506 94 m506.pep	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60
501 m506/a506 94 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF III RRF 60
501 m506/a506 94 m506.pep	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG
m506/a506 94 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG
501 m506/a506 94 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF 60 120 CVG RVG
m506/a506 94 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG
m506/a506 94 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF 60 120 CVG II RVG 120
m506/a506 94 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120
m506/a506 94 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 20 CVG RVG 20 80 FGO
m506/a506 94 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * .8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF 60 120 CVG II RVG 120 180 FGQ
m506/a506 94 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF 60 120 CVG 11 RVG 120 180 FGQ 111 FGQ
m506/a506 94 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * .8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 20 CVG RVG 20 80 FGQ
m506/a506 94 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ
m506/a506 94 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ
m506/a506 94 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ 180 240 ALL
m506/a506 94 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ 180 ALL
m506/a506 94 m506.pep a506 m506.pep a506 m506.pep a506 m506.pep	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFFFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF
m506/a506 94 m506.pep a506 m506.pep a506 m506.pep a506 m506.pep	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFFFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ 180 ALL
m506/a506 94 m506.pep a506 m506.pep a506 m506.pep a506 m506.pep	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFFFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ 180 180
m506/a506 94 m506.pep a506 m506.pep a506 m506.pep a506 m506.pep a506	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ 180 240 ALL ALL 240
m506/a506 94 m506.pep a506 m506.pep a506 m506.pep a506 m506.pep	GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ 180 240 ALL ALL 240 ALL
m506/a506 94 m506.pep a506 m506.pep a506 m506.pep a506 m506.pep a506 m506.pep	GOMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ 180 ALL ALL ALL ALL
m506/a506 94 m506.pep a506 m506.pep a506 m506.pep a506 m506.pep a506	GOMGYRAFGG XHRSCSFSQV GOXGGKRLTV RFGGKRIRNR FLDCNKFLES TFYFPFVKTM DATIRQDFRY * 8% identity in 520 aa overlap 10 20 30 40 50 MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQ	RRF RRF 60 120 CVG RVG 120 180 FGQ FGQ 180 ALL ALL ALL ALL

PCT/US99/09346 WO 99/57280

752

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFV	QVGELTRVAQ	EEHGRVVADI	HIPVAFFGIKI	QGKTADVAF	CIGCAAF
			1111111111	1111111:	1111111	1111111
a506	RAHIGARVAFDGFV	QVGELTRVAQ	EEHGRVVADI	HIPVAFFGIE	LQRKTADVAF	CIGCAAF
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFF	ADFAEDFGAG	VFGDVVRYGK	(RTERARTFG)	HTAFGDDFA:	HEVGEFF
		11111111	111111111	1111111111	11111111	111111
a506	ACHGGETGEHLGFF	ADFAEDFGAG	VFGDVVRYGK	RTERARTFG	HTAFGDDFA	HEVGEFF
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQQRAART	GGQAVLIVGN	RRAVVHGQMG	YRAFGGSHRS	CSFSQVGQM	GGKRLTV
		111111111	1111111111	11111111	1111111	
a506	IQPQILRQQRAART(GGQAVLIVGN	RRAVVHGQMG	YRAFGGXHRS	CSFSQVGQX	GGKRLTV
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDC	VKFLESTFYF	PFVKTMDAT I	RQDFRYX		
			1111111111	111111		
a506	RFGGKRIRNRFLDC	NKFLESTFYF	PFVKTMDATI	RQDFRYX		
	490	500	510	520		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1381>: g507.seq

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ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
  1
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51
101 CCTTTGCGCT CTTCGTGCTT GGCAACGGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGACTTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCGGT
```

- 301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT 351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
- 401 TCGCGTTCGA TGCGTTGGTG CAGGTTTTGC CGGTGGCGGA TTTGTTCTTC
- 451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTTG CTCAATTCGT
- 501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
- 551 TTATTTAA

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>: g507.pep

- MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL 1
- 51 LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
- 101 LLFFDLQLVF LKLHADLLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
- 151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1383>: m507.seq

- ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG 1
- TTTCGGCTTC GTCGGGCAGG TTTAAGGCTT GGTTTTCCTG TTTCAGACGA
- 101 CCTTTGCGCT CTTCGTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
- 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
- 201 GGGTTTGGAA GGCGGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
- 251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAGCTCGGT
- 301 TTGTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
- 351 GCTGCTGCTC TTGATGAATG CGTTGTAACT GCGCCTGCGC TGCCTGCTTG
- 401 TCGCGTTCGA TGCGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC
- 451 CAAACGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTTG CTCAATTCAT
- 501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
- 551 TCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>: m507.pep

MLLLTLQQGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFGMGKL

PCT/US99/09346 WO 99/57280

753

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLLVFG NLHRPFRQLG 101 LFFFDLQLVF FKLHADLLLL LMNALXLRLR CLLVAFDALV QVLLMADLFF OTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV* Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from N. gonorrhoeae: m507/q507 20 30 10 40 50 60 MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQROFAAD m507.pep MLLPALQQGGGFLSGGGFGLVGQVQGLVFLLQTAFALFVLGNGLFGMGKLLLLQROFAAD g507 20 1.0 40 80 90 100 110 120 AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL m507.pep g507 AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL 70 80 90 100 110 140 150 130 160 170 180 LMNALXLRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG m507.pep LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG g507 140 150 160 180 VYFVV m507.pep | | | | : q507 VYFVI The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1385>: a507.seq ATGCTCTTGC TGGCTTTGCA ACAAGGCGGC AGCTTCCTGC GCGGCGGCGG 1 TTTCGGCTTC GTCAGGCAGA TTCAGGGCTT GGTTTTCCTG TTTCAGACGA 51 CCTTTGCGCT CTTCGTGCTT GGCAACGGTT TGTTCGGCAT GGGCAAGCTG 101 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT 201 GGGTTTGGAA GGCGGCATTG AGTGTGGCTT GGGTTTCTTC CAATTCGGGC AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCG CCAATTCGGT 251 TTGCTTTTCT TCCGCCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT 301 GCTGCTGCTC CTGATGGATG CGCTGCATCT GCGCCTGCGC CGCCTGCTTG 351 401 TCGCGTTCGA TGCGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC CAAACGGGCA ATCTGTTCGC GCAACACGCC GCGTTTGTTG CCCAATTCGT 451 GCACCGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG 501 TCGTTTAA This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>: a507.pep 1 MLLLALQQGG SFLRGGGFGF VRQIQGLVFL FQTTFALFVL GNGLFGMGKL LLLQRQFAAD AVCLVLLGLE GGIECGLGFF QFGQTLFVFG NLHRPFRQFG LLFFRLQLVF FKLHADLLLL LMDALHLRLR RLLVAFDALV QVLLMADLFF QTGNLFAQHA AFVAQFVHRL LLRLFGSLQG VYFVV* m507/a507 89.7% identity in 185 aa overlap 30 10 20 40 MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNRLFGMGKLLLLQRQFAAD m507.pep MLLLALQQGGSFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNGLFGMGKLLLLQRQFAAD a507 10 20 30 40 50 60 70 80 90 100 110 120

m507.pep	AVCLVLLGLEGGVER	GLGFFQFGQ	TLLVFGNLHF	RPFRQLGLFFE	DLQLVFFKL	HADLLLL
	1111111111111	311111111	11:1111111	11111:11:11	11111111	
a507	AVCLVLLGLEGGIEC	GLGFFQFGQ	TLFVFGNLHF	RPFRQFGLLFE	RLQLVFFKL	HADLLLL
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRLRCLLVA	FDALVQVLL	MADLFFQTGN	ILLAQHAALVA	QFMHCLLLR:	LFGSLQG
				1:11111:11		1111111
a507	LMDALHLRLRRLLVA	FDALVQVLL	MADLFFQTGN	ILFAQHAAFVA	QFVHRLLLR:	LFGSLQG
	130	140	150	160	170	180
m507.pep	VYFVVX					
	11111					
a507	VYFVVX					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1387>: a508.seq

```
1 ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
```

- 51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGTACG
- 101 CGGGCGTATT GCTCCCTGCC CTGTTCCTGA ATCTGCGCGA GTTTTTCCTG
- 151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
- 201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
- 251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
- 301 GGCGATTTGC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG 351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
- 401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
- 451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
- 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>: 9508.pep

- 1 MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLREFFL
- 51 HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
- 101 GDLLPVVLFL RVEFVDGDFG KPVLAVGFQQ GKLRLFQTAL LLLAAVRGGL
- 151 LLVFEFGGGF LQSSDVV

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1389>: m508.seq

- 1 ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAAGGCGG
- 51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGCAG GGTTTGCACT
- 101 TTAGCGTATT GCTCCCTGCC CTGTTCCTGA ATCTGCGCGA GTTTCTCTTG
- 151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
- 201 CAAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
- 251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
- 301 GGCGATTTGC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
- 351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
- 401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
- 451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAGGTA ACGATGTCGT
- 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>: m508.pep

- 1 MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLREFLL
- 51 HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLLAF LPVEGLLFKL
- 101 GDLLPVVLFL LVEFVDGDFG KPVLAVGFQQ GKLRLFQTAL LLLAAVRGGL
- 151 LLVFEFGGGF LQGNDVV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae:*

m508/g508

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLL	QQGGLGGGLK	LRQLGLQGLHF	SVLLPALFLNI	REFLLHNNIFF	VQGL
g508	MVAFGVDQGLLLLL	QQGGLGGGLK	LRQLGLQGLYA	GVLLPALFLNI	: ::: REFFLHGDVFF	: VQRV
	10	20	30	40	50	60
	70	80	90	100	110	120
	YGFAXFFKLDVLL' : : :		GKLLLAFLPVE :		VVLFLLVEFVD	GDFG
g508	YGFGQLVELDVLLY		GKLLPAFLPVQ	GLLFEPGDLLF		
	70	80	90	100	110	120
m508.pep 1	130 KPVLAVGFQQGKLI	140 PLEOTALLL:	150	160	377	
g508 I	KPVLAVGFQQGKLI 130	RLFQTALLLL 140	AAVRGGLLLVF 150	EFGGGFLQSSD 160	VV	
The following		equence was	s identified i	n <i>N. mening</i>	itidis <seq< td=""><td>ID 1391>:</td></seq<>	ID 1391>:
a508.seq 1		TTGGCGT T GA	TCAGGGCTTC	CTGCTGCTGC	AACAGGGCGG	
51	TTTGGGTGGC (GGCCTGAAGC	TGCGGCAGCT	TGGTTTGCAG	GGTTTGTACG	
101 151						
201	CGAGCTTGAT (GTGCTGCTCG	TCGTTTTGGA	ACTCGGTTTC	ATAGGCGAGG	
251		GCTGGCGTTC	CTGCCAATCG	AAGGTTTGTT	GTTCAAGCTG	
301		TGTTGGTAGT	TTTGTTTTTG	CTGGTTGAGC	TTGTGGACGG	
351 401	CGACTTCGGC A					
451	CTGCTGGTGT 1					
501	CTGA		000000110	01001111110	00011101001	
This correspond	ds to the amino	acid seque	nce <seo ii<="" td=""><td>D 1392: OR</td><td>F 508 a>·</td><td></td></seo>	D 1392: OR	F 508 a>·	
a508.pep		avia boque	5241	5 155 2 , 010	300.4	
1	MVAFGVDQGF I	LLLQQGGLGG	GLKLRQLGLQ	GLYAGVLFPT	LLLNLREFLL	
51	YDNIFFVQTL Y	YGFAQLFELD	VLLVVLELGF	IGEGKLLLAF	LPIEGLLFKL	
101	GNLLLVVLFL I		KPVLAVGFQQ	GKLRLFQTT <u>L</u>	LLLAAVRGGL	
151	LLVFEFGGGF I	LQNGDVV*				
m508/a508 88	8.6% identity in	n 167 aa ov	erlap			
mE00 non			20 30		50 LFLNLREFLLHI	60
m508.pep					T: PETNEKEEFFFHI	
a508	MVAFGVDOG	GFLLLOOGGLO	GGLKLROLGL	OGLYAGVLFPT	LLLNLREFLLYI	· I I I I I I DNTFFVOTI.
			20 30		50	60
			30 90		110	. 120
m508.pep	YGFAXFFKI	DVLLVVLELO	FIGEGKLLLA	TLPVEGLLFKL	GDLLPVVLFLL	VEFVDGDFG
a508	YGFAOLFEI	DVLLVVLELG		T.PTEGIJ.FKI	: GNLLLVVLFLL	II:
			30 90		110	120
	13	30 14	10 150	160		
m508.pep			LLLLAAVRGGI	LLVFEFGGGF		
a508	KPVLAVGFQ 13		LLLLAAVRGGI		LQNGDVVX	
	1.3	14	130) 160		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1393>: g509.seq

```
atggtcgctg tatgtgatga acgggctgta cagcggacgt tggtggccca
            1
               attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgttgtag
           51
               tcttccaagc ctgcgtgttg gaaaagctcg gcaaccacat cggcgtgttt
          101
               gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
          151
              acacggaacg gatgaggtet gecaaacgge etteggeaag caggeggetg
          251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatcat cqaqaaattt
          301 ttgggccgaa gcataaggct cgagaaagcc gaatttqcaq cccatqccca
          351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
          401 gcgcggcggt aaggttette ggtgcggcg atttettegt caggcgagag
          451 ggctgccagt gccattacgt cgtcgttgac tttgacgcgg cggatggaaa
          501 gcggcagttc gcggtaaagt ttgtcgagtt cgctgcggta aaaacggaac
          551 acggcatcgg cgtggcggcg gaaggcaaag cgcagggttt cgccagaaac
          601 aaacggattg ccgtcgcggt cgccgccgat ccagccgccg attttaagga
          651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
          701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
          751 cacgccgttg ttgatttcgt cgttgacgct gagtttgtgg cggcgcgttt
          801 cgctggtctg ccacaagccc agaagcacgg tgtcgatttc gcggcgcagc
          851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
          901 gcggatgcgg cggttgaaat tcaaaacggt ttggcgttgc acttcggtcg
          951 ggtgcgcggt caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
         1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
         1051 caggetgeet tetgetgegt tgtggeegge atettegtgg attttggeqge
         1101
               ggcgttcgtg gtgcacgtct tcggcgatat tcaqaatctq qqcqaacaqc
               ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
         1151
         1201
              tactttttca atcaatgccg cgctgtcgtc ggaagtggac aagagtttga
         1251 ccgtttcgac aaccaacggc gaggcttctt cgtgcaggag gttgaacagg
         1301 gactgtttca aaaattccgc gtccgccgcc aaagccgcgt ccttcggatt
         1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
         1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
         1451 ctcatgtccc gaaatgccgt ctgaagttga acgccgcccg acggcggcgt
         1501 tacaategee egeaactgtt ttttteegaa cateateatg accgegaecg
         1551 aacacqacaa cgacgacqca ctcctqctqc qqtacaqccq ccacatcctc
         1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
         1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgcccct gccctatctc
         1701 gccgcctcgg gggtcggcac gctga
This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:
     g509.pep
              MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
            1
           51 ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LOFFOIIEKF
          101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
          151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
          201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGO GFKKAHREDG
          251 HAVVDFVVDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQQR
          301 ADAAVEIQNG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
          351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
              YFFNQCRAVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
          401
          451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTTHVPKCR LKLNAARRRR
          501 YNRPQLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
          551 FGRRLRRIGR RRPCPISPPR GSAR*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1395>:
     m509.seq
              ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
              ATTCGCGCAA CAGGGCGGTT TGTTTTTGCT CTTCGTTCAG GCGGTTGTAG
              TCTTCCAAGC CTGCGTGTTG GAAAAGCTCG GCAACCACAT CGGCGTGTTT
          101
          151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
          201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCGGCAAG CAGACGGCTG
          251
              CCGTTGTCGA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAAACTC
              TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
          301
              AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
          351
          401 GCGCGGCGGT AGGGTTCTTC GGCGCGGGCG ATTTCTTCGT CGGGCGATTT
          451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
```

501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCGCGATA GAAGCGGAAC

```
ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
      AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
 601
      TGTCCGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
      TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
      CACGCCGTTG TTGATTTCGT CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
      CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTLC GCGGCGCAGC
     CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCGCGTTGCG GCAACAGTGC
     GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
     GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001
      ACCGATTTGC CGTCGGCTTT CCCCGCTTTG AGCCTGCGGA CGGTTTCCGT
     CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1051
1101
     GGCGTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAA
1201 TACTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTCA GAAATTCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTTCT CTCTCGTCTG CCGTAAATAT
1401 TGTAAATGTA CCCCAAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTLTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCCTGC TGCGGTACAG CCGCCACATC
1601 CTCTTGGACG AAATCGGCAT CGAAGGGCAG CAGAAACTTT CCGCCGCGCA
     TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1651
     CTTGCCGCTT CGGGTGTCGG CACGCTGA
1701
```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```
m509.pep

1 MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51 ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
```

101 BCKSTKBEKA EFAMITQTEK AKTAIDAKIN VOLGARVOFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFEKAHREDG
251 HAVVDFVVDA EFVAARFAGL PQAQQDSVDF AAQPCQRVGI GAAFALRQQC
301 ADAAVEAXDG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR

351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRAVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI

451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNAARRQ 501 RYNRPQLFFS EHHHDHDRTR QRRCIPAAVQ PPHPLGRNRH RRAAETFRRA

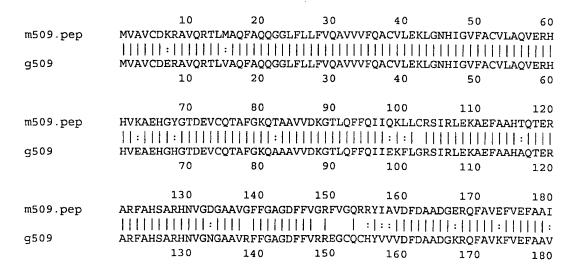
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from N. gonorrhoeae:

m509/g509



		190	200	210	220	230	240
m509.pep	EAEHG:				DFEDVRNADAG		
					: :		
g509					FKDIRNADIG		
3		190	200	210	220	230	240
		250	260	270	280	290	300
m509.pep	GFEKAI	HREDGHAVVI	DFVVDAEFVA	ARFAGLPQAC	QDSVDFAAQP		
					: :		
q509					KHGVDFAAQP		
J ===		250	260	270	280	290	300
		310	320	330	340	350	360
m509.pep	ADAAVI	EAXDGLALHI	FGRVRGQNGG	NGRIVQLPLH	RFAVGFPRFE	PADGFROAAI	RAAASG
					HHHHHH		
g509	ADAAVI	EIQNGLALH	FGRVRGQNGG	NGRIVQLPLH	RFAVGFPRFE	PADGFRQAAF	CCVVAG
3		310	320	330	340	350	360
		370	380	390	400	410	420
m509.pep	FFVDLA	AAAFVVHVFO	GDVQNLGEQA	AGQGXIVGLL	FVQLRQYFFN	QCRAVVGSGC)EFDCFD
g509					FVQLRQYFFN		
5		370	380	390	400	410	420
		430	440	450	460	470	480
m509.pep	NQRRGE	FVQEVEQGI	FQKFRVRRQ	SRVLWIVQNM	QLHDFSLSSA	VNIVNVPQMF	PHPCQTV
	11111			1111 111:1	11111 1 1		111111
g509	NORRGE	FVQEVEQGI	FOKFRVRRQ	SRVLRIVQDM	QLHDFPLI-A	VNTVNVPQMP	HPCQTV
•		430	440	450	460	470	
•		490	500	510	520	530	540
m509.pep	HTLTAR	VPKCRLKLN	NAARRQRYNR	PQLFFSEHHH	DHDRTRQRRC:	I PAAVQPPHP	LGRNRH
	: :	111111111		111111111	1:111111		
g509	HTLTTH	IVPKCRLKLN	JAARRRRYNR	PQLFFSEHHH	DRDRTRQRRR'	TPAAVQPPHP	LGRNRH
	480	490	500	510	520	530	
		550	560	570			
m509.pep	RRAAET	FRRAYFGRE	LRRFGCRRT	CPTLPLRVSA	R		
	:		:		İ		
g509				CPISPPRGSA	R		
_	540	550	560	570			
following pa	rtial DNA	sequence	was identi	fied in N. n	neningitidis	<seo id<="" td=""><td>1397>·</td></seo>	1397>·
a509.seq			20 1001101				10717.
2303.3eq							

The fo

1509.seq					
1	ATGGTCGCTG	TATGTGATGA	ACGGACTGTA	CAGTGGACGT	TGATGGCTCA
51	ATTCGCGCAA	CAGGGCGGCT	TGTTTTTGCT	CTTCGTTGAG	GCTGTTGTAG
101	TCTTCCAAGC	CTGCGTGTTG	GAAAAGCTCG	GCAACCACAT	CGGCGTGTTT
151	GCCTGCGTGT	TGGCGCAGGT	CGAGCGGCAT	CATGTGGAAG	CCGAACACGG
201	ATACGGAACG	GATGAGGTCT	GCCAAACGGC	CTTCGGCAAG	CAGGCGGCTG
251	CCGTTGTCGA	TAAGGGAATG	TTGCAATTTT	TTCAAATCAT	CGAGAAATTC
301	TTGTGCCGAA	GCATAAGGCT	CGAGAAAGCC	GAATTTGCAG	CCCATACCCA
351	AACCGAGCGC	GCGCGCTTTG	CCCATAGCGC	GCGCCATAAT	GTAGGCAATG
401	GCGCGACGGT	AGGGTTCTTC	GGCGCGGGCG	GTTTCTTCGT	CGGGCGATTT
451	GTCGGACAAC	GCCATCACAT	CGCCGTTGAC	TTTGACGCGG	CGGATGGAGA
501	GCGGCAGTTC	GCGGTAGAGT	TTGTCGAGTT	CGCCACGGTA	AAAACGGAAC
551	ACGGCATCGG	CGTGGCGGCG	GAAGGCAAAA	CGCAAGGTTT	CGGCAGAAAC
601	GAACGGATTG	CCGTCGCGGT	CGCCGCCGAT	CCAGCCGCCG	ATTTTGAGGA
651	TGTCCGGAAC	GCGGACATCG	GGATAGGCCG	TCTGAAAGTC	GTGTTCCATC
701	TTGCGGTAGA	GCTTGGGCAG	GGCTTCAAAA	AAGCTCATCG	GAAAGATGGA
751	CACGCCGTTG	TTGATTTCGT	CGTTGACGCT	GAGTTTGTGG	CGGCGCGTTT
801	CGCTGGTCTG	CCACAAGCCC	AGCAGGATAG	TGTCGATTTC	GCGGCGCAGC
851	CGTGCCAGCG	CGTCGGCATT	GGTACAGCGT	TCGCGTTGCG	GCAGCAGCGC

901	GCGGATGCGG	CGGTTGAAAT	TCAAGACGGT	CTGGCGTTGC	ACTTCGGTCG
951	GGTGCGCGGT	CAAAACGGCG	GTAACGGACG	TATTGTCCAA	CTGCCGCTGC
1001	ACCGATTTGC	CGTCGGCTTT	CCCCGCTTTG	AGCCTGCGGA	CGGTTTCCGT
1051	CAGGCTGCCT	TCCGCGCCGC	CGCGTCCGGC	TTCTTCGTGG	ATTTGGCGGC
1101	GGCGTTCGTG	GTGCACGTCT	TCGGCGATGT	TCAAAATCTG	GGCGAACAGG
1151	CCGCAGGCCA	AGGTTAAATC	GTGGGTTTGT	TGTTCGTCCA	ATTGCGGCAA
1201	TACTTTTTCA	ATCAATGCCG	CGCTGTCGTC	GGAAGTGGAC	AAGAGTTTGA
1251	CCGTTTCGAC	AACCAACGGC	GAGGCTTCTT	CGTGCAGGAG	GTTGAACAGG
1301	GATTGTTTCA	GAAATTCCGC	GTCCGCCGCC	AAAGCCGCGT	CCTTTGGATT
1351	GTTCAGAATA	TGCAGTTGCA	TGATTTTTCT	CTCATTGCCG	TAAATACTGT
1401	AAATGTACCT	CAAATGCCGC	ATCCGTGCCA	AACCGTTCAC	ACTTTAACCG
1451	CCCGTGTCCC	GAAATGCCGT	CTGAAGTTGA	ACGCCGCCCG	ACGGCAGCGT
1501	TACAATCGCC	CACAACTGTT	TTT.TCCGAA	CATCATCATG	ACCACGACCG
1551	AACACGACAA	CGACGATGCA	TTCCTGCTGC	GGTACAGCCG	CCACATCCTC
1601	TTGGACGAAA	TTGGCATCGA	AGGGCAGCAG	AAACTTTCCG	CCGCGCATAT
1651	TTTGGTCGTC	GGCTGCGGCG	GTTTGGGTGC	CGCCG.CCCT	GCCCTATCTC
1701	GCCGCTTCCG	GCATCGGCAC	GCTGA		

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

09.pep					•
1	MVAVCDERTV	QWTLMAQFAQ	QGGLFLLFVE	AVVVFQACVL	EKLGNHIGVF
51	ACVLAQVERH	HVEAEHGYGT	DEVCQTAFGK	QAAAVVDKGM	LQFFQIIEKF
101	LCRSIRLEKA	EFAAHTQTER	ARFAHSARHN	VGNGATVGFF	GAGGFFVGRF
151	VGQRHHIAVD	FDAADGERQF	AVEFVEFATV	KTEHGIGVAA	EGKTQGFGRN
201	ERIAVAVAAD	PAADFEDVRN	ADIGIGRLKV	VFHLAVELGQ	GFKKAHRKDG
251	HAVVDFVVDA	EFVAARFAGL	PQAQQDSVDF	AAQPCQRVGI	GTAFALRQQR
301	ADAAVEIQDG	LALHFGRVRG	QNGGNGRIVQ	LPLHRFAVGF	PRFEPADGFR
351	QAAFRAA <u>ASG</u>	FFVDLAAAFV	VHVFGDVQNL	GEQAAGQG*I	VGLLFVQLRQ
401	YFFNQCRAVV	GSGQEFDRFD	NQRRGFFVQE	VEQGLFQKFR	VRRQSRVLWI
451	VQNMQLHDFS	LIAVNTVNVP	QMPHPCQTVH	TLTARVPKCR	LKLNAARRQR
501	YNRPQLFXSE	HHHDHDRTRQ	RRCIPAAVQP	PHPLGRNWHR	RAAETFRRAY
551	FGRRLRRFGC	${\tt RXPCPISPLP}$	ASAR*		

m509/a509 93.0% identity in 575 aa overlap

mE00 man	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTI			/FQACVLEKLG		
a509	MVAVCDERTVQWTI					
4307	10	20	30	40	50	60
					30	00
	70	80	90	100	110	120
m509.pep	HVKAEHGYGTDEVO					
		1111111:11	11111 1111	1111:1:111	111111111	
a509	HVEAEHGYGTDEVO				IRLEKAEFA	AHTQTER
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVGDO					
500	111111111111111111111111111111111111111					
a509	ARFAHSARHNVGNG	SATVGEFGAGG. 140				
	130	140	150	160	170	180
	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKA					
msos.pep	::					
a509	KTEHGIGVAAEGKT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFEKAHREDGHAVV	DFVVDAEFVA	ARFAGLPQAÇ	QDSVDFAAQP	CQRVGIGAA	FALRQQC
		1111111111	1111111111		111111:11	
a509	GFKKAHRKDGHAVV	'DFVVDAEFVA	ARFAGLPQAÇ	QDSVDFAAQP	CQRVGIGTA	FALRQQR
	250	260	270	280	290	300
	310	320	330	340	350	360

```
ADAAVEAXDGLALHFGRVRGQNGGNGRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG
     m509.pep
                         ADAAVEIQDGLALHFGRVRGQNGGNGRIVQLPLHRFAVGFPRFEPADGFRQAAFRAAASG
     a509
                        310
                                 320
                                          330
                        370
                                 380
                                          390
                                                    400
                                                             410
                                                                      420
                 FFVDLAAAFVVHVFGDVQNLGEQAAGQGXIVGLLFVQLRQYFFNQCRAVVGSGQEFDCFD
     m509.pep
                 FFVDLAAAFVVHVFGDVQNLGEQAAGQGXIVGLLFVQLRQYFFNQCRAVVGSGQEFDRFD
     a509
                        370
                                 380
                                          390
                                                             410
                        430
                                 440
                                          450
                                                   460
                                                             470
                                                                      480
                 NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV
     m509.pep
                 NQRRGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLI-AVNTVNVPQMPHPCQTV
     a509
                        430
                                          450
                                 440
                                                   460
                        490
                                 500
                                          510
                                                   520
                                                             530
                 HTLTARVPKCRLKLNAARRQRYNRPQLFFSEHHHDHDRTRQRRCIPAAVQPPHPLGRNRH
     m509.pep
                 \verb|HTLTARVPKCRLKLNAARRQRYNRPQLFXSEHHHDHDRTRQRRCIPAAVQPPHPLGRNWH|
     a509
                         490
                                  500
                                           510
                                                    520
                        550
                                 560
                                          570
     m509.pep
                 RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRVSARX
                 11111111111
                 RRAAETFRRAYFGRRLRRFGCRXPCPISPLPASARX
     a509
               540
                        550
                                  560
                                           570
The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 1399>:
     g510.seq
           1
              atgeettege ggacacegea gggaaaaagg ggttatteet geeceaageg
          51
              ggatagtgcc ttttggcagg cgttgtccat atcggttatt ttacgcgcaa
              aatcgccgat tgccaaatcg ccgccgttca gggaggtttt caataggtcg
              tggacgacgt tgagcgcggc cataatgacg attttttcgc tgtccgcgac
              gcggccgcct tcgcggatgg cttcggcttt gccgttgagc attccgactg
              cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
         301
              ggcgtgcatg acttcgatgt agacttgttc gatgttcatc ctttaatcct
              tattgctgcg tttcctgccg ttgggggagg cgcgctgcca gtgcgctga
         351
This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:
     g510.pep
              MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
              WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
              GVHDFDVDLF DVHPLILIAA FPAVGGGALP VR*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1401>:
    m510.seq
              ATGCCTTCGC GGACACCGCA GGGNAAAAGG GGTTATTCCT GCGCCAAGCG
              GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
          51
              AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
              TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTTCGC TGTCCGCGAC
              GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCCGACTG
         201
              CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTTGAC GGTCAGCCGG
         251
              GGCGTGCAWG ACTTCsAtGT GGACTTGTTC GATGTTCATC CTTTAATCCT
         301
              TATTGCTGCG TTTCCTGCCA TTGGGGGAGG CGCGCTGCCA GTGCGCTGA
         351
This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:
    m510.pep
           1
             MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
          51
             WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
```

GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR* Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from N. gonorrhoeae:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCA	KRDSAFWQ	ALSISAILRAK	SPIAKSPPFF	REVFNRSWTT	LSAAIMT
	1111111111		11111:1111	11111111111	1111111	
g510	MPSRTPQGKRGYSC	KRDSAFWQ	ALSISVILRAK	SPIAKSPPFF	REVENRSWITT	LSAAIMT
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMAS	ALPLSIPTA	ACNSVSFSSAG	VLTVSRGVX	FXVDLFDVH	PLILIAA
		11111111		111111111111111111111111111111111111111	1 11111111	
g510	IFSLSATRPPSRMAS	ALPLSIPTA	ACNSVSFSSAG	VLTVSRGVHE	FDVDLFDVH	PLILIAA
_	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	111:11111111					
q510	FPAVGGGALPVRX					
7	130					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1403>:

```
a510.seq

1 ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTTATTCCT GCGCCAAGCG
51 GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTTCGC TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTTGAC GGTCAGCCGG
301 G.CGTGCATG ACTTCGATGT GGACTTGTTC GATGTTCATC CTTTAATCCT
351 TATTGCTGCG TTTCCTGCCG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

1 MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS 51 WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR

101 XVHDFDVDLF DVHPLILIAA FPAVGGGALP VR*

m510/a510 97.0% identity in 132 aa overlap

	•					
	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCA	KRDSAFWQA	LSISAILRAK	SPIAKSPPFR	EVFNRSWTT	LSAAIMT
	1111111111111		11111111111	111111111	111111111	
a510	MPSRTPQGKRGYSCA	KRDSAFWQA	LSISAILRAK	SPIAKSPPFR	EVFNRSWTT	LSAAIMT
	10	20	30	40	50	60
	70	80	90	100	110	100
m510.pep	IFSLSATRPPSRMASA					120
moro.pcp	11111111111111		DACCICVEND	ATIASKGAVD		
a510	TECTCATEDECEMAC		CNOUCECORO			
a310	IFSLSATRPPSRMASA	ADEPOTEIN	CNOVOLODAG	ATLASKYAHD	LDADTEDAHI	STILLAA
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
a510	FPAVGGGALPVRX					
4310						
	130					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1405>: 9512.seq

¹ atgaaagtgc ttgttttagg tgcgggtgtt gccggcgtat cctccgtgtg

g512

762

```
51 gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
          101 gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
          151 tataccacge cttgggctge acceggtatt ccgaccaaag cactgaaacg
          201 gctgtttaaa agccatccgc ctttactgtt ccgccctgac ggcggcctgt
          251 atcaaatcga atggctgtgg cggatgctgc aaaactgcac ggcaacgcgc
          301 tatcaaatca ataaagagcg catggtcagg atttccqaat acagccqtqa
          351 aatgttccgc cgttttgaag cgcaaaccga catgaatttt gagggacgca
          401 aaaaagggac gttgcagatt ttccgccaaa ccgaagaagt cgaaqcqqca
          451 aaacaagaca ttgccgtttt ggaacgctac ggcgtgccgt accgccgtct
          501 gaageeegaa gaatgegeag aattegagee tgegetggea egegttaeeg
          551 ccaaaattgt cggcggtctg cacctgcctg cggatgcgac cggcqactqc
          601 cgcctcttca ccgaaaacct gtacaaattg tgtcaagaga agggggtacg
          651 gttctacttc aaccaaacca tcagccgcat cgaccacaac gggctgcgca
          701 tcaaagccgt tgaaacgaaa cagggcggtt tgaaacagat gccgttgtct
          751 gcgcgctcgg ctgcttcagc aggactgtgt tggcgcagtt ggatctcaat
          801 ctgcccattt atcccgtcaa aggctattcc ttga
This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:
     g512.pep
              MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGOLSYG
              YTTPWAAPGI PTKALKRLFK SHPPLLFRPD GGLYQIEWLW RMLONCTATR
          101 YQINKERMVR ISEYSREMFR RFEAQTDMNF EGRKKGTLQI FRQTEEVEAA
          151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
          201 RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
          251 ARSAASAGLC WRSWISICPF IPSKAIP*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1407>:
     m512.seq
              (partial)
               ..GTTTTGGAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
           51
                 TGCAGAATTT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
                 GCCTGCACCT GCCTGCAGAT GCGACCGGCG ACTGGCGCCT CTTCACTGAA
          101
                 AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
          151
                AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAAA ACCGTTGAAA
          201
                 CCAAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
          251
                 TCAGCAGGAC GGTTTTGGCG CAGTTGGATC TCAATCTGCC CATTTATCCC
          301
                 GTCAAAGGCT ATTCCTTGA
          351
This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:
     m512.pep
                (partial)
              ..VLERYGVPYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
           1
                NLYKLCQEKG VRFHFNQNIS RIDHNGLRIK TVETKQGGLK QMPLSARSVA
           51
                 SAGRFWRSWI SICPFIPSKA IP*
          101
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng)
from N. gonorrhoeae:
    m512/g512
                                                      10
                                                                         3.0
    m512.pep
                                              VLERYGVPYRRLKPEECAEFEPALARVTAK
                                              TDMNFEGRKKGTLQ1FRQTEEVEAAKQD1AVLERYGVPYRRLKPEECAEFEPALARVTAK
    q512
                             140
                                      150
                                                160
                                                          170
                         40
                                   50
                                                      70
                                            60
                 IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
    m512.pep
                 IVGGLHLPADATGDCRLFTENLYKLCQEKGVRFYFNQTISRIDHNGLRIKAVETKQGGLK
    g512
                   190
                             200
                                      210
                                                220
                                                          230
                        100
                                  110
                                           120
                 QMPLSARSVASAGRFWRSWISICPFIPSKAIP
    m512.pep
```

QMPLSARSAASAGLCWRSWISICPFIPSKAIP

250 260 270

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1409>:

a512.seq ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG 1 51 GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG GCGTGGCGAT GGAAACCAGT TTTGCCAACG CAGGCCAGCT TTCTTACGGC TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT 251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA 351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA 401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCGTGCCGT ACCGCCGTCT 451 GAAGCCCGAA GAATGCGCAG AATTCGAGCC TGCGCTGGCA CGCGTTACCG 551 CCAAAATTGC CGGCGGCCTG CACCTGCCCG CAGACGCGAC CGGCGACTGC 601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG 651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA 701 TCAAAACCGT TGAAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT 751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT 801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

a512.pep

- MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG YTTPWAAPGI PTKALKWLFK SHPPLLFRPD GSLYOIEWLW OMLOHCTAAR
- 101 YQINKERMVR MSEYSREMFR RFEAQTGMNF EGRKKGTLQI FRQTKEVEAA
- 151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
- RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS 201
- ARSAASAGRF WRKWISICRF IPSKAIP*

m512/a512 95.9% identity in 122 aa overlap

	•				10	20	30
m512.pep				VLERYGV	PYRRLKPEE	CAEFEPALA	RVTAK
				111111	11111111	1 1 1 1 1 1 1	Ш
a512	TGMNFEGRK	KGTLQIFR	.QTKEVEAAK(DIAVLERYGV	PYRRLKPEE	CAEFEPALAF	RVTAK
	130	140	150	160	170	180	
		_					
	4 (-	50	60	70	80	90
m512.pep	IAGGLHLPAI	DATGDWRL	FTENLYKLC	QEKGVRFHFNQ	NISRIDHNG:	LRIKTVETKO	QGGLK
					:	[1111
a512	IAGGLHLPAI	DATGDCRL	FTENLYKLC	QEKGVRFHFNQ	TISRIDHNG	RIKTVETKO	QGGLK
	190	200	210	220	230	240	
	10/	`	110	100			
	100		110	120			
m512.pep	QMPLSARSVA	ASAGREWR	SWISICPFI	PSKAIPX			
a512	QMPLSARSA <i>I</i>	ASAGREWR	KWISICRFI	PSKAIPX			
	250	260	270				

The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 1411>: g513.seq

```
ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
    TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
    GATTTGAGCG GTGCGGCGCT GACGCAGGGG GCGATTGTCA GCCAAGTGGG
    GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
    CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
    AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
    GGTCTATTTC GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
351
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

```
AATGGGCAAA GACCCCGAGT TCAAACTTTC CGAACATCCG GGCCTGAAAC
         GCCGCATCAA ATCCGATGTT TGGTAA
This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:
q513.pep
         MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
      1
         DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
     51
         KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
    101
         LSPLAFMLLR DYTAKLKMGK DPEFKLSEHP GLKRRIKSDV W*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1413>:
m513.seq
         ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
      1
         TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTCGAT ACCATCATCG
     51
         TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
    101
         GATTTGAGCG GTGCGGCGCT GACGCAGGCG GCGATTGTCA GCCAAGTGGG
    201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
    251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
    301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
    351 GGTCTATTTC GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
    401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
    451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
    501 AATGGGCAAA GACCCCGAGT TCAAACTTTC CGAACATCCG GGCCTGAAAC
        GCCGCATCAA ATCCGATGTT TGGTAA
This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:
m513.pep
         MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
         DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
     51
         KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
         LSPLAFMLLR DYTAKLKMGK DPEFKLSEHP GLKRRIKSDV W*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 513 shows 99.5% identity over a 191 as overlap with a predicted ORF (ORF 513.ng)
from N. gonorrhoeae:
m513/g513
                             20
                                       30
            MGSAPNAAAAAEVKHPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTOA
m513.pep
            MGSAPNAAAAEVKHPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTOA
g513
                             20
                                      30
                                                40
                                                         50
                                                                   60
                    10
                    70
                             80
                                      90
                                               100
                                                        110
                                                                  120
            AIVSOVGOWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF
m513.pep
            AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF
q513
                                      90
                    70
                             80
                                               100
                                                        110
                                                                  120
                            140
                                      150
                                               160
            GAVANVPLVWDMADMAMGIMAWINLVAILLLSPLAFMXLRDYTAKLKMGKDPEFKLSEHP
m513.pep
            GAVANVPLVWDMADMAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMGKDPEFKLSEHP
g513
                   130
                            140
                                      150
                                               160
                                                        170
                                                                  180
```

The following partial DNA sequence was identified in N. meningitidis <SEO ID 1415>: a513.seq

190 **GLKRRIKSDVW**

111111

GLKRRIKSDVW 190

m513.pep

g513

1	ATGAACGAGA	ACTTTACCGA	ATGGCTGCAC	GGCTGGGTCG	GCGCCATCAA
51	CGATCCGATG	TGGTCATACT	TGGTTTATNT	GCTTTTGGGT	ACGGGGCTTT
101	TCTTCACCGT	AACCACGGGC	TTTGTCCAAT	TCCGCCTGTT	CGGGCGCAGC
151	ATCAAAGAAA	TGCTCGGCGG	CCGCAAACAG	GGGGACGACC	CTCACGGCAT
201	CACGCCGTTT	CAGGCATTTG	TAACCGGCCT	TGCCAGCCGC	GTGGGCGTGG
251	GCAATATCGC	GGGCGTGGCC	ATCGCCATCA	AAGTCGGCGG	ACCGGGCGCG
301	GTGTTTTGGA	TGTGGGTAAC	CGCCTTAATC	GGTATGAGTT	CGGCGTTTGT
351	CGAATCTTCG	CTGGCGCAGC	TCTTTAAAGT	CCGCGACTAC	GACAACCACC
401	ATTTCCGGGG	CGGCCCTGCC	TACTACATCA	CTCAAGGGCT	GGGGCAGAAA
451	TGGCTGGGCG	TGTTGTTCGC	CCTGAGCCTG	ATTTTCTGTT	TCGGCTTTGT
501	GTTTGAAGCG	GTTCAGACCA	ATACCATTGC	CGATACCGTC	AAAGCGGCGT
551	GGGGTTGGGA	GCCTCATTAT	GTCGGCGTCG	CCCTGGTGAT	TTTAACCGCG
601	CCGATTATCT	TCGGCGGCAT	CAGGCGCATA	TCTAAAGCGG	CGGAAATCGT
651	CGTCCCCCTG	ATGGCGGTTT	TGTACCTCTT	TATCGCGCTT	TTCATCATTT
701	TGACCAATAT	TCCGATGATT	CCGGACGTGT	TCGGTCAGAT	TTTTTCGGGC
751	GCGTTCAAAT	TCGACGCGGC	AGCAGGCGGC	TTACTCGGCG	GTCTGATTTC
801	GCAAACGATG	ATGATGGGCA	TCAAACGCGG	CCTGTATTCC	AACGAGGCGG
851	GTATGGGTTC	CGCGCCGAAC	GCCGCCGCCG	CCGCCGAAGT	GAAACACCCT
901	GTTTCGCAAG	GTATGATTCA	AATGCTGGGC	GTGTTTGTCG	ATACCATCAT
951	CGTTTGTTCT	TGCACCGCCT	TCATCATCTT	GATTTACCAA	CAGCCTTACG
1001	GCGATTTGAG	CGGTGCGGCG	CTGACGCAGG	CGGCGATTGT	CAGCCAAGTG
1051	GGGCAATGGG	GCGCGGGCTT	CCTCGCCGTC	ATCCTGTTTA	TGTTTGCCTT
1101	TTCCACCGTT	ATCGGCAACT	ATGCCTATGC	CGAGTCCAAC	GTCCAATTCA
1151	TCAAAAGCCA	TTGGCTGATT	ACCGCCGTTT	TCCGTATGCT	GGTTTTGGCG
1201	TGGGTCTATT	TCGGCGCGGT	TGCCAATGTG	CCTTTGGTCT	GGGATATGGC
1251	GGATATGGCG	ATGGGCATTA	TGGCGTGGAT	CAACCTTGTC	GCCATCCTGC
1301	TGCTCTCGCC	CTTGGCGTTT	ATGCTGCTGC	GCGATTACAC	CGCCAAGCTG
1351	AAAATGGGCA	AAGACCCCGA	GTTCAAACTT	TCCGAACATC	CGGGCCTGAA
1401	ACGCCGTATC	AAATCCGACG	TTTGGTAA		

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```
a513.pep

1 MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTTG FVQFRLFGRS
51 IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGGPGA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGFVFEA VQTNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPMI PDVFGQIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGLYS NEAGMGSAPN AAAAAEVKHP
301 VSQGMIQMLG VFVDTIIVCS CTAFIILIYQ QPYGDLSGAA LTQAAIVSQV
351 GQWGAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

	•		-	10	20	30
m513.pep			MC	SSAPNAAAAAI	EVKHPVSQGM:	IQMLGVFVD
			• •			
a513	DAAAGGLLGGL:					_
	260	270	280	290	300	310
	40	50	60	70	80	90
m513.pep	TIIVCSCTAFI:		- -	· -		
moro.pep	111100011111)	111111111
a513	TIIVCSCTAFI	LIYOOPYGDI	SGAALTOAA	EVSOVGOWGA	FLAVILEME	AFSTVIGNY
4015	320	330	340	350	360	370
	100	110	120	130	140	150
m513.pep	AYAESNVQFIK:	SHWLITAVFRM	1LVLAWVYFG	AVANVPLVWD	ADMAMGIMA	WINLVAILL
						1111111
a513	AYAESNVQFIK:	SHWLITAVFRM	1LVLAWVYFG/	AVANVPLVWDI	/ADMAMGIMA	WINLVAILL
	380	390	400	410	420	430
	160	170	180	190	_	
m513.pep	LSPLAFMLLRD	TAKLKMGKDE	PEFKLSEHPGI	LKRRIKSDVW	ζ.	
					i	

766

LSPLAFMLLRDYTAKLKMGKDPEFKLSEHPGLKRRIKSDVWX

a513

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 1417>:
     q515.seq
               atggttcaaa tacaggttgt gcgcgccgcc ggcgttgccc gtggtctgca
               ttccgagttt gcgcgcgctg taactgccga ggaaatagcc ttcgacaatg
               ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa
          151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga
          201 ggaaatcggg caggactttt ttgccgatgc tgtcgatcag gaaactgctt
          251 tggcggtaga gcgcgccgcc ggagagtgtg ccgacgaggt gtccqatcaq
          301 cccgcccgaa acggtggtat cgaagaggac ggggtagctg cctgtcggga
          351 tgctgcggct gccgagtcgg cgcaaagtgc ggcgggcggc ggtttgaccg
          401 atggtttcgg ggctgtccat atccggatgg cggcaggcgg aatcgtacca
          451 gtagtcgcgc tgcattccgt tttcgtcggc ggcgacgacg ctgcaggaaa
          501 tgctgtggtg cgtgctttgc cggtgtgcgg caaaaccgtg ggtgttgccg
          551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc
          601 gatgcggctg tccgtgtcca acgctgcctg ttcgcattgt tttgccaagc
          651 cgacggcggc ttccgtatcc aaatcccatt cgtggtaaag gtcggggtcg
          701 ccgatgtgtt gcgccatcaa ctcggggtcg gcaagtccgg cgcaaccgtc
          751 ttcggcggtg tggcgggcga tgtcggcggc ggcgcggacg gtgtcgcgca
          801 gggcttgttc ggagaagtcg gcggtgccgg cgcggccttt gcgtttgccg
          851 acgtaaacgg taatgtccag cgatttgtcc tgctggaact cgatttgttc
          901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
          951 cggcttcggc ggcggtcgcg cccgctgctt ttgccaagtc gagcgtqcqq
         1001 cggcagaggt cgaggagttc ggaaqcqqtq tqqttqaaca qcataacaat
         1051 ctttcttggt ggagcgttgt ggcattttaa
This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:
     g515.pep
               MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RRGGNTFRIK
            1
           51
              IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADEVSDQ
              PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
               VVALHSVFVG GDDAAGNAVV RALPVCGKTV GVAVNVLVLS GLHRRAFGVF
          201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
          251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLELDLF
          301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
          351 LSWWSVVAF*
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1419>:
     m515.seq
               (partial)
               ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
                 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
                 GCGCCGCCGG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
                 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
                 CGAGTCGGCG CAAAGTGCGG CGGGCGGCGG TTTGACCGAT GGTTTCGGGG
                 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
          251
                 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
          301
                 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTTGCCGTA AACGTATTGG
          351
                 TAATGGCCGG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TGCGCTCATC
          401
                 CTCGTTCAGG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTk
          451
          501
                 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
                 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG
          551
                 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGCAGG GCTTTTTCGG
          601
          651
                 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA
          701
                 ATGTCCAGCG ACTTGTCCTG CTGGAACTCG ATTTGTTsGA TTTsGCCCAG
                 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
          751
          801
                 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGCGGCG GCAGAGGTCG
          851
                 AGGAGTTCGG AAGCGGTGTG GTTGAACAGC ATAGAAATCT TTCTTGATGA
                 TGCTTTGCGG CATTTTAA
This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:
     m515.pep
                (partial)
```

```
..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
                GGIEEDGVAA CRDAAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
           51
                HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
          101
          151
                LVQGGLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
                AGDVDGGFDG VLQGFFGEVG STGAAFAFAD VNGNVQRLVL LELDLXDXAO
          201
          251
                PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEOHRNLSXX
                CFAAF*
          301
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng)
from N. gonorrhoeae:
     m515/g515
                                                   10
                                                            20
                                                                     30
     m515.pep
                                           GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                                  AEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
     g515
                                      50
                                               60
                       40
                                50
                                         60
                                                            80
                                                                     90
                 VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAAESAQSAAGGGLTDGFGAVHIRMAA
     m515.pep
                 VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAAESAQSAAGGGLTDGFGAVHIRMAA
     q515
                            100
                                     110
                                              120
                                                       130
                      100
                               110
                                        120
                                                 130
                                                           140
                 GGIVPVVALHAVFVGGNDAAGNAVVRALPVCGKTVGVAVNVLVMAGLHRRAFGVFDALIL
     m515.pep
                 GGIVPVVALHSVFVGGDDAAGNAVVRALPVCGKTVGVAVNVLVLSGLHRRAFGVFDAAVR
     q515
                  150
                                     170
                            160
                                              180
                                                       190
                                                                200
                               170
                                        180
                                                 190
                                                           200
                VQGGLFALFCQADGGXRIQIPFVVKVGVADVFCHQTGIGKSGATVFGGVAGDVDGGFDGV
    m515.pep
                    VQRCLFALFCQADGGFRIQIPFVVKVGVADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
    g515
                            220
                  210
                                     230
                                              240
                                                       250
                                                                260
                      220
                               230
                                        240
                                                 250
                                                           260
                                                                    270
                {\tt LQGFFGEVGSTGAAFAFADVNGNVQRLVLLELDLXDXAQPHADALSQXFAEIGFGGGCAR}
    m515.pep
                  AQGLFGEVGGAGAAFAFADVNGNVQRFVLLELDLFDFAQAHADALSERFAEVGFGGGRAR
    g515
                  270
                            280
                                     290
                                              300
                                                       310
                               290
                                        300
                      280
                RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAF
    m515.pep
                 CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAF
    g515
                  330
                           340
                                     350
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1421>:
    a515.seg
             ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GGCGTTGCCC GTGGTCTGCA
           1
             TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
          51
             CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
         101
             ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
         151
             GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
         201
         251
             TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
             ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
         301
             TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTTGACCG
         351
             ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
         401
             GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
         451
```

TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTTGCCG

551 601 651 701 751 801 851 901 951 1001 1051	TAAACGTATT GGTAATGGCC GGTTTGCACC GCCGCGCCTT CGGAGTTTTC GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATGT TTTGCCAAGC CGACGGCGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG CGATGTGTT GCGCGCAACACCGTC TTCGGCGGTG TGGCGGCGA TGTCNNNNGC GGCGCGGACG GTGTCGCCA GGGCTTGTTC GGAGAAATCG GCGTTGCCG CGCGGCCTTT GCGTGAAACT CGATTTGTCC AGCCGCACGC TGACGCTTTG TCCCAATGAT TCGCTGAAAT CCGCTTCGGC GGCGCTTT TCCCAATGAT TCGCTGAAAT CCGCTTCGGC GGCGGTTCGC CGGCAGAGTC GAGCGTGCGG CCGCAAGAATC CGGCTTCGGC GGCGGTTGCG CCCGTCGCTT TTGCCAAGTC GAGCGTGCGG CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAGAAAT CTTTCTTGAT GATGCTTTGC GGCATTTTAA
a515.pep	5 to the annio acid sequence SEQ 15 1422, Old 513.45.
1 51 101 151 201 251 301	MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RCGGNAFRIK IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADEVSDK TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP VVALHAVFVG GNDAAGNAVV RALPVCGKTV GVAVNVLVMA GLHRRAFGVF DALILVQGGL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV FGGVAGDVXX GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF DFAQPHADAL SQ*FAEIGFG GGCARRFCQV ERAAAEVEEF GSGVVEQHRN LS**CFAAF*
m515/0515 02	.1% identity in 304 aa overlap
m515.pep	10 20 30 GKSGGCAFFAQVEEIGQDFSADAVDQETALA ::
a515	AEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
	30 40 50 60 70 80
m515.pep a515	40 50 60 70 80 90 VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAAESAQSAAGGGLTDGFGAVHIRMAA :
m515.pep a515	100 110 120 130 140 150 GGIVPVVALHAVFVGGNDAAGNAVVRALPVCGKTVGVAVNVLVMAGLHRRAFGVFDALIL
m515.pep a515	160 170 180 190 200 210 VQGGLFALFCQADGGXRIQIPFVVKVGVADVFCHQTGIGKSGATVFGGVAGDVDGGFDGV
m515.pep a515	220 230 240 250 260 270 LQGFFGEVGSTGAAFAFADVNGNVQRLVLLELDLXDXAQPHADALSQXFAEIGFGGGCAR : :
m515.pep a515	280 290 300 RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1423>: g515-1.seq

1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GGCGTTGCCC GTGGTCTGCA

```
51 TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
 101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
 151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
 201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
 251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
 301 CCCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
 351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTTGACCG
     ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
 451 GTAGTCGCGC TGCATTCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
 501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
     TAAACGTATT GGTAGTGTCC GGTTTGCACC GCCGCGCCTT CGGAGTTTTC
 551
 601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGCATTGT TTTGCCAAGC
     CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
     CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
 701
     TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GGCGCGGACG GTGTCGCGCA
     GGGCTTGTTC GGAGAAGTCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
 851 ACGTAAACGG TAATGTCCAG CGATTTGTCC TGCTGGAACT CGATTTGTTC
     GATTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CGGCTTCGGC GGCGGTCGCG CCCGCTGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGGT GGAGCGTTGT GGCATTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>: g515-1.pep

- 1 MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RRGGNTFRIK
- 51 IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADEVSDQ
- 101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
- VVALHSVFVG GNDAAGNAVV RALPVCGKTV GVAVNVLVVS GLHRRAFGVF
- 201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
- 251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLELDLF 301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN 351 LSWWSVVAF*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1425>: m515-1.seq

```
1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GGCGTTGCCC GTGGTCTGCA
 51 TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCCTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAATGGCC GGTTTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGTCTTGCA
801 GGGCTTTTC GGAGAAGTCG GCAGTACTGG CGCGGCCTTT GCGTTTGCCG
```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>: m515-1.pep

ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGGAACT CGATTTGTTC

1 MVQIQVVRAA GVARGLHTEF ARAVTAEEIA FDNAVLNHEA RCGGNAFRIK

901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

- 51 IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADEVSDK
- TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
- VVALHAVFVG GNDAAGNAVV RALPVCGKTV GVAVNVLVMA GLHRRAFGVF 151
- 201 DALILVQGGL FALFCQADGG FRIQIPFVVK VGVADVFCHQ TGIGKSGATV
- 251 FGGVAGDVDG GFDGVLQGFF GEVGSTGAAF AFADVNGNVQ RLVLLELDLF
- DFAQPHADAL SQ*

91.7% identity in 312 aa overlap m515-1/g515-1

```
20
                                      40
         {\tt MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNAVLNHEARRGGNTFRIKIAAAERAGDV}
q515-1.pep
         MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDV
m515-1
                       20
                                      40
```

g515-1.pep	70 RFFAQVEEIGQDFF RFFAQVEEIGQDFF 70	$\Pi\Pi\bar{\Pi}\Pi\Pi$	1111111111	111111: 111	1111111111	ШНН
g515-1.pep m515-1	130 AESAQSAAGGGLTDG AESAQSAAGGGLTDG 130	111111111	THEFTH	1:1111111	111111111	HILLI
g515-1.pep m515-1	190 GVAVNVLVVSGLHRI :: GVAVNVLVMAGLHRI 190		11 11111	шин		$\Pi : \tilde{\Pi}$
g515-1.pep m515-1	250 LGVGKSGATVFGGVI I: TGIGKSGATVFGGVI 250	1111 11 11	1 11:1111	::	1111111:1	
g515-1.pep m515-1	310 DFAQAHADALSERFA : DFAQPHADALSQX 310	320 \EVGFGGGRA	330 RCFCQVERAA	340 AEVEEFGSGV	350 VVEQHNNLSWV	360 SVVAFX
The following partial DNA sequence was identified in N. meningitidis <s< td=""></s<>						

SEQ ID 1427>: a515-1.seq

```
1 ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GGCGTTGCCC GTGGTCTGCA
51 TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
     GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTTGACCG
401
     ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
     TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTTGCCG
551 TAAACGTATT GGTAATGGCC GGTTTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
     TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GGCGCGGACG GTGTCGCGCA
801 GGGCTTGTTC GGAGAAATCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGAAACT CGATTTGTTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA
```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>: a515-1.pep

- 1 MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RCGGNAFRIK 51 IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADEVSDK
- 101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
- 151 201 VVALHAVFVG GNDAAGNAVV RALPVCGKTV GVAVNVLVMA GLHRRAFGVF DALILVQGGL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
- 251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
- 301 DFAQPHADAL SQ*

94.9% identity in 312 aa overlap m515-1/a515-1

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVA	RGLHSEFARAV	/TAEEIAFDNA	VLNHEARCGG	NAFRIKIAAA	ERAGDV
• •	1111:1111111	:	11111111111	111111111	111111111	HHHH
m515-1	MVQIQVVRAAGVA	RGLHTEFARAV	/TAEEIAFDNA	VLNHEARCGG	NAFRIKIAAA	ERAGDV
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDF	FADAVDQETAI	LAVERSAGECA	DEVSDKTARN	GGIEEDGVVA	CRDAAA
	11111111111111			[11][[][[][]	11111111111	111111

```
RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
m515-1
                 70
                          80
                                  90
                                         100
                130
                         140
                                 150
                                         160
                                                 170
                                                         180
           AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCGKTV
a515-1.pep
           m515-1
           AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCGKTV
                130
                         140
                                 150
                                         160
                                                 170
                190
                         200
                                 210
                                         220
                                                 230
          GVAVNVLVMAGLHRRAFGVFDALILVQGGLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
a515-1.pep
           GVAVNVLVMAGLHRRAFGVFDALILVQGGLFALFCQADGGFRIQIPFVVKVGVADVFCHQ
m515-1
                190
                         200
                                 210
                                                 230
                                                         240
                250
                         260
                                 270
                                         280
a515-1.pep
          LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
           m515-1
          TGIGKSGATVFGGVAGDVDGGFDGVLQGFFGEVGSTGAAFAFADVNGNVQRLVLLELDLF
                        260
                                 270
                                         280
                                                 290
                310
          DFAOPHADALSOX
a515-1.pep
          11111111111111
m515-1
          DFAQPHADALSQX
                310
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1429>:

```
atgttgttcc gtaaaacgac cgccgccgtt ttggcggcaa ccttgatact
  1
 51
     gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101
     caatcacccg caaacacgtt gacaaagacc aaatccgcgc cttcggtgtg
     gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
151
     cgggaaatac tggttcgccg tcaatcccga agattcggcg aagctgacgg
201
251
     gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
     ccqagctatg cccgccacca agccctgccg gtcaaattcg aagcgcccgg
    cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
351
401
    gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcggtcaaa
    ctcgacaatc ggaccattta cacgcgctgc gtatccgcca aaggcaaata
451
501
     ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagtg
     tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601
    aagctgtttg gaaatatctt atatacgccc cccttgttga tattqqatqc
    ggcggccgcg gtgctggtct tgcctatggc tctgattgca gccgcgaatt
651
701
    cctcagacaa atga
```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

- 1 MLFRKTTAAV LAATLILNGC TMMLRGMINP VSQTITRKHV DKDQIRAFGV
- 51 VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
- 101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDDIAK LKQLEFKAVK
- 151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
- 201 KLFGNILYTP PLLILDAAAA VLVLPMALIA AANSSDK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1431>: m516.seq

- ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT 1 GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA 51 101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCGC CTTCGGTGTG 151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCGGCG AAGCTGACGG 201 251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACTCG AATCGCCTGG 301 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
- 451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```
772
            CTACGCCACA CCGCAAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
             TGCCTGCCGA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC
             AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTTGA TACTGGATGC
         651 GGCGGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGGTCGTGG
         701 ATGCCGCCCG CAAATGA
This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:
    m516.pep
             MLFRKTTAAV LAATLMLNGC TLMLWGMNNP VSETITRKHV DKDOIRAFGV
             VAEDNAQLEK GSLVMMGGKY WFVVNPEDSA KLTGILKAGL DKPFOIVEDT
          51
             PSYARHOALP VKLESPGSON FSTEGLCLRY DTDKPADIAK LKOLGFEAVK
             LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEEHTDKS
             KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng)
from N. gonorrhoeae:
    m516/q516
                                20
                                        30
                                                 40
                                                          50
                MLFRKTTAAVLAATLMLNGCTLMLWGMNNPVSETITRKHVDKDQIRAFGVVAEDNAQLEK
    m516.pep
                MLFRKTTAAVLAATLILNGCTMMLRGMNNPVSQTITRKHVDKDQIRAFGVVAEDNAQLEK
    q516
                       10
                                20
                                        30
                                                 40
                                                          50
                                80
                                        90
                                                100
                                                         110
                                                                  120
                GSLVMMGGKYWFVVNPEDSAKLTGILKAGLDKPF0IVEDTPSYARHOALPVKLESPGSON
    m516.pep
                GSLVMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN
    g516
                       70
                                80
                                        90
                                                100
                                                         110
                      130
                               140
                                       150
                                                160
                                                         170
                                                                  180
    m516.pep
                FSTEGLCLRYDTDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF
                FSTGGLCLRYDTGRPDDIAKLKQLEFKAVKLDNRTIYTRCVSAKGKYYATPOKLNADYHF
    g516
                      130
                               140
                                       150
                                                160
                                                         170
                      190
                               200
                                       210
                                                220
                                                         230
                                                                 23.9
               EQSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK
    m516.pep
```

WO 99/57280

g516

The following partial DNA sequence was identified in N. meningitidis <SEO ID 1433>:

200

190

EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAAAVLVLPMALIAAANSSDK

210

220

```
a516.seq
         ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCCGCCAA CCTTGATGTT
      1
      51
         GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
         CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
    101
         GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
    151
         CGGGAAATAC TGGTTCGTCG TCAATCCTGA AGATTCGGCG AAGCTGACGG
    201
    251
         GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
    301 CCGCGCTTTG CCTACCAAGC CCTGCCGGTC AAACTCGAAT CGCCCGCCAG
    351 CCAGAATTTC AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
         CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTCGAACTC
         GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA
    451
         CGCCACACCG CAAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
         CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
         TTGTTTGAAA ATATTGCATA TACGCCCACC ACGTTGATAC TGGATGCGGT
         GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
         CCTCAGACAA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>: a516.pep

PCT/US99/09346 WO 99/57280

```
MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
           1
              VAEDNAQLEK GSLVMMGGKY WFVVNPEDSA KLTGILKAGL DKQFQMVEPN
          51
              PRFAYOALPV KLESPASONF STEGLCLRYD TDRPADIAKL KOLEFEAVEL
              DNRTIYTRCV SAKGKYYATP QKLNADYHFE QSVPADIYYT VTKKHTDKSK
              LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*
          201
m516/a516 86.1% identity in 238 aa overlap
                         10
                                           30
                                                     40
                 MLFRKTTAAVLAATLMLNGCTLMLWGMNNPVSETITRKHVDKDQIRAFGVVAEDNAQLEK
     m516.pep
                 MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDKDQIRAFGVVAEDNAQLEK
     a516
                                           30
                                                    40
                        70
                                  80
                                           90
                                                   100
                                                             110
                                                                      120
                 GSLVMMGGKYWFVVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
     m516.pep
                 GSLVMMGGKYWFVVNPEDSAKLTGILKAGLDKQFQMVEPNPRFA-YQALPVKLESPASQN
     a516
                                  80
                                           90
                                                   100
                                                              110
                       130
                                 140
                                          150
                                                   160
                                                             170
     m516.pep
                 FSTEGLCLRYDTDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF
                 FSTEGLCLRYDTDRPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYYATPQKLNADYHF
     a516
               120
                        130
                                  140
                                           150
                                                    160
                                                              170
                       190
                                 200
                                          210
                                                   220
                                                             230
                                                                     239
                 EOSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
     m516.pep
                 EQSVPADIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX
     a516
                        190
                                  200
                                           210
               180
                                                    220
                                                              230
The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 1435>:
    g517.seq
              atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
              egtaggette gacgattttt tgeaccagag gatgeeggae aacgtetteg
              ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacq
             tgcgtctttc aatcccgatt tgatgttttt gggcaggtcg atttggctgg
         201 tgtcgccggt aatgacggct ttcgcgccga agccgatgcg ggtcaggaac
         251 attttcattt gttcgggcgt ggtgttttgc gcttcgtcga ggatgatgta
         301 tgcgccgttg agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa
              tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcaggtca
         401
              tagagggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
         451
              gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaqqccqaa
         501
This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:
    q517.pep
              MHRVSDGIGV SVVFCRFVGF DDFLHQRMPD NVFAGEGMEI OSCHAVOFLT
             CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
          51
              CAVERPAAHI GERGDFNQAF FNQLGYTVKA HOVIEGIIKR TEVGVDFLGO
         101
         151 VSGQEAQFLT GFDGRPN*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1437>:
    m517.seq
             ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
              CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
          51
              CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
         101
              CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
         151
              TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
         201
         251
              ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
              TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCGATTTCAA
         301
              TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
              TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
```

```
GTCTCCGGGC AGGAAGCCCA GTTTCTCGCC GGCTTCGACG GCTGGGCGCA
          451
         501
This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:
     m517.pep
              MHRVSDGIGM SVVFCRFVGF DDFLHQRMPD NVFAGKGVEI QPFHVVQFLT
              RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
              CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
              VSGQEAQFLA GFDGWAH*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng)
from N. gonorrhoeae:
     m517/g517
                         10
                                   20
                                                       40
                                                                5.0
                 MHRVSDGIGMSVVFCRFVGFDDFLHQRMPDNVFAGKGVEIQPFHVVQFLTRIFXSRFDVF
     m517.pep
                  MHRVSDGIGVSVVFCRFVGFDDFLHQRMPDNVFAGEGMEIQSCHAVQFLTCVFQSRFDVF
     g517
                                                       40
                                                                50
                         10
                                   20
                                             30
                                                     100
                                                               110
                         70
                                   80
                                             90
                  GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF
     m517.pep
                  GOVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF
     g517
                         70
                                   80
                                             90
                                                     100
                                                               110
                                                                         120
                                  140
                                            150
                        130
                 FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH
     m517.pep
                  {\tt FNQLGYTVKAHQVIEGIIKRTEVGVDFLGQVSGQEAQFLTGFDGRPN}
     g517
                                                     160
                                  140
                                            150
                        130
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1439>:
a517.seq
        ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
        CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
     51
        CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTTCTCACG
        CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
        TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
    201
    251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
        TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCAATCTCAA
        TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCGAAGCC CATCAGGTCA
    351
        TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
    401
    451
        GTCACCGGGC AGAAAACCCA GTTTCTCGCC GGCTTCGACG GCAGGCCGCA
    501
This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:
a517.pep
        MHRVSDGIGM SVVFCRFVGF DDFLHQRMPD NVFAGKGVEI QPFHAVQFLT
        RIF*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
     51
        CAVERPAAHI GERGNLNQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
    151 VTGQKTQFLA GFDGRPH*
m517/a517
           93.4% identity in 167 aa overlap
                                            40
                                                     50
           MHRVSDGIGMSVVFCRFVGFDDFLHQRMPDNVFAGKGVEIQPFHVVQFLTRIFXSRFDVF
m517.pep
           \verb|MHRVSDGIGMSVVFCRFVGFDDFLHQRMPDNVFAGKGVEIQPFHAVQFLTRIFXSRFDVF|
a517
                  10
                           20
                                   30
                                            40
                                                     50
                                                             60
                           80
                                   90
                                           100
                                                    110
           GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF
m517.pep
           GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLNQTF
a517
```

80

775

100

110

120

90

```
130
                           140
                                    150
                                            160
            FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX
m517.pep
            FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX
a517
                           140
                                    150
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1441>:
      q518.seq
               atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttgtgtct
            1
               ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
           51
               aaggcagcat cttattcaac cattttttca gcataaatat tctgacccga
          101
          151
               agagcggcat ctccacgggc aaccgtgttc agactgcatc aggcggtacg
          201
               attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
               tecgaateae geogeeteet egggeggeaa egetteatta taacagattg
               ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga
This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:
     g518.pep
               MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
               RAASPRATVF RLHQAVRFHK MPKTISKMRR NYAVRITPPP RAATLHYNRL
           51
               PLKKSDPAFV AESEI*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1443>:
     m518.seq
               ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
           51
               TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTTTACTG CTCCGACCGG
               AAGGCAGCAT CTTATTCAAC CATTTTTTCA GCATAAATAT TCTGACCCGA
               AGAGCGGCAT CTCCACAGGC AACCGTGTTC AGACGGCATC AGGCGCGGTT
               TGCAAGATGC CGTACCATAA ACAAAAGGCG TAGAAACTAC GCCGTCCGAA
          201
               TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
          251
               GCGGCAGGCT TAGTGCGCCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
               TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
          351
          401
This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:
     m518.pep
               MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
               RAASPQATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
               AAGLVRRERR RCAVILSNGR KKSDPAFVAE SEI*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng)
from N. gonorrhoeae:
     m518/g518
     m518.pep
                  MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPQATVF
                  MTFSAAKLNISALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
     q518
                          10
                                    20
                                             30
                                                       40
                           70
                                     80
                                               90
                                                        100
                                                                  110
                 RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSN
     m518.pep
                  1 111 11 : :11:1 1111111111 111 111111
                 RLHQAVRFHKMPKTISKMRRNYAVRITPPPRAATLHYNRLPL----
     g518
                         70
                                   80
                                             90
                                                      100
                 120
                          130
     m518.pep
                 GRKKSDPAFVAESEI
                   11111111111111
     g518
                 --KKSDPAFVAESEI
```

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1445>:
a518.seq
        ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
      1
        TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTTTACTG CTCCGACCGG
     51
        AAGGCAGCAT CTTATTCAAC CATTTTTTCA GCATAAATAT TCTAACCCGA
    101
        AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
    151
    201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
        GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
    251
    301
        351
    401 TTTGA
This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:
a518.pep
        MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
        RAASPRATVF RRHQAVRFRK MPTINKRRN YAVRITPSSX AATRHYNRLP
     51
        S...... .KKSDPAFVA ESEI*
    101
m518/a518
           79.9% identity in 134 aa overlap
                                    30
                                             40
                  10
                           20
           MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPQATVF
m518.pep
           MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
a518
                  10
                                                              60
                           20
                                    30
                                             40
                                     90
                                             100
                                                     110
                                                             119
                   70
                            80
           RRHQA-RFARCRTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSNG
m518.pep
           RRHQAVRFRKMPTINKRRRNYAVRITPSSXAATRHYNRLPS-
a518
                           80
         120
                  130
           RKKSDPAFVAESEIX
m518.pep
            11111111111111111
           -KKSDPAFVAESEIX
a518
                 110
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1447>:
     q519.seq
              atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
               atcetttqtc gtcatccccc agcaggaagt ccacgttgtc gaaaggctcg
           51
          101 ggcgtttcca tcgcgccctg acggccggtt tgaatatttt gattcccttt
              atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
          201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
          251 gcatcatcta tttccaagta accgatccca aactcgcctc atacggttcg
          301 agcaactaca ttatggcaat tacccagett geccaaacga egetgegtte
          351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
          401 tcaacagtac cgtcgtctcc gccctcgatg aagccgccgg ggcttggggt
          451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
          501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
          551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
          601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
              ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
          651
               gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
          701
               cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atgcggtcaa
               tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
          851
               aagacaatac gcggattaag cccgccaagg ttgccgaaat cgggaaccct
               aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaaata
          951
This corresponds to the amino acid sequence <SEO ID 1448; ORF 519.ng>:
     q519.pep
               MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
               IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
```

```
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
               VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
               GOREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAN
               RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
           301 NFRRHEKFSP EAKTAK*
 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1449>:
      m519.seq
               (partial)
               ..TCCGTTATCG GGCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
                 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGGCTTGGG
                 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
          101
                 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
          151
                 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
          201
                 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
          251
                 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
          301
          351
                 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
                 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
          401
          451
                 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
                 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
          501
                 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA
          551
This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:
     m519.pep
                (partial)
            1
               ... SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPOE
                 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA
           51
                 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
          101
                 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng)
from N. gonorrhoeae:
     m519/q519
                                                      10
                                                               20
     m519.pep
                                              SVIGRMELDKTFEERDEINSTVVAALDEAA
                                              YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
     q519
                    90
                                     110
                                               120
                                                         130
                                                                  140
                                   50
                                            60
                 GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
     m519.pep
                  GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
     q519
                   150
                            160
                                     170
                                               180
                                                        190
                                                                  200
                                  110
                                           120
                                                     130
                                                              140
                 IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQGGADAV
     m519.pep
                 IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAEANRQIAAALQTQSGADAV
     q519
                  210
                            220
                                     230
                                               240
                                                        250
                        160
                                 170
                                           180
                                                     190
                 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK
     m519.pep
                 1:
                 NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSPEAKTAK
     9519
                  270
                            280
                                     290
                                               300
                                                        310
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1451>:
        ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
```

a519.seq

- 51 ATCCTTTGTT GTCATCCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
- 101 GGCGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
- 151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT

```
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
    GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
    AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
    CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
351
401
    TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
    GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
551
    GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651
    GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
    GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
701
    CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
751
    TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
    AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>: a519.pep

```
MEFFIILLAA VVVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
    IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
51
101
    SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
```

201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI

251 RQIAAALQTQ GGADAV 301 ISAGMKIIDS SKTAK* RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL

m519/a519 99.5% identity in 199 aa overlap

		-		•			
					10	20	30
m519.pep				SVIGRME	LDKTFEERDE	INSTVVAALD	EAA
				1111111	111111111	11111111111	$\Pi\Pi$
a519	YFQVTDPKLAS	SYGSSNYIMA	ITQLAQTT	LRSVIGRME	LDKTFEERDE	INSTVVSALD	EAA
•	90	100	110	120	130	140	
	40	50	(60	70	80	90
m519.pep	GAWGVKVLRYE	IKDLVPPQE	ILRSMQAQ:	(TAEREKRA)	RIAESEGRKI	EQINLASGQR	EAE
	- 11111111111	111111111	11111111		111111111	HIIIIIII	111
a519	GAWGVKVLRYE	IKDLVPPQE	ILRSMQAQ:	TAEREKRA	RIAESEGRKI	EQINLASGQR'	EAE
	150	160	170	180	190	200	
	100	110					150
m519.pep	IQQSEGEAQAA	VNASNAEKI	ARINRAKGI	EAESLRLVA	EANAEAIRQI.	AAALQTQGGA!	DAV
		1111111	111111111				111
a519	IQQSEGEAQAA	VNASNAEKI	ARINRAKGE	CAESLRLVA	EANAEAIRQI.	AAALQTQGGA !	DAV
	210	220	230	240	250	260	
	160	170	18	30 :	190	200	
m519.pep	NLKIAEQYVAA	FNNLAKESN	TLIMPANVA	DIGSLISA	MKIIDSSKT	AKX	
	11111111111	11111111	111111111	11111111	1111111111	111	
a519	NLKIAEQYVAA	FNNLAKESN'	TLIMPANVA	DIGSLISA	MKIIDSSKT	AKX	
	270	280	290	300	310		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1453>: g519-1.seq

```
1 ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
 51 ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
    ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
151
    ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251
    GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
     CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451
    GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
    GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
701
    CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGGGG ATGCGGTCAA
```

```
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
      851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
      901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA
 This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:
 g519-1.pep
       1 MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
          IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
      101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
      151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
      201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
      251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
      301 ISAGMKIIDS SKTAK*
 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1455>:
 m519-1.seq
       1 ATGGAATTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
      51 ATCCTTTGTT GTCATCCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
     101 GGCGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
     151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
     201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
     251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
     301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
     351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
     401 TCAACAGTAC TGTTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
     451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
     501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
         GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
     601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
     651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
     701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
     751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
         TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
     801
     851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
     901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA
This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:
m519-1.
         MEFFIILLVA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
         IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
      51
     101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
         VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
     151
     201
         GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAT
     251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
     301 ISAGMKIIDS SKTAK*
m519-1/g519-1 99.0% identity in 315 aa overlap
                             20
                                                40
                                                         50
            {\tt MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL}
q519-1.pep
            m519-1
            MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
                   10
                             20
                                      30
                                                40
                             80
                                       90
                                                        110
                                                                 120
            KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
g519-1.pep
            m519-1
            KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
                   70
                             80
                                      90
                                              100
                                                        110
                                                                 120
                            140
                                     150
                                               160
                                                        170
            RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
g519-1.pep
            RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
m519-1
                  130
                                     150
                                              160
                                                        170
                                                                 180
```

g519-1.pep

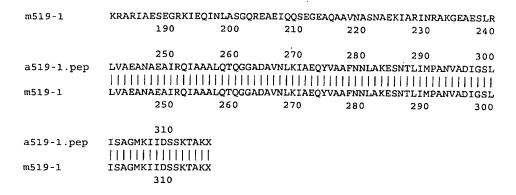
200

210

KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR

220

m519-1	KRARIA	ESEGRKIEQI 190	NLASGQREAI 200	EIQQSEGEAQ 210	AAVNASNAEKI 220	ARINRAKGE 230	AESLR 240
		250	260	270	280	290	300
g519-1.pep					aafnnlakesn 		
m519-1					AAFNNLAKESN 280		
g519-1.pep	ISAGMKI	310 IDSSKTAKX	:				
m519-1		 IDSSKTAKX					
	22	310					
	ing parti	al DNA s	equence v	vas identi	fied in N. 1	neningitia	lis <seq 1457="" id="">:</seq>
a519-1.seq 1 A	rggaattti	TCATTATC	TT GCTGGCA	GCC GTCGT	GTTT TCGGC	TTCAA	
					TTGTC GAAAG ATTTT GATTC		
151 A	rcgaccgcg	TCGCCTAC	CG CCATTC	CTG AAAGA	ATCC CTTTA	GACGT	
					GCTG ACTGT		
					ACGA CGCTG		
					AGAA CGCGA CCGG AGCTT		
					CCGC CGCAA		
					TCAA CCTTG		
					GAGG CTCAG CAAC CGCGC		
701 GT	rgaagcgga	ATCCTTGC	GC CTTGTTG	CCG AAGCCA	ATGC CGAAG	CCATC	
					GCGG ATGCG CAAT CTTGC		
851 A	AGCAATAC	GCTGATTA'	TG CCCGCCA	ATG TTGCCG	ACAT CGGCA	GCCTG	
901 A7	TTTCTGCCG	GTATGAAA	AT TATCGAC	AGC AGCAAA	ACCG CCAAA	TAA	
This correspasses.	ponds to	the amin	o acid seq	uence <s< td=""><td>EQ ID 145</td><td>8; ORF 5</td><td>19-1.a>:</td></s<>	EQ ID 145	8; ORF 5	19-1.a>:
1 <u>M</u> E					HRAL TAGLN		
			-		TVVS ALDEA		
		·-			ESEG RKIEQ ESLR LVAEA		
251 RQ	QTQLAAAIQ	GGADAVNLI			TLIM PANVA		
301 IS	SAGMKIIDS	SKTAK*					
m519-1/a519-	1 99.	0% identit	ty in 315	aa overlap			
a519-1.pep	MERETTI	10 	20 2557777 DOOR	30	40 HRALTAGLNI	50	60
asis-i.pep		[:[]:4]]]]		111111111			1111
m519~1	MEFFIIL	LVAVAVFGFF 10	KSFVVIPQQE 20	VHVVERLGRF 30	HRALTAGLNII 40	LIPFIDRVAY 50	RHSL 60
a519-1.pep	KEIPLDV	70 PSQVCITRDN	80 NTQLTVDGII	90 YFQVTDPKLA	100 SYGSSNYIMA:	110 ITOLAOTTLR	120 SVIG
-510 1		1111111111		111111111			1111
m519-1	KEIPLDV	70	80	90 90	SYGSSNYIMA: 100	ITQLAQTTLR 110	SVIG 120
		130	140	150	160	170	180
a519-1.pep	RMELDKT	FEERDEINST	TVVSALDEAA	GAWGVKVLRY	EIKDLVPPQE:	LRSMQAQIT	AERE
m519-1	RMELDKT	 FEERDEINST	: VVAALDEAA		 EIKDLVPPQE:	 LRSMQAOIT.	 AERE
		130	140	150	160	170	180
		190	200	210	220	230	240
a519-1.pep	KRARIAE!	SEGRKIEQIN	ILASGQREAE:	IQQSEGEAQA	avnasnaekia 	ARINRAKGEA:	ESLR
	111111	1111(1111)	111111111		1:11111111		1111



Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, J. Immunol 143:3007; Roberts et al. 1996, AIDS Res Human Retroviruses 12:593; Quakyi et al. 1992, Scand J Immunol Suppl 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1459>:
```

```
g520.seg
               atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
               catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
           51
               atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
          101
          151
               ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgttttc
               cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
          201
          251
               cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
          301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
               cgcgaacagt tcgaacggat cttttgacaa gggcgggcga cgggccgatt
          351
               ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
          401
          451 cgcgcccaa gcggcgggaa atttcctctg cgttgtcccg caacacggca
               gccgcaccgc cgccgaccgt acctaagcct aaaagaccga tgtttactgg
          551
               cttcattgtg tctccttgta agccgactga aatgtaaata ttqa
This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:
     q520.pep
              MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDLILFAA KPSRTALMIG
            1
               IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
           51
               AMPVPPNNST KTSTSLRANS SNGSFDKGGR RADFGGLFLR LSRTWOKYGF
              RAPSGGKFPL RCPATROPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1461>:
     m520.seq
            1
               ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
           51
              CATTTCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
          101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
          151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
          201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTTGTTGG
          251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
```

```
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
          351 TGCGACCAGT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
          401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
          451 CGCGCCCCAA GCGACGGGAA ATTTCCTCCG CGTTGTCsCG CAACACGGCA
          501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
              CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA
          551
This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:
     m520.pep
               MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDLILFAA KPSRRALMIG
               IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
               AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTROKYGF
              RAPSDGKFPP RCXATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng)
from N. gonorrhoeae:
     m520/g520
                         .10
                                   20
                                            30
                                                      40
                                                               50
                                                                         60
                 MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDLILFAAKPSRRALMIGIPPATAASNW
     m520.pep
                  MPALLSIRRANALPFSRISERMKLLVPLIMPAMDLILFAAKPSRTALMIGIPPATAASNW
     g520
                         10
                                   20
                                            30
                                                     40
                                                               50
                         70
                                   80
                                            90
                                                     100
                                                              110
                                                                        120
     m520.pep
                 TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
                  g520
                 TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
                         70
                                   80
                                            90
                                                    100
                                                              110
                        130
                                  140
                                          150
                                                    160
                                                              170
                                                                        180
                 {\tt SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR}
     m520.pep
                 SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLKDR
     g520
                        130
                                  140
                                           150
                                                    160
                                                              170
                        190
     m520.pep
                 CLLASLCLLVSRLKCKY
                 1111111111
     g520
                 CLLASLCLLVSRLKCKY
                        190
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1463>:
     a520.seq
              ATGCCTGCGC TTCTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
          51
             CATTTCGGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
         101
             ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
         151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
         201
              CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTTGTTGG
              CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
          251
              GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
              TGCGACCAGT TCGAACGGAT CTTTGACAAA GGCTG..CGG ACGGGCAGGT
         351
         401
              TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
         451
              CGCGCCCCAA GCGACGGGAA ATTTCCTCCG CGTTGTCCCG CAACACGGCA
              GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
         501
              CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA
This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:
     a520.pep
           1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDLILFAA KPSRRALMIG
             IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
          51
```

101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

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151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALP	FSRISXRMKLI	LVPLIMPAM	DLILFAAKPSR	RALMIGIPPA	WIZAATA
		11111 11111	11111111	1111111111	111111111	
a520	MPALLSVHRXNALP	FSRISERMKLI	LVPLIMPAM	DLILFAAKPSR	RALMIGIPPA	TAASNW
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISL	PYSASSFLLAV	TMCLPFSM	AFNTASLAMPV	PPNNSTTTSI	SSRATS
		11111111111			1111111111	111111
a520	TMTFCFSASGKISL	PYSASSFLLAV	TMCLPFSM	AFNTASLAMPV	PPNNSTTTSI	SSRATS
	. 70	80	90	100	110	120
	130	140.	150	160	170	180
m520.pep	SNGSLTKAXRTGRF	VGLFLHSNRTF	ROKYGFRAP	SDGKFPPRCXA	TRQPYRRRPY	PNLKDR
					111/111111	
a520	SNGSLTKAXRTGRF		RQKYGFRAPS	SDGKFPPRCPA	TRQPYRRRPY	PNLKDR
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRLK	CKYX				
		1111				
a520	CLLASLCLLVSRLK	CKYX				
	190					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1465>: g520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA 101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTTCCGC CAGCGGGAAG 151 ATTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG 201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGccgAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG 301 AACGGATCTT TGACAAAGGC GGCGGACGGG CAGATTTGGC GGGCTTTTTC 351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC 401 GGGAAATTTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG 451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC 501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>: g520-1.pep

- 1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK 51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
- 101 NGSLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
- 151 TVPKPKRPMF TGFIVSPCKP TEM*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1467>: m520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT 51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA 101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTTCCGC CAGCGGGAAG 151 ATTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG 201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC 251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTCACGTGC GACCAGTTCG 301 AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTTGTC GGGCTTTTTC TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC 351 401 GGGAAATTTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG 451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC 501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>: m520-1.pep

- 1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK 51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```
NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
         TVPKPKRPMF TGFIVSPCKP TEM*
g520-1/m520-1
               97.1% identity in 173 aa overlap
                   10
                            20
                                    30
                                             40
                                                      50
           MKLLVPLIMPAMDLILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF
q520-1.pep
            m520-1
           MKLLVPLIMPAMDLILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF
                                    30
                                             40
                                                               60
                            80
                                    90
                                            100
                                                    110
                                                             120
           \verb|LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSLRATSSNGSLTKAADGQIWRAFSSLK|
g520-1.pep
           LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK
m520-1
                   70
                           80
                                    90
                                            100
                                                    110
                  130
                           140
                                   150
                                            160
                                                    170
           SHMAEIRISRPKRREISSALSRNTAAAPPPTVPKPKRPMFTGFIVSPCKPTEMX
g520-1.pep
           m520-1
           SHTAEIRISRPKRREISSALSRNTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX
                                   150
                                            160
                                                    170
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1469>:
a520-1.seq
        ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
      1
     51
        TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
    101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTTCCGC CAGCGGGAAG
    151
        ATTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
        TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
    201
        CGCCGAACAA TTCGACGACG ACATCGACGT CTTCACGTGC GACCAGTTCG
        AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTTGTC GGGCTTTTTC
    301
        TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
    351
        GGGAAATTTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
        ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
    451
        TTGTAAGCCG ACTGAAATGT AA
This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:
a520-1.pep
      1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
     51
        ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
    101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
        TVPKPKRPMF TGFIVSPCKP TEM*
m520-1/a520-1
              100.0% identity in 173 aa overlap
                  10
                           20
                                    30
                                            40
a520-1.pep
           MKLLVPLIMPAMDLILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF
           m520-1
           MKLLVPLIMPAMDLILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF
                  10
                           20
                                    30
                                            40
                                                     50
                                                              60
                  70
                           80
                                    90
                                           100
                                                    110
                                                             120
a520-1.pep
           LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK
           m520-1
           LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK
                  70
                                                    110
                 130
                          140
                                   150
           SHTAEIRISRPKRREISSALSRNTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX
a520-1.pep
           m520-1
           SHTAEIRISRPKRREISSALSRNTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX
                 130
                          140
                                   150
                                           160
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1471>: 9521.seq

- 1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTCAAG
- 51 CCCATTGGGT GCGAATGCGG CCAAAATCTA TACCTGCACA ATCAACGGAG
- 101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTTG

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- 151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAAACTCC
- 201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
- 251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
- 301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
- 351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAaqcac
- 401 qtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cqcattqtaa
- 451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAqAATt
- 501 GGGACGTATG TAA

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>: g521n.pep

- 1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTDL
- 51 PPIGNYSSER YILPQTPEPA PSPSNGGQAV KYKAPVKTVS KPAKSNTPPO
- 101 QAPVNNSRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
- SNVLDRQQNI QALQRELGRM *

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1473>:

- m521.seq
 - ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTCAAG
 - CCCATTGGGT GCGAATGCGG CCAAAATCTA SACCTGCACA ATCAACGGAG
 - AAACCGTTTA CACCASCAAG CCGTCCAAAA GCTGCCACTC AACCGATTTG
 - CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
 - 201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACWGGTTGTC AAATATAAAG
 - 251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCArTAC GCCGCCGCCG
 - 301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
 - 351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
 - 401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
 - 451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
 - 501 ACTGGGGCGT ATGTAA

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

m521.pep

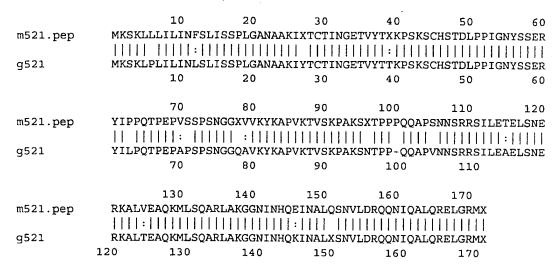
- MKSKLLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTDL
- PPIGNYSSER YIPPQTPEPV SSPSNGGXVV KYKAPVKTVS KPAKSXTPPP
- 101 QQAPSNNSRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
- QSNVLDRQQN IQALQRELGR M*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from N. gonorrhoeae:

m521/g521



The following partial DNA sequence was identified in N. meningitidis <SEO ID 1475>: a521.seq

ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAAG

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786
           51 CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
          101 AAACCGTTTA CACCACCAAG CCGTCCAAAA GCTGCCTCTC AACCGATTTG
          151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACATC
          201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
          251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
              CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
              GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
          401
              CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
          451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
         501 ATTGGGACGT ATGTAA
This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:
     a521.pep
              MKSKLPLILI NFSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCLSTDL
              PPIGNYSSER YIPPQTSEPT PSPSNGGQAV KYKAPVKTVS KPAKSNTPPP
          51
              QQAPSNNSRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
          101
              QSVLDRQQN IQALQRELGR M*
         151
           94.2% identity in 171 aa overlap
m521/a521
                                            30
                                                     40
                                                               50
                                                                        60
                 MKSKLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER
     m521.pep
                 a521
                 MKSKLPLILINFSLISSPLGANAAKIYTCTINGETVYTTKPSKSCLSTDLPPIGNYSSER
                         10
                                  20
                                            30
                                                     40
                                                              50
                                                                        60
                         70
                                  80
                                                    100
                                            90
                                                             110
                                                                       120
                 YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNSRRSILETELSNE
    m521.pep
                 YIPPQTSEPTPSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNSRRSILETELSNE
     a521
                         70
                                  80
                                            90
                                                    100
                                                             110
                        130
                                 140
                                          150
                                                    160
                                                             170
                 RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDRQQNIQALQRELGRMX
    m521.pep
                 RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDRQQNIQALQRELGRMX
     a521
                        130
                                 140
                                          150
                                                    160
                                                             170
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1477>:
         atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
        caaaaaaqca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
        ttttqqcqtt qctcqcttca accgccctqc tctcccaatq cqcqatqtcc
    151 aaaccqcaqq caaaacaqaa aattqtcqaq tcttqcatqa aaaatattcc
    201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
    251 acaatacccq tctcqccqtc qactactqca aatqtatqtq qqaqcaqcct
    301 ttqqacqqat tqaqcqaqaa acaqatcaqc tccttcqqca aactcqqtqc
         acaagaacag cttgacctgc tcggcggcgc aaacgcgttt gaaactcgag
         acaaacaatg tgtcgcggat ttgaaagccg attga
This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:
         MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
         KPOAKOKIVE SCMKNIPFAE KWONDLKARG LDADNTRLAV DYCKCMWEOP
         LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1479>:
        ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
     51 CAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCGTGGGTCA
    101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
```

151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC 201 GTTTGCCGAA AAATGGCAAA ACGATTTGCG GGCCCGCGGT TTAGATTCAA 251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

g522.seg

g522.pep

m522.seg

```
TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
          ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
          ACAAGCAGTG TGTTGCCGAT TTGAAATCAG AATAA
 This corresponds to the amino acid sequence <SEO ID 1480; ORF 522>:
m522.pep
          MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSOCAMS
         KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEOP
         LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKOCVAD LKSE*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng)
from N. gonorrhoeae:
m522/q522
                             20
                                      30
                                               40
                                                         50
            MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE
m522.pep
            q522
            MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE
                             20
                    10
                                      30
                                               40
                                                         50
                    70
                             80
                                      90
                                              100
                                                        110
m522.pep
            SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGKLGAOEO
            q522
            SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGKLGAQEQ
                    70
                             80
                                      90
                                              100
                                                        110
                   130
                            140
m522.pep
            LDLLGGANAFEARDKOCVADLKSEX
            q522
            LDLLGGANAFETRDKQCVADLKAD
                            140
                  130
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1481>:
     a522.seq
              ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
           1
              CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
          51
         101
              TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
         151
              AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
              GTTTGCCGAA AAATGGCAAA ACGATTTGCG GGCCCGCGGT TTAGATTCAA
         201
              ACAATACCCG CCTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
         251
              TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
              ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
         351
              ACAAGCAGTG TGTTGCCGAT TTGAAATCAG AATAA
This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:
     a522.pep
              MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
           1
              KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
              LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*
m522/a522 95.8% identity in 144 aa overlap
                                 20
                                          30
                                                             50
                MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE
    m522.pep
                 MTEPKHEMPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE
     a522
                        10
                                 20
                                          30
                                                    40
                                                             50
                        70
                                          90
                                                  100
                SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGKLGAQEQ
    m522.pep
                 a522
                SCVKNIPFAEKWQNDLRARGLDSNNTRLTVDYCKCMWEQPLDRLSEKQISSFGKLGAQEQ
                        70
                                 80
                                          90
                                                  100
                                                            110
                                                                     120
```

130 140 LDLLGGANAFEARDKQCVADLKSEX m522.pep LDLLGGANAFETRDKQCVADLKSEX a522 130 140

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1483>: q523.seq

- . 1 atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
- qacqqqaacq qtttatcttt tgqttqtcaq cqcggctttq qcqqqttcqq 51
- 101 quattgecta egggetgact ggeageaege etgeegeegt ettgaeegee
- 151 gcactgcttt ccgcgctggg catttggttc gtacatgcca aaaccgccgt
- 201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
- 251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
- 301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
- 351 aacgcgcgcc ctcatcgtcc gcaaagaagg taaccttctt atcatcgcaa
- 401 acccttaa

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>: g523.pep

- MTVWFVAAVA VLIIELLTGT VYLLVVSAAL AGSGIAYGLT GSTPAAVLTA
- ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYAEILRYT GGNRYEVFYR
- GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1485>: m523.seq (partial)

- ..GCCGTCTTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT 1
- nagcgcggct ttggcgggtt cgggcattgc ttacgggctg accggcagta 51
- CGCCTGCCGC CGTCTTGACC GnCGCTCTGC TTTCCGCGCT GGGTATTTnG 101
- TTCGTACACG CCAAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA 151
- GGATTTGGAT GCCGGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA 201
- ACCGTTACGA AGTTTTLTAT CGCGGTACGC ACTGGCAGGC TCAAAATACG 251
- 301 GGGCAAGAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGCAAGGA
- AGGCAACCTT CTTATTATCA CACACCCTTAA

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>: (partial) m523.pep

- ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX 7
- FVHAKTAVRK VETDSYQDLD AGQYVEILRH TGGNRYEVFY RGTHWOAONT 51
- GQEELEPGTR ALIVRKEGNL LIITHP* 101

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF523 shows 91.3% identity over a 126 as overlap with a predicted ORF (ORF 523.ng) from N. gonorrhoeae: m523/g523

10 20 AVLIIELLTGTVYLLVVSAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF m523.pep q523 MTVWFVAAVAVLIIELLTGTVYLLVVSAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF 10 20 30 40 50 60 70 80 90 100 VHAKTAVRKVETDSYQDLDAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA m523.pep g523 VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA 70 80 90 100

120

LIVRKEGNLLIITHP m523.pep 111111111111::1

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LIVRKEGNLLIIANPX g523

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1487>:
```

- ATGACTGTAT GGTTTGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT 51 GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG 101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC 151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT 201 GGGAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
- 251 CCGAAATCCT CCGGCACGCA GGCGGCAACC GTTACGAAGT TTTTTATCGC 301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
- 351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
- 401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep

- MTVWFVAAVA VLIIELLTGT VYLLVVSAAL AGSGIAYGLT GSTPAAVLTA
- 51 ALLSALGIWF VHAKTAVGKV ETDSYODLDA GOYAEILRHA GGNRYEVFYR
- 101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*

130

m523/a523 94.4% identity in 126 aa overlap

		4				
		10	20	30	40	50
m523.pep	AVLIIE	LLTGTVYL	LVVSAALAGSG	IAYGLTGST	PAAVLTXALL	SALGIXF
	11111	1111111	111111111111		111111 111	11111 1
a523	MTVWFVAAVAVLIIE	LLTGTVYI	LVVSAALAGSG	SIAYGLTGST	PAAVLTAALL	SALGIWF
	10	20	30	40	50	60
	60	70	80	90	100	110
m523.pep	VHAKTAVRKVETDSY	QDLDAGQY	VEILRHTGGNR	YEVFYRGTH	WQAQNTGQEE	LEPGTRA
		1111111	: :			111111
a523	VHAKTAVGKVETDSY	QDLDAGQY	AEILRHAGGNR	YEVFYRGTH	WQAQNTGQEE	LEPGTRA
	70	80	90	100	110	120
	120					
m523.pep	LIVRKEGNLLIITHP	X				
	11111111111111::1	1				
a523	LIVRKEGNLLIIAKP	Х				

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1489>:

q525.seq

- 1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca 51 ageggegget geegaaatgg tteaaatega aggeggeage taeegeeege 101 tttatctgaa aaaagatacc ggcctgatta aagtcaaacc gttcaaactg 151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca 201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaacccgctt 251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg 301 ggcgaattga aacagccggt taccaatatt tcctggtttg ccgccaacgc 351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat 401 ttgccggact tgcttccgcc acgcagaaaa aacggctcaa acgaacccgg 451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc 501 tgcacgatgt cggcaaagca ccgcccgaac tactggggtg tttatgatat
- 551 gcacgggctg a This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>: g525.pep
 - 1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 - 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
 - 101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRTR
 - 151 LOPHYSRLVC RRRTERPARC ROSTARTTGV FMICTG *

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1491>:

```
m525.seq
               ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG CCrrCACTCA
            1
               Arcggcggct gccgaaatgg ttcaaatcga aggcggcagc taccgcccrc
           51
               TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACTG
          101
               GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
          151
          201
              CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
               ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
          251
               GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGwTTG CCGCCAAcGC
          301
               CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
          351
               TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
          401
               CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
          451
               TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
          501
               GCACGGGCTG A
          551
This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:
     m525.pep
               MKYVRLFXLG AALAXTQXAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
               DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
           51
               GELKQPVTNV SWXAANAYCA AQGKRLPTID EWEFAGLASA TQKXRLKRTR
          101
               LQPHYSRLVC RRRTERPARC RXKAARTTGA FMICTG*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng)
from N. gonorrhoeae:
     m525/g525
                         10
                                  20
                                            30
                                                      40
                                                                         60
     m525.pep
                 MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
                  MKYVRLFFLGTALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
     g525
                         10
                                   20
                                            30
                                                      40
                                                               50
                                                                         60
                         70
                                   80
                                            90
                                                     100
                                                              110
                                                                        120
                 AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
     m525.pep
                 AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTNISWFAANAYCA
     g525
                         70
                                  80
                                            90
                                                    100
                                                              110
                                                                        120
                        130
                                  140
                                           150
                                                    160
                                                              170
                                                                        180
                 AQGKRLPTIDEWEFAGLASATQKXRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
     m525.pep
                 AQGKRLPTIDEWEFAGLASATQKKRLKRTRLQPHYSRLVCRRRTERPARCRQSTARTTGV
     q525
                        130
                                 140
                                           150
                                                    160
                                                              170
                                                                        180
     m525.pep
                 FMICTGX
                 FMICTGX
     g525
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1493>:
     a525.seq
              ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
           1
              AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
          51
              TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACTG
         101
              GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
         151
         201
              CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
              ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
         251
         301
              GGCGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTCG CCGCCAACGC
              CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
         351
              TTGCCGGACT TGCCTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
         401
              CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
         451
              TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
         501
```

551 GCACGGTCTG A

```
This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:
```

```
a525.pep

1 MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
```

51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA 101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR

151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*

m525/a525 90.8% identity in 185 aa overlap

25/a525 90.89	% identity in 185 a	aa overlap				
	10	20	30	40	50	60
m525.pep	MKYVRLFXLGAALAX	XTQXAAAEM	VQIEGGSYRPL	YLKKDTGLIF	KVKPFKLDKY:	PVTNAEF
	11::11: 1 1111		1111111111			111111
a525	MKFTRLLFLCAALAG	GTQAAAAEM'	VQIEGGSYRPL	YLKKDTGLI	(VKPFKLDKY	PVTNAEF
	10	20	30	40	50	60
	70	80.	90	100	110	120
m525.pep	AEFVNSHPQWQKGR:	IGSKQAEPA:	YLKHWMKNGSR	SYAPKAGELK	(QPVTNVSWX	AANAYCA
		11111111		1111111:11	, , , , , , , , ,	
a525	AEFVNSHPQWQKGR1		YLKHWMKNGSR	SYAPKAGDLK	QPVTNVSWF	AANAYCA
	70	80	90	100	110	120
	120	1.40	4.50			
505	130	140	150	160	170	180
m525.pep	AQGKRLPTIDEWEFA		KRLKRTRLQPH	YSRLVCRRRT		
505			111111111			
a525	AQGKRLPTIDEWEFA				_	
	130	140	150	160	170	180
m525.pep	FMICTGX					
a525	FMICTVX					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1495>: g525-1.seq

```
1 ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACTCA
 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101
    TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGACC GCCCGAACTA CTGGGGTGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
    TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACTATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
    GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCGCAAGC
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>: g525-1.pep

- 1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
 101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
 151 YNRTILDWYA DGGRKGLHDV GKDRPNYWGV YDMHGLIWEW TEDFNSSLLS
 201 SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCAS
- 251 R*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1497>: m525-1.seq

- 1 ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
- 51 AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
- 101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACTG

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```
GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
151
    CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
    ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
251
    GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
301
    CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
351
    TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
401
    TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
451
    GCACGATGTC GGCAAAGGCC GCCCGAACTA CTGGGGCGTT TATGATATGC
    ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
551
    TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
601
    GAGCGACTCG TCCAACTATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
651
    GCCTGCAATC CAAATATGTC TTGCACAACT TGGGCTTCCG TTGCACAAGC
701
```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>: m525-1.pep

```
MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
      1
        DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
     51
        GELKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
    101
        YNRTILDWYA DGGRKGLHDV GKGRPNYWGV YDMHGLIWEW TEDFNSSLLS
        SGNANAOMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
    201
    251
              97.6% identity in 251 aa overlap
m525-1/q525-1
                                           40
                 10
                        20
                                  30
                                                   50
           MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
m525-1.pep
           MKYVRLFFLGTALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
g525-1
                          20
                                  30
                                           40
                                   90
                                          100
                                                  110
                                                           120
                 70
                          80
           AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTNVSWFAANAYCA
m525-1.pep
           AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTNISWFAANAYCA
g525-1
                          80
                                  90
                                          100
                                                  110
                                                           120
                 70
                         140
                                 150
                                          160
           AOGKRLPTIDEWEFAGLASATOKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWGV
m525-1.pep
           AQGKRLPTIDEWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKDRPNYWGV
g525-1
                                                  170
                130
                         140
                                 150
                                          160
                                                          180
                190
                         200
                                 210
                                          220
                                                  230
                                                           240
           YDMHGLIWEWTEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLQSKYV
m525-1.pep
           g525-1
           YDMHGLIWEWTEDFNSSLLSSGNANAQMFCSGASVGASDSSNYAAFLRYGIRTSLQSKYV
                190
                         200
                                                  230
                250
          LHNLGFRCTSRX
m525-1.pep
           1111111111111
g525-1
          LHNLGFRCASRX
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1499>: a525-1.seq

```
ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
    AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
51
    TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACTG
101
    GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
151
    CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
201
    ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
251
    GGCGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTCG CCGCCAACGC
301
    CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
351
    TTGCCGGACT TGCCTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
401
    TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAAGACCT
451
    GCACGATGTC GGCAAAGGTC GCCCGAACTA CTGGGGCGTT TATGATATGC
501
    ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
551
     TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
    GAGCGACTCG TCCAACTATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
651
701
    GCCTGCAATC CAAATATGTC TTGCACAACT TGGGCTTCCG TTGCACAAGC
751
    CGATAA
```

```
This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:
 a525-1.pep
       1
          MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
          DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
      51
          GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
     101
          YNRTILDWYA DGDRKDLHDV GKGRPNYWGV YDMHGLIWEW TEDFNSSLLS
     201
          SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
     251
         R*
 m525-1/a525-1
               97.2% identity in 251 aa overlap
                   10
                            20
                                     30
                                              40
            MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
 m525-1.pep
            a525-1
            MKFTRLLFLCAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
                                     30
                                              40
                                                      50
                   70
                            80
                                     90.
                                             100
                                                      110
            AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVTNVSWFAANAYCA
 m525-1.pep
            {\tt AEFVNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA}
 a525-1
                   70
                            80
                                     90
                                            100
                  130
                           140
                                    150
                                             160
                                                     170
                                                              180
            AQGKRLPTIDEWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWGV
m525-1.pep
            a525-1
            AQGKRLPTIDEWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWGV
                  130
                           140
                                    150
                                            160
                                                     170
                                                              180
                           200
                                    210
                                            220
                                                     230
m525-1.pep
            YDMHGLIWEWTEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLQSKYV
            a525-1
            YDMHGLIWEWTEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLQSKYV
                  190
                           200
                                    210
                                            220
                                                     230
                  250
            LHNLGFRCTSRX
m525-1.pep
            1111111111
a525-1
            LHNLGFRCTSRX
                  250
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1501>:
     g527.seq
               atggttttac cagteteett ttttcageet gtecagttgg cggcggtege
               gcttggtcgg tctgccgtcg ggatgggcgg aagtgatgcg gctgaattgg
           51
          101
               tegagetgtt tgcactette ceteaatget geegtttteg egtettette
          151
               atacagaagc cgcgcctcgg gtgccgggcg gcgttggtgg ttcaaacctt
               taaccttgat tttatgggga agggaattga gcgtcaggtc gataatatcg
               ccgatgtcta tggttttact gtttttgact ttcgagccgt ttacttgaac
               cctacccagt tcgatatgct tttgcgcaag ggaacgggtc ttgaaaaaac
               gtgccgccca aagccatttg tccagccgca tggcggaaga atcgtgcttg
               tettteatac gattttgttt gaaataattg aatttgttte gagtttagea
          401
          451
This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:
     g527.pep
               MVLPVSFFQP VQLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFF
               IQKPRLGCRA ALVVQTFNLD FMGKGIERQV DNIADVYGFT VFDFRAVYLN
           51
          101
               PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1503>:
     m527.seq
               ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
            1
              GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
           51
              TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTwTCG CGTCCTCTTC
          101
              ATACAGAAGC CGCGCYTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
```

```
201 TAACCKTGAT TTTATAGGGA AGGG.AATTK AGCKTCaGTy GrTwATaTCG
           251 CSGATGTMTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
           301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
               GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
               TCTTTCATAC GATTTTGTTT GAAATAATTG AATTTGTTTC GAGTTTAGCA
           401
           451
 This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:
      m527pep
               MVLPVSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLF
               IOKPRXGCRA ALVVQTFNXD FIGKXNXASV XXIADVYGFT VFDLRAVYLN
            51
           101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 Computer analysis of this amino acid sequence gave the following results:
 Homology with a predicted ORF from N. gonorrhoeae
 ORF 527 shows 90.0% identity over a 150 as overlap with a predicted ORF (ORF 527.ng)
 from N. gonorrhoeae:
     m527/g527
                          10
                                   20
                                                      40
                  MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA
     m527.pep
                  MVLPVSFFQPVQLAAVALGRSAVGMGGSDAAELVELFALFPQCCRFRVFFIQKPRLGCRA
     g527
                         10
                                            30
                                                      40
                                                               50
                                                                        60
                                            90
                                                    100
                                                                       120
                  {\tt ALVVQTFNXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP}
     m527.pep
                  {\tt ALVVQTFNLDFMGKGIERQVDNIADVYGFTVFDFRAVYLNPTQFDMLLRKGTGLEKTCRP}
     q527
                         70
                                   80
                                            90
                                                    100
                                                              110
                        130
                                  140
                                           150
     m527.pep
                  KPFVQPHGGRIVLVFHTILFEIIEFVSSLA
                  q527
                  KPFVQPHGGRIVLVFHTILFEIIEFVSSLA
                        130
                                  140
                                           150
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1505>:
     a527.seq
              ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
            1
              GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
              TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
          101
          151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
              TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
          251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
          301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
          351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
          401 TCTTTCATAC GATTTTGTTT GAAATAATTG AATTTGTTTC GAGTTTAGCA
          451 TAA
This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:
     a527.pep
              MVLPVSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLF
             IQKPRLGCRA ALVVQTFNLD FIGKGIERQV DNIADVYGFT VFDLRAVYLN
          51
         101
             PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
m527/a527 93.3% identity in 150 aa overlap
                        10
                                  20
                                           30
                                                     40
                                                              50
                 MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA
    m527.pep
                 MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRFRVLFIQKPRLGCRA
     a527
                        10
                                  20
                                           30
                                                    40
                                                              50
```

	•
	70 80 90 100 110 120
m527.pep	
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP 70 80 90 100 110 120
m527.pep	130 140 150 KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX
a527	
a327	130 140 150
	partial DNA sequence was identified in N. gonorrhoeae <seq 1507="" id="">:</seq>
g528.seq 1	
51	
101	ccggctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 201	- 55 55 5 5 5 5 1
251	
301	acgcgtgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 401	ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc gatggtaa
	ds to the amino acid sequence <seq 1508;="" 528.ng="" id="" orf="">:</seq>
g528.pep	52Q 12 1500, Old 520.ngs.
1	MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51 101	GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*
	partial DNA sequence was identified in N. meningitidis <seq 1509="" id="">:</seq>
	(partial)
1	ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51 101	TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151	GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201	CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 301	ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351	CTGCTTGGAA AAG
This correspond	ls to the amino acid sequence <seq 1510;="" 528="" id="" orf="">:</seq>
m528.pep	(partial)
1 51	METRATKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
101	GGESPPSLGD YEIPLSDGNS SVRANEYESA QQSYFYRKIG KFEXCGLDWR TRDGKPLIET FKQGGFDCLE K
Computer analy	rsis of this amino acid sequence gave the following results:
	a predicted ORF from N. gonorrhoeae
	89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng)
from N. gonorri	hoeae:
m528/g528	
	10 20 30 40 50 60
m528.pep	10 20 30 40 50 60 MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
	1111:14111 11:4:1111111111111111
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECLSLSGWCKPRKPAAIDFWDIGGESPLSLED 10 20 30 40 50 60
	10 20 30 40 50 60
500	70 80 90 100 110 120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
	70 80 90 100 110 120

```
m528.pep
              К
q528
              KQGLRRNGLSERVRW
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1511>:

796

```
a528.seq
           ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
       1
      51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
     101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
     151 GGCGGCGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
     201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
     251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT 301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
     351
           TTGTTTGAAA AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
     401
          GATGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

a528.pep

WO 99/57280

- MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI 1
- GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR 51
- TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

m528/a528 95.0% identity in 121 aa overlap

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALL	AFTVAGCRLA	AGWYECSSLT	GWCKPRKPAA	IDFWDIGGES	SPPSLGD
		HHHHHH		1111111111	1111111111	1111
a528	MEIRAIKYTAMAALL	AFTVAGCRLA	AGWYECSSLS	GWCKPRKPAA	IDFWDIGGES	SPPSLED
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRAN	EYESAQQSYE	YRKIGKFEX	CGLDWRTRDG	KPLIETFKQG	GFDCLE
		1111111		1111111111	11111111	11111:
a528	YEIPLSDGNRSVRAN	EYESAQQSYE	YRKIGKFEA	CGLDWRTRDG	KPLIETFKQE	GFDCLK
	70	80	90	100	110	120
m528.pep	К					
MOZO PCP	i					
a528	KQGLRRNGLSERVRW	Х				
•	130					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1513>: g528-1.seq

```
1 ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCTTGT
    CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
101
151 GGCGGCGAGA GTCCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
    ACGCGTGACG GCAAACCTTT GGTTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGGAA AAGCAGGGGT TGCGGCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>: g528-1.pep

- MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
- 1 51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
- 101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1515>: m528-1.seq

1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

PCT/US99/09346

```
WO 99/57280
                                          797
     51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
         CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
    101
         GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
    151
    201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
    251 ACTITTACAG GAAAATAGGG AAGTITGAAG CCTGCGGGCT GGATTGGCGT
         ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
    301
         CTGCTTGGAA AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
    351
    401 GATGGTAA
This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:
m528-1.pep..
         MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
      1
         GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
     51
        TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*
g528-1/m528-1 92.6% identity in 135 aa overlap
                   10
                            20
                                      30
                                               40
                                                        50
           MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
q528-1.pep
            MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
m528-1
                            20
                                     30
                                               40
                   70
                            80
                                      90
                                              100
                                                       110
            YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
g528-1.pep
            YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
m528-1
                   70
                            80
                                     90
                                             100
                                                       110
                  130
           KQGLRRNGLSERVRWX
q528-1.pep
            m528-1
            KQGLRRNGLSERVRWX
                  130
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1517>:
      1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
     51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
         CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
    151 GGCGGCGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
    201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
    251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
    301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
```

a528-1.seq

```
351 TTGTTTGAAA AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>: a528-1.pep

MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI 1

GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR 51 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

97.0% identity in 135 aa overlap a528-1/m528-1

	10	20	30	40	50	60
a528-1.pep	MEIRAIKYTAMAALLA	FTVAGC	RLAGWYECSSLS	GWCKPRKPA	AIDFWDIGGES	PPSLED
		HHHH	111111111111111111111111111111111111111		11111111111	
m528-1	MEIRAIKYTAMAALLA	FTVAGC	RLAGWYECSSLT	GWCKPRKPA	AIDFWDIGGES	PPSLGD
	10	20	30	40	50	60
	70	80	90	100	110	120
a528-1.pep	YEIPLSDGNRSVRANE	YESAQQ	SYFYRKIGKFEA	CGLDWRTRD	GKPLIETFKQE	GFDCLK
	111111111111111111	111111	111111111111	1111111		11111:
m528~1	YEIPLSDGNRSVRANE	YESAQQ	SYFYRKIGKFEA	CGLDWRTRD	GKPLIETFKQG	GFDCLE
	70	80	90	100	110	120
	130					
a528-1.pep	KQGLRRNGLSERVRWX					

11111111111111 m528-1 KOGLRRNGLSERVRWX 130

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1519>:
         (partial)
q529.seq
         atgacccata tcaaacccgt cattgccgcg ctcgcactca tcgggcttgc
       1
      51 cgcctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
     101 ggtcgcaccg cctgatcaaa ctcgaagtcc cgcctgattt gaacaacccc
     151 gaccaaggca acctctaccg cctgcctgcc ggttcgggag ccgtccgcgc
     201 cggggatttg gaaaaacgcc gcacacccgc cgtccaacag ccagcggatg
     251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
     301 gccaacgcct ggcttgtcgt tgacggcaaa tcccccgccg aaatctccgc
     351 cgctttctg.
This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:
g529.pep
         (partial)
         MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
         DOGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
      51
         ANAWLVVDGK SPAEISAAF..
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1521>:
m529.seq
         ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
         CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
         GGTCGCACCG CCTGATCAAA CTTGAAGTCC CACCTGATTT GAACAACCCC
     151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
     201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
     251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
    301 CAACGCTGGC TCGTTGTCGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
    351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
    401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
    451 CCCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
    501 CTACTCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
    551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
    601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
    651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTGGGCG
    701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAAACC TACCCTTCCC
    751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
    801 CGACTACGGC AGAAACTGGC GGCGCACCGT GCTCGCCCTC GACCGCATCG
    851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
    901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
    951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
    1001 AACTGATTGT CTATGCAGAA CCTGTCGCCA ACGGCTCGCG CATCGTCCTG
    1051 CTCAACAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
    1101 GGGCAAACTC CATTCCGAAC TGCGTTAA
This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:
m529.pep
      1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
     51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAEVLKSV KGVRLERDGS
    101 QRWLVVDGKS PAEIWPLLKA FWQENGFDIK SEEPAIGQME TEWAENRAKI
    151 PQDSLRRLFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
    201 YGGKDKDTTV WQPSPSDPNL EAAFLTRFMQ YLGVDGQQAE NASAKKPTLP
    251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
         KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
     351 LNKDGSAYAG KDASALLGKL HSELR*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng)
from N. gonorrhoeae:
g529/m529
                                         3.0
```

MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA

g529.pep

WO 99/57280 PCT/US99/09346

m529 I	10	20	30	40	50	60 60
	70	80	90	100	110	120
	SSGAVRAGDLEKR :					AFX
	SGAVRASDLEKR 70					LLK
m529 A	AFWQENGFDIKSE) 130	EPAIGQMETEV 140	AENRAKIPQDS 150	SLRRLFDKVGL 160	GGIYSTGERDKF 170	IVR
The following	nartial DNA so	equence was	identified i	n N menina	itidis <sfo i<="" td=""><td>D 1523>-</td></sfo>	D 1523>-
a529.seq		oquonoc was		ii i i i ii ii ii ii ii ii ii ii ii ii	arais ADEQ I	D 13232.
1	ATGACCCATA					
51						
101						
151						
201						
251	CCGAAGTATT					
301	CAACGCTGGC					
351						
401	CCGCCATCGG					
451	CCCCAAGACA					
501 551	CTACTCCACC				GAACAGGGCA GAAAGAAGTG	
601	TACGGCGGCA					
651	TCCCAACCTC					
701	TTGACGGACA					
751	GCCGCCAACG					
801	CGACTACGGC					
851	GGCTGACCGT					
901	AAAGCCCCGA					
951	CAAACGCCTG					
1001	AACTGATTGT					
1051	CTCAACAAAG					
1101	GGGCAAACTC			ANAGACGCAT	CCGCATTATT	
This correspond	is to the amino	o acid seque	nce <seo ii<="" td=""><td>D 1524: ORI</td><td>7 529 a>·</td><td></td></seo>	D 1524: ORI	7 529 a>·	
a529.pep	is to the diffin	o dora soque	nee abb@m	5 152 i, Old	, 32).ω.	
a529.pep	MTHIKPVIAA	TALTCLAACS	CCKALUDKID	VU6D6HD11K	TEUDDOLNND	
51	DQGNLYRLPA					
101	QRWLVVDGKS					
151	PQDSLRRLFD					
201	YGGKDKDTTV					
251	AANEMARIEG					
301	KAPNESNAVT					
351	LNKDGSAYAG			- L		
m529/a529 99	9.2% identity i	n 375 aa oy	erlan			
1110 25, 40 25	•		:0 30	40	50	60
m529.pep					LEVPPDLNNPDQ	
mozo.pep						
a529					LEVPPDLNNPDQ	
a323			0 30		50 50	60
			0 90		110	120
m529.pep					QRWLVVDGKSPA	
	1111111	1111111111	1111111111			
a529					RWLVVDGKSHA	EIWPLLKA
		70 8	0 90	100	110	120
	_	20	0			
	1	30 14	0 150	160	170	180

m529.pep	FWQENG	FDIKSEEPAI	GQMETEWAENI	RAKIPQDSLR	RLFDKVGLGG	IYSTGERDKF	IVRI
a529	FWQENG	FDIKSEEPAI	GQMETEWAENI	RAKIPQDSLR	RLFDTVGLGG	IYSTGERDKF	IVRI
		130	140	150	160	170	180
		190	200	210	220	230	240
m529.pep		VSDIFFAHKA					
		11111111					,
a529	EQGKNG'	VSDIFFAHKAI					
		190	200	210	220	230	240
		250	260	270	280	290	300
m529.pep	NASAKK	PTLPAANEMAI	RIEGKSLIVFO			_	
	11111	1 1			:		
a529	NASAKK	PTLPAANEMAI					
		250	260	270	280	290	300
		210	200	220	240	250	2.60
	*** *********	310	320	330	340	350	360
m529.pep	KAPNESI	NAVTEQKPGLI	KKLLGKGKAL	SKPAEQPELI	YAEPVANGSI	KIVLLNKDGS/	
500	11111		IIIIIIIIIIIIIIIII			77177 7 2277	
a529	KAPNESI	NAVTEQKPGLI					
		310	320	330	340	350	360
		370					
m529.pep	KDASALI	LGKLHSELRX					
mozo.pep							
a529		LGKLHSELRX					
4525		370	•				
		- ·	•				

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1525>:

```
q530.seq
```

```
1 atgagtgcga gcgcggcaat gacgggtttg atatgggtca tcgtgtcatc
```

51 ctgtgtgatg gatattaaag tgtttgtcat gttatgccgt ccgaacggtt

101 cagacggcat ggctatattt aaagttgtcc tgaggctttc agggcggcgc

151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg

tgcggtccgc atccgcccaa ggcggatacc gcccatttcg gtgcggcggg

251 actgggttcg cagaacatgg tgtcgtaaat cggaatcagc cggtcgttga

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

g530.pep

- MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLRLSGRR
- 51 GLLPVRLPSA ERAAGARAVR IRPRRIPPIS VRRDWVRRTW CRKSESAGR*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1527>:

m530.seq

- wTGAGTGCGA GCGCGGCAAT GACGGGTYTG ATATGGGTCA TCGTGTCATC
- 51 STGTGTGATG GATATTAAAG TGTyTGTTGC GWTATGCCGT CCGAACGGTT
- 101 CGGACGGCAT GGMTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
- 151 GGACTKTTGC WTGTCCGTTT YCCGTCAGCG GAACGAGCGG CAGGCGGACG
- 201 TGCGGTTCGC ATCTGCCCAg GGCGGATACC GCCCATTTCG GTGCGGCGGG
- 251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

m530.pep

- XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLRLSGRR
- GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESVGR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from N. gonorrhoeae:

m530/g530

XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA m530.pep

```
MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA
     a530
                                    20
     m530.pep
                  ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSESVGR
                  a530
                  ERAAGARAVRIRPRRIPPISVRRDWVRRTWCRKSESAGR
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1529>:
     a530.seq
               ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCATC
               CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
           51
              CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
          101
          151 GGACTTTTGC CTGTCCGCCT TCCGTCAGCG GAACGAGCGG CAGGCGGACG
               TGCGGTTCGC ATCTGCCCAG GGCGGATACC GCCCATTTCG GTGCGGCGGG
          251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGC CGGTCGTTGA
This corresponds to the amino acid sequence <SEQ ID 1530; ORF 530.a>:
     a530.pep
               MSASAAMTGL IWVIVSSCVM DIKVFVALCR PNGSDGMAIF KVVLRLSGRR
            1
               GLLPVRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESAGR*
m530/a530 93.9% identity in 98 aa overlap
                          10
                                   20
                                             30
                                                      40
                                                                50
                  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA
     m530.pep
                   MSASAAMTGLIWVIVSSCVMDIKVFVALCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA
     a530
                         10
                                   20
                                            30
                                                      40
                                                                50.
                          70
                                   80
                                             90
                                                     100
     m530.pep
                  ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSESVGRX
                  a530
                 ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSESAGRX
                         70
                                   80
                                            90
                                                     100
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1531>:
g531.seq
         ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
      1
         GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTTGGCATTG ATGTTTGCCG
     51
         GAACATGGCT GCTTGCCTAT GCCGGCGGCT ATCAAATCTA CGGCGCAGGC
        ATCTTGTGGA CGGTCGGACT CATCAGCCTT GGCGGCATAC TGGCGGACTA
         TATGGCAGGC ATGTTGGGGG TAAAATACAC TGGGGCAGGC AAACTCGCCG
     251 TCCGAGGTGC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCCTTCCC
    301 GGACTAATAC TCGGCCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
    351 TCGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
    401 GGCTTGTCGT CGGCACGGCG TTCAAAATCG GCTGCGCCGT ATCCATCTTG
     451 TTTATCCTGT TGGTGAAATA CATCGCATAC CTGTTTTAA
This corresponds to the amino acid sequence <SEQ ID 1532; ORF 531.ng>:
g531.pep
      1
         MTALLVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
         ILWTVGLISL GGILADYMAG MLGVKYTGAG KLAVRGALAG SIIGIFFSLP
         GLILGPFIGA AAGELIDRRN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
         FILLVKYIAY LF
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1533>:
m531.seg
         ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
      1
         GGCGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
     51
    101 GAACATGGCT GCTTGCCTAT GCCGGCGGCT ACCAAATCTA CGGCGCGGGC
    151 GTTTTGTGGA CGGTCGGACT CATCAGCCTT GCCGGCATAC TGGCGGACTA
    201 TGTGGCAGGC ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
    251 TTCGCGGCGC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCCTTCCC
    301 GGACTAATAC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
```

WO 99/57280 PCT/US99/09346

```
351 ACGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
         GGCTTGTCGT CGGCACGGCG TTCAAAATCG GCTGCGCnGT ATCCATCTTG
         TTTATCCTGT TGGTGAaATA CATCGCCTAC CTGTTTTAA
This corresponds to the amino acid sequence <SEQ ID 1534; ORF 531>:
m531.pep
         MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
         VLWTVGLISL AGILADYVAG IWGTKYTGAG KLAVRGALAG SIIGIFFSLP
      51
     101
         GLILGPFIGA AAGELIERRN MLOAGKAGLG TLLGLVVGTA FKIGCAVSIL
         FILLVKYIAY LF*
     151
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 531 shows 94.4% identity over a 162 as overlap with a predicted ORF (ORF 531.ng)
from N. gonorrhoeae:
m531/g531
                    10
                             20
                                       30
                                                40
                                                         50
                                                                   60
            MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL
m531.pep
            MTALLVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGILWTVGLISL
g531
                             20
                                       30
                                                40
                    10
                                                         50
                    70
                                       90
                             80
                                               100
                                                        110
                                                                  120
            AGILADYVAGIWGTKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERRN
m531.pep
            GGILADYMAGMLGVKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIDRRN
g531
                    70
                             80
                                       90
                                               100
                   130
                            140
                                      150
                                               160
            MLOAGKAGLGTLLGLVVGTAFKIGCAVSILFILLVKYIAYLF
m531.pep
            MLQAGKAGLGTLLGLVVGTAFKIGCAVSILFILLVKYIAYLF
q531
                   130
                            140
                                     150
                                               160
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1535>:
     a531.seq
              ATGACCGCCT TGCTCGTCAT CCTCGCCCTC GCCCTGATAG CCGCCGGTAC
              GGCGGGCATC GTTTACCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
          51
         101
              GAACCTGGCT GCTCGCCTAC TCCGGCGGCT ACCAAATCTA CGGCGCGGGC
              GTTTTGTGGA CGGTCGGACT CATCAGCCTT GCCGGCATAC TGGCGGACTA
         151
              TGTGGCAGGC ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
         201
              TTCGCGGCGC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCCTTCCC
         251
              GGACTAATAC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
         301
              ACGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
         351
              GGCTTATCGT CGGTACGGCG TTCAAAATCG GCTGCGCCGT ATCCATCTTG
         401
              TTTATCCTGT TGGTGAAATA CATCGCCTAC CTGTTTTAA
This corresponds to the amino acid sequence <SEQ ID 1536; ORF 531.a>:
     a531.pep
              MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
          51
              VLWTVGLISL AGILADYVAG IWGTKYTGAG KLAVRGALAG SIIGIFFSLP
              GLILGPFIGA AAGELIERRN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
              FILLVKYIAY LF*
           96.9% identity in 162 aa overlap
m531/a531
                                           30
                                                     40
                                                              50
                 MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL
    m531.pep
                 MTALLVILALALIAAGTAGIVYPALPGLALMFAGTWLLAYSGGYOIYGAGVLWTVGLISL
     a531
                         10
                                  20
                                                     40
                                           30
                                                              50
                         70
                                  80
                                           90
                                                    100
                                                             110
                                                                       120
                 AGILADYVAGIWGTKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERRN
    m531.pep
```

```
AGILADYVAGIWGTKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERRN
a531
              70
                     80
                           90
             130
                    140
                           150
        MLQAGKAGLGTLLGLVVGTAFKIGCAVSILFILLVKYIAYLFX
m531.pep
        a531
        MLQAGKAGLGTLLGLIVGTAFKIGCAVSILFILLVKYIAYLFX
             130
                    140
                           150
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1537>: g532.seq (partial)

```
l atggctgaaa caatgaaaaa acaggcggat tcgcctgatt tggtgtacgg
```

- 51 tttggaagac aggccgccgt tcggtaatgc gctcttgagc gcggttaccc
- 101 atcttttggc gattttcgtg ccgatgatta cgcccgcgct gattgtgggc
- 151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgtcgatggc
- 201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
- 251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
- 301 cggcgcgggg atgaaagagg gcggtttgag ...

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>: g532.pep (partial)

- 1 MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
- 51 GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDCA
- 101 RRGDERGRFE ...

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1539>: m532.seq

```
1 ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
  51 TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
 101 ATCTTTTGGC GATTTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
 151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
 201 GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
 251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CGGTGAATTT TTCGTTCGTT
 301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
 351 GGATGCGATG ATTTCGACGC TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
 401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
     CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
     CGTCGGCATT ACCGATTTCG GCGGCGGCTT CGGCGCGAAG GCGGACGCA
     CGTTCGGCTC GATGGAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
     GTGTTGGTGT TCAACTGCAT GAAAAACCCG CTGTTGCGCA TGAGCGGCAT
     TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
     TGGATTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
 751 TTTAAATACG GTTTTGCTTT CGACTGGCAC GCGTTTATTG TGGCGGGCGC
 801 GATTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
 851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
 901 CGCGGCGGCG TGTTGGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
 951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCGGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA
```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>: m532.pep

- 1 MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
- 51 GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
- 101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
- 151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

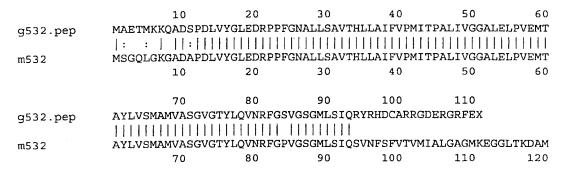
```
VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLPVP
201
    FKYGFAFDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
    RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
    VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
    VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
    EAAVKFDTDH LEH*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from N. gonorrhoeae:

g532/m532



The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1541>:

```
a532.seq
          ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
       1
         TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
      51
         ATCTTTTGGC GATTTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
         GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
     151
          GATGGTTGCG TCGGGTGTCG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
     201
         CGGTCGGTTC GGGGATGCTG TCCATCCAGT CGGTGAATTT CTCGTTCGTT
     251
         ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
     301
     351
          GGATGCGATG ATTTCGACGC TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
     401
          TGGTGTGTTT TTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
          CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
     451
          CGTCGGTATT ACCGATTTCG GCGCGGCTT CGGCGCAAAG GCGGACGGCA
     501
          CGTTCGGCTC GATGGAAAAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
     551
          GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCGGA TGAGCGGCAT
     601
          TGCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
     651
          TGGATTTTTC GGCACTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
     701
          TTTAAATATG GTTTTGCTTT TGACTGGCAC GCATTTATTG TGGCGGGTGC
     751
     801
         GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTG ACGCCGACGG
     851
         CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
     901
         CGCGGCGGC TGTTGGCGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
     951
         GGGTTCGCTG CCGCTGACGA CGTTTGCACA AAACAACGGC GTGATTCAGA
   1001
         TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
   1051
          GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
          GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCGGC TTGATTGCGA
   1101
   1151
          TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
          GTAATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
   1201
          GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAAACTCT ATTTCCGCCG
   1251
          GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
   1301
          GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA
```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pep

MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG 1 51 GALELPVEMT AYLVSMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

101	TVMIALGAGM	KEGGLTKDAM	ISTLLGVSFV	GAFLVCFSAW	LLPYLKKVIT
151	PTVSGVVVML	IGLSLVHVGI	TDFGGGFGAK	ADGTFGSMEN	LGLASLVLLI
201				LGKVDFSALQ	
251	FKYGFAFDWH	AFIVAGAIFL	LSVFEAVGDL	TATAMVSDQP	IEGEEYTKRL
301	RGGVLADGLV	SVIATALGSL	PLTTFAQNNG	VIQMTGVASR	HVGKY <u>IAVIL</u>
351	VLLGLFPVVG	RAFTTIPSPV	LGGAMVLMFG	LIAIAGVRIL	VSHGIRRREA
401	VIAATSVGLG	LGVAFEPEVF	KNLPVLFQNS	ISAGGITAVL	LNLVLPEDKT
451	EAAVKFDTDH	LEH*			

m532/a532 100.0% identity in 463 aa overlan

32/a532	100.0% iden	tity in 46.	s aa overi	ap			
		10	20	30	40	50	60
m532.pe	p MSGQLGK	GADAPDLVYG	LEDRPPFGN#	LLSAVTHLLA	IFVPMITPAL	LIVGGALELPV	EMT
	111111		1111111111		1111111111		111
a532	MSGQLGK					LIVGGALELPV	
		10	20	30	40	50	60
		70	80	90	100	110	120
m532.pe	AYI.VSMA					SAGMKEGGLTK	
MODE: pc	1111111			1111111111	1111111111	1111111111	111
a532						SAGMKEGGLTK	
		70	80	90	100	110	120
			140	150	160		180
m532.pe						VGITDFGGGF	
F 3.0						 VGITDFGGGF	
a532			34W55F15AF	150	160		180
	•	130	140	130	100		100
	1	190	200	210	220	230	240
m532.pe	ADGTFGSN	1ENLGLASLV	LLIVLVFNCN	KNPLLRMSGI	AVGLIAGYIV	ALFLGKVDFS	ALQ
- '						411111111	
a532						ALFLGKVDFS	
	1	190	200	210	220	230	240
	,	250	260	270	280	290	300
m532.pe						DOPIEGEEYT	
m332.pe						1111111111	
a532						DOPIEGEEYT	
	2	250	260	270	280	290	300
			320	330	340		360
m532.pe						VILVLLGLFP	
						 VILVLLGLFP	
a532			GSLPLTTFAÇ 320	330 330	340		360
	•	,10	320	33.0	340	330	300
	3	370	380	390	400	410	420
m532.pe	-		MFGLIAIAGV	RILVSHGIRE	REAVIAATSV	GLGLGVAFEP	EVF
			1111111111	4111111111	HIHIHI	111111111	111
a532						GLGLGVAFEP	
	3	370	380	390	400	410	420
			4.40	450	460		
			440 Aut i ni ui be	450 DKTEAAVKFD	460		
m532.pe		_		DKTEAAVKEL			
a532				DKTEAAVKFD			
4552	-	-	440	450	460		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1543>: g535.seq

```
1 atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
 51 ttttgccgta ggtcggattc tcgaatccga catttccaac agcggttttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatttaca tcgcttccaa tttcgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt
```

PCT/US99/09346 WO 99/57280

```
806
               categatgat tttgtcccgt tgtacggtgg tttggcgcgt gttgccqtaq
              ctqtcqaaqq cqqqtttttt qacggacaqq taqtqcaata cttctqqcqq
               gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccqtqca
               qeatqeqttq ctgtgecatg gtgatgtaga ggcgtttgcg qqcqcqqqtq
              atggcgacgt acatgaggcg gcgttcttct tcgaggccgc cgcgctcggc
          601 aaggeteatt tegetgggga aaegeeete tteeataeeg gtgaggaaga
          651 cggcgttgaa ttccaagcct ttggcggcgt ggacggtcat cagttggacg
          701 gctttttcgc ctgccctgc ttggttttcg ccggattcga gggcggcgtt
          751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga
This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:
     q535.pep
               MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFFVGYEYP
               ACISNLHRFO FRKLGIOFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
           51
               DVLSDAEACV GLRLFEVIDD FVPLYGGLAR VAVAVEGGFF DGOVVOYFWR
               DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
               KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
               AQEGEDGEGG IV*
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1545>:
     m535.seq
               aTGCCCTTtC CCGTTTTCAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
            1
               TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTTCCAAC AGCGGTGTTT
           51
               CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
               TACATTTCAA ATTTACATCT CTTCCAATTT CGCAAACTTG GTGTCCAACT
               CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTCGCCT
               TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTTGG CGTGGCGGAC
               GTTTTGTCCG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
          351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGTT GCCGTAACTG
          401 TCGTAGGCAG GCTTTTTGAC GGACAGGTAG TGCAATACTT CGGGTGGGAT
          451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
          501 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
          551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
          601 GCTCATTTCG CTGGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
          651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
          701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTCGAGGG CGGCATTGCT
          751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA
This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:
     m535.pep
              MPFPVFRRPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
           51 YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEFGVAD
          101 VLSDTETCVG LGLFVVVDDF IFGCGGLARV AVTVVGRLFD GOVVOYFGWD
          151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEAAAFGK
          201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
              XEGENGEGGV V*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng)
from N. gonorrhoeae:
     m535/g535
                          10
                                    20
                                             30
                                                       40
                                                                  50
                                                                           59
                 MPFPVFRRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFO
     m535.pep
                  1111111: 11 111 1111::11 1111111 1111:11111: 11111: 11111
     g535
                 MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFO
                          10
                                    20
                                             30
                                                       40
                                                                 50
                 60
                                              90
                                                       100
                  FRKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDD
     m535.pep
                  {\tt FRKLGIQFFHALFAEVDGQSGGFAFVCGIDNHAGAEFGVTDVLSDAEACVGLRLFEVIDD}
```

g535

70

80

90

100

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m535.pep		170 179 GLSVQHALLRHGDVEAFA
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAEL	
m535.pep]
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVEFQ 190 200 210 220	AFGGVDGHQLDGFFACPC 230 240
m535.pep	: :	
g535	LVFAGFEGGVAQEGEDGEGGIV 250 260	
	partial DNA sequence was identified in N. meningitia	is <seq 1547="" id="">:</seq>
a535.seq	<pre>f (partial) . TTCAGACGGC CTTTTGCCTT GTCCTTGCTA CAGTTTTTTG CC</pre>	TATTACCTOC
51		
101	. CGTCAAATAT TTTTGTCGGA TACGAGTATC CAGCCTGCAT TT	CAAATTTA
151 201		
251	. ATAATCACGC CGGTGCCGAA TTTGGCGTGG CGGACGTTTT GT	CCGATACG
301	GAAACCTGCG TAGGTTTGGG GCTGTTTGTA GTCGTCGATG AT	TTTGTCTT
351 401		CGGGTTTT
451		TTGCGCCA
501	TGGTGATGTA GAGGCGTTTG CGGGCGCGGG TGATGGCGAC GT	ACATCAGG
551 601	· · · · · · · · · · · · · · · · · · ·	
651		
701	GCTTGGTTTT CGCCGGATTC GAGAGCAGCA TTGCTTAGGA AA	
751	GGGGAAGGCG GGGTCGTCTG A	
This correspond	ds to the amino acid sequence <seq 1548;="" 53<="" id="" orf="" td=""><td>35 25.</td></seq>	35 25.
	(partial)	J.J.a .
1	FRRPFALSLL QFFAIGRILE SDISNSGFSE TIDASNIFVG YE	
51	Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z	
101 151		GRDFFDEA FGKAHFAG
201		SIA*ESED
251	GEGGVV*	
m535/a535 88	8.7% identity in 256 aa overlap 10 20 30 40	50 60
m535.pep	MPFPVFRRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF	VGYEYPTYISNLHLFOF
25.25		111111: 11111 111
a535	FRRPFALSLLOFFAIGRILESDISNSGFSETIDASNIF 10 20 30	VGYEYPACISNLHRFQF 40 50
		10 30
	70 80 90 100	110 120
m535.pep	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLS	
a535	RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLS	
		00 110
	130 140 150 160	170 100
m535.pep	130 140 150 160 IFGCGGLARVAVTVVGRLFDGQVVQYFGWDLFDEAGDDAELGL	170 180 SVOHALLRHGDVEAFAG
- -	:11	
a535	VFGRGGLARVAIAVVGGFFDGQVVQYFGRDFFDEAGDDAELGL	SVQHALLRHGDVEAFAG
	120 130 140 150 16	60 170

```
200
                                210
                                         220
                                                 230
          AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFOAFGGVDGHELDGLFACACI.
m535.pep
          a535
          AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL
                    190
                            200
                                    210
                                             220
                                                     230
                250
m535.pep
          VFTGFEGGIAXEGENGEGGVVX
          ||:||::|||::||
a535
          VFAGFESSIAXESEDGEGGVVX
            240
                    250
```

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1549>: g537.seq
```

```
1 atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
  51 tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
 101 cgtccgcacc gcaaatcagg gacggcggcg atgcgctgca ctacctcaac
 151 cgcatccgca cacaaatcgg tttgcacgcg ctggcacacg cgccggtttt
 201 ggaaaattcc gcccgcaggc acgcacgcta tctcacgctc aatcccgaag
 251 acggacacgg cgaacaccat cccgacaatc cgcactacac cgcacaaaag
 301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
 351 aaacatcagc acggaagagg aagccqccqa atcqtccqac aqcqacatcc
     qcacqcaqca acqccaaqtq qacqctttqa tqaqcqcaat ctaccaccqc
     ctttcgctgc ttgaccgcca taccgacgaa gcaggtqcqq catttqtqcq
 501 cgaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
 551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaaatat
 601 taccgcaacg cttgccacaa cggtgcggcc gtttatgctg acgaagccat
 651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcgqcqcqc
 701 tqccttattt ttacgqqqaa cqtcccqacc ccqtqccqqa atatqaaatc
 751 acaggcaatc etgccagcat tgatttttcc gaggcggcag gcaaaattgc
 801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
 851 qqqttttaac cgccggcaac gaccctaacg gcaggctgac cgcgcaccaa
 901 ttcgcccttt tcccgctcaa acctttggaa tacggcacgc tttatacggc
 951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatqqcaqt
1001 ttagaacccg aaaacccgat tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgcgg ttagaaaagg cgaaaaatat ttcatccact ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatac ctaccggcgg cagttcggca
1151 acagcctgtc catactccgg cacgaagcgg gcggcattgt cttcagcgtc
1201 ageggaatgg egggaageeg cateaggett acteeggaag acageeegga
     acgcggtgta accctttatt tgcaggattg a
```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

```
MKSLFIWLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
LTERTRLAGY LYNGVHENIS TEEEAAESSD SDIRTQQRQV DALMSAIYHR
LSLLDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RRQPEAGRKY
RNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDPVPEYEI
TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAHQ
TGNPASIDFS YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
```

351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV

401 SGMAGSRIRL TPEDSPERGV TLYLQD *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>: m537.seq (partial)

```
1 ATGAAATCCC TTTTTATTCG GCTGCTCCTG TTGGGTTCGG CGGCAGGCGT
51 TTTCTACCAT ACCCAAAMCC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGC ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
201 GGAAAACTCC GCCCGCAGGC ACGCAAGCTA CCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
```

```
CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
               AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
               GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
               CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...
This corresponds to the amino acid sequence <SEO ID 1552; ORF 537>:
     m537.pep
               (partial)
               MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
               RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
          101 LTERTRLAGY LYNGVHENIS TEEEAAESSD SDIRTQQRQV DGLMSAIYHR
              LSLLDRHTDE SGAA...
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng)
from N. gonorrhoeae:
     m537/g537
                         10
                                   20
                                                                50
                                                                          60
     m537.pep
                  MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLNRIRAQIGLHK
                  MKSLFIWLLLLGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLNRIRTQIGLHA
     q537
                         10
                                   20
                                            30
                                                      40
                                                                50
                                   80
                                            90
                                                     100
                                                               110
                                                                         120
     m537.pep
                 LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
                  LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
     q537
                         70
                                   80
                                            90
                                                     100
                                                               110
                                                                        120
                                  140
                                           150
                                                     160
     m537.pep
                 TEEEAAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDESGAA
                  TEEEAAESSDSDIRTQQRQVDALMSAIYHRLSLLDRHTDEAGAAFVRENGKTVLVFNQGN
    g537
                        130
                                  140
                                           150
                                                     160
                                                               170
                 GSFERACAKGRRQPEAGRKYYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE
     g537
                        190
                                  200
                                           210
                                                     220
                                                               230
                                                                        240
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1553>:
    a537.seg
              ATGAAATCCC TTTTTATTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
           1
              TTTCTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
          51
              CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
         101
              CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
              GGAAAATTCC GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
         201
              ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
         251
              CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
         301
              AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
         351
              GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
         401
              CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTTGTGCG
         451
              CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
         551
              AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
              TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
         601
              GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
         651
              TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
         701
              ACGGGCAATC CTGCCAGCAT TGATTTTCC GAGGCGGCAG GCAAAATTAC
         751
              GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA
         801
         851
              GGGTTTTAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
              TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
         901
         951
              GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
        1001 TTAGAACCCG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG
```

ACACTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG

CTGGTGTTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

```
GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTCAGCGTT
         1151
               GACGGAATGG CGGCCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
              ACGAGGCGTA ACCCTTTATT TACAGGATTG A
This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:
     a537.pep
              MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
           1
              RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
           51
              LTERTRLAGY LYNGVHENIS TEEEAAESSD SDIRTQQRQV DGLMSAIYHR
          101
              LSLLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
          151
              YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDPVPEYEI
              TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ
          251
              FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
          301
              TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPGSRLSIGR HKAGGIVFSV
          351
              DGMAGSRITL APEGETERGV TLYLQD*
m537/a537 98.2% identity in 164 aa overlap
                 MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLNRIRAQIGLHK
     m537.pep
                 MKSLFIRLLLLGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLNRIRAQIGLHK
     a537
                         10
                                   20
                                            30
                                                     40
                                                               50
                                                                         60
                         70
                                   80
                                            90
                                                    100
                                                              110
                                                                        120
                 LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAOKLTERTRLAGYLYNGVHENIS
     m537.pep
                 a537
                 LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS
                         70
                                  80
                                            90
                                                    100
                        130
                                  140
                                           150
                                                    160
                 TEEEAAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDESGAA
     m537.pep
                 TEEEAAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDEAGAAFVRENGKTVLVFNQGN
     a537
                                 140
                                           150
                                                    160
                 GRFERHCAQGRNQPEAGRKYYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE
     a537
                        190
                                  200
                                           210
                                                    220
                                                              230
                                                                        240
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1555>:
     q538.seq
              atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
           1
          51
              egteatgetg gtgggegtaa tgttggataa agatgataeg ggeageaatg
         101 ccgcccgtct gaacggtttt cagacggcat tggcggaagc cgtcgagctg
         151 qtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaacqcqa
         201 ccqccqcac actqcqctqt ttqtcqqcac qqqcaaqqcq qcqqaqctqt
             cqqaagcagt tgccgcaqac ggcattgatt tggtcgtatt caaccacqaa
         301 cttactccca cgcaggaacg caatttggaa aaaatcctcc aatgccgcgt
         351
              attggacaga gtggggctga ttctggcgat tttcgcccgc cgcgcccgca
         ,401
             cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
         451
              ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
         501
              cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa
              ccgcccatcg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
         551
         601
              cagcgcgccc tgcgccgcaa gtcccgcgag tcgggcagaa tcaaaacgtt
         651
              tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
         701
              tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
              acgacggcgc ggcggctgta catcagtccc gcatgcagca ttatcctgac
         801
              cgataccgtc ggattcgtca gcgatctgcc gcacaaactg atttccgcct
         851
              tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc
         901
              gtcgatgctg ccgcccggaa cagcgggcag cagattgaag acgtggaaaa
         951
              cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aaggtgtaca
        1001
              acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
```

gacgctgcgg gaaaaattgc cgccgtccgc atttccqttq ctqaaaatac

```
This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:
     g538.pep
          MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QTALAEAVEL
       1
      51
          VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVVFNHE
     101 LTPTQERNLE KILQCRVLDR VGLILAIFAR RARTQEGRLO VELAOLSHLA
     151 GRLIRGYGHL OSORGGIGMK GPGETKLETD RRLTAHRINA LKKOLANLKK
     201 ORALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDOLFATLD
          TTARRLYISP ACSIILTDTV GFVSDLPHKL ISAFSATLEE TVOADVLLHV
     251
     301 VDAAARNSGO QIEDVENVLQ EIHAHDIPCI KVYNKTDLLP SEEONTGIWR
     351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAAPNTDETE MP*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1557>:
     m538.seq
               ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
            1
              CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGTAGTG
              CCGCCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
          151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
          201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
          251 CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
          301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTSA AATGCCGCGT
          351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
          401
              CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTTGGCG
              GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
          451
              CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
              TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
               CAGCGCGCCC TGCGCCGCAA GTCnCGCGAA TCGGGCACAA TCAAAACGTT
               TGCGCTGGTC GGCTATACAA ATGTCGGAAA ATCCAGCCTG TTCAACCGGC
               TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
          751 ATTATCCTGA CCGATACCGT CGGATTCGTn AGCGATCTGC CGCACAAACT
          801 GATTTCCGCC TTTTCGCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
          851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
          901 GACGTGGAAA ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
          951 CAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
         1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCCGTCCG CATTTCCGTT
         1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCCATTG CCGAGTCTTG
              TGCCGCCGCA CCAAACACAG ACGAAACCGA AATGCCATGA
This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>;
     m538.pep
              MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QTALAEAVEL
           51 VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVVFNHE
          101 LTPTQERNLE KELKCRVLDR VGLILAIFAR RARTQEGRLQ VELAQLSHLA
          151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKOLANLKK
          201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
          251 IILTDTVGFV SDLPHKLISA FSXTLEETAQ ADVLLHVVDA AAPNSGQQIE
          301 DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
              AENTGIDALR EAIAESCAAA PNTDETEMP*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng)
from N. gonorrhoeae:
     m538/g538
                         10
                                   20
                                             30
                                                      40
                                                                50
                 {\tt MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR}
     m538.pep
                 MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR
     g538
                                   20
                                            30
                                                      40
                                                                50
                         70
                                   80
                                             90
                                                     100
                                                               110
     m538.pep
                 VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLVVFNHELTPTQERNLEKELKCRVLDR
                 g538
                 VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLVVFNHELTPTQERNLEKILQCRVLDR
```

			812			
		70	80 9	00 100) 110	120
			40 15			180
m538.pep					QSQRGGIGMKGPGI	ETKLETD
	,,,,,,,					
g538	VGLILAI	FARRARTQEGR	LQVELAQLSHL	AGRLIRGYGHI	QSQRGGIGMKGPGI	ETKLETD
		130 1	40 15	0 160	170	180
			00 21			240
m538.pep	RRLIAHR	INALIKQLANL	KKQRALRRKSR	ESGTIKTFALV	GYTNVGKSSLFNRI	TKSGIY
	[] [] [] [111111111		
g538					GYTNVGKSSLFNRI	
		190 2	00 21	0 220	230	240
			250	260	270 200	
mE30 non	7 KDKI				270 280 ISAFSXTLEETAQA	DITT T TITT
m538.pep				IIIIIIIIIIIII		
a=20		דע.זססגייית.זיי				
g538			60 27		290	
	•	250 2	27	0 200	290	300
	290	300	310	320	330 340	
m538.pep					SEEQNTGIWRDAAG	KTAAVD
	11111				111111111111	
g538 [.]					SEEQNTGIWRDAAG	
.			20 33			360
	350	360	370	380		
m538.pep	ISVAENT	GIDALREAIAES	SCAAAPNTDET	EMPX		
	111111			1111		
g538	ISVAENT	GIDALREALAE	YCAAAPNTDET	EMPX		
The following p	artial DNA s	equence was	s identified in	n N. meningi	itidis <seq id<="" td=""><td>1559>:</td></seq>	1559>:
a538.seq		_		_	•	
ĺ	ATGACAGGCA	GAACAGGCCG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG	
51	CGTCATGCTG	GTGGGCGTAA	TGTTGGACAA	AGATGGTACG	GGCAGCAGTG	
101	CCACCCGTCT	GAACGGTTTT	CAGACGGCAT	TGGCGGAAGC	TGTCGAGCTG	
151				GTGGAGACTG		
201				GGGCAAGGCG		
251				TGGTCGTATT		
301	•			AAAATCCTCC		
351				TTTCGCCCGC		
401				CACAATTGAG	CCATTTGGCG GCGGCGGTAT	
451 501					CGCCGATTGA	
551					CCTCAAAAAA	
601				TCGGGCACAA		
651				ATCCAGTCTG		
701				AGCTTTTCGC		
7.1	7.007.00000		CAMCACMOO		EMA MOCENCA	

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

CAAACACAGA CGAAACCGAA ATGCCATGA

1051

1101 1151

a538.pep MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL

CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC

751 ACGACGCCC GGCGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC 801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAAACTG ATTTCCGCCT 851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC 901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA 951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA 1001 ACAAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC

- 51 VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVVFNHE
- 101 LTPTQERNLE KILQCRVLDR VGLILAIFAR RARTQEGRLQ VELAQLSHLA
- GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

201 251 301 351	QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD TTARRLYISP ECSILLTDTV GFVSDLPHKL ISAFSATLEE TAQADVLLHV VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR DAAGKIAAVR ISVAENTGID ALREAIAEYC AAAPNTDETE MP*	
m538/a538 94	4.6% identity in 392 aa overlap	
	10 20 30 40 50 6 MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSV	
m538.pep		ı
a538	MTGRTGRNGSTQAQPERVMLVGVMLDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVI 10 20 30 40 50 60	
	10 20 30 40 50 60	ر
m538.pep	70 80 90 100 110 120 VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLVVFNHELTPTQERNLEKELKCRVLDI	
mood.pep		1
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLVVFNHELTPTQERNLEKILQCRVLDI 70 80 90 100 110 120	
	1	,
m538.pep	* 130 140 150 160 170 180 VGLILAIFARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETI	
• •		ŀ
a538	VGLILAIFARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETI 130 140 150 160 170 180	
		-
m538.pep	190 200 210 220 230 240 RRLIAHRINALIKQLANLKKQRALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY	
a538	RRLIAHRINALKKQLANLKKQRALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY 190 200 210 220 230 240	
	250 260 270 280	
m538.pep	AKDKLSPECSIILTDTVGFVSDLPHKLISAFSXTLEETAQADVLLHV	
a538	: AKDQLFATLDTTARRLYISPECSIILTDTVGFVSDLPHKLISAFSATLEETAQADVLLHV	
2550	250 260 270 280 290 300	
	290 300 310 320 330 340	
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR	
. a538		
. 2330	310 320 330 340 350 360	
	350 360 370 380	
m538.pep	ISVAENTGIDALREAIAESCAAAPNTDETEMPX	
a538		
	370 380 390	

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1561>: g539.seq

```
atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
 51 teggeagege gaacateate gtetgeatea tacceagtee ggeaaeggea
101 aggcggacga tgtattgttt gcgttctttt tggttggcgg cttcgatttt
151 ttgcgcgtca tagggtgcgg cggtgtagcc tgtctgccgg attttcaaca
    gaatgtcgga gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggattgg
401 acttcgggca ggtcgtacag gcggatttgg tcgaggattt cttggggcgg
451 cagttcggtt tttttcgcgt cggcggtgcg tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggt cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtgga aacaggtttt tttcatggca tttcggtttc
```

```
651 qtctqtqttt qqtgcggcgg cacaatactc ggcaatggct tcgcgcagtg
          701 cqtctatacc qqtattttca gcaacggaaa tqcggacggc qqcaattttt
          751 cccqcagcqt cgcgccatat gcccgtgttt tgttcttcag acggcagcag
          801 gtcggttttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
          851 cttgcagtac gttttccacg tcttcaatct gctgcccgct gttccgggcg
          901 qcaqcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
          951 ggtggcggaa aaggcggaaa tcagtttgtg cggcagatcg ctgacgaatc
         1001 cgacggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
         1051 egegeegteg tgtegagagt ggegaaaage tggtettteg catatatgee
         1101 cgacttggtc agccggttga acaggctgga tttgccgaca ttggtatag
This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:
     q539.pep
               MEDLOEIGFD VAAVKVGROR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
               LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAAVRAVIEV DADDAVCAQK
               LLFDOPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
              OFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMQVFG
          201 NVOPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
          251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPLFRA
          301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPTVSVRI MLHAGLMYSR
          351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1563>:
     m539.seq
                (partial)
              ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
              TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
               AGGCGGACGA TGTATTGTTT GCGTTCTTTT TGGTTGGCGG CTTCGATTTT
               TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
              GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCaGCqG
          251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
          301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
          351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
          401 ACTTCGGGCA GGTCGTACAG GCGGATTTGG TCGAGGATTT CTTGGGGCGG
          451 CAGCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTTGTAA TAACTGCCCA
          501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaCAGG
          551 GTTTCGCGGT CTTCGTTTTC GTAACGGACA GTCAGGTGGA GGTGTTCGGG
          601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
          651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATGGCT TCGCGCAGTG
          701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTTT
          751 CCCGCAGCGT CGCGCCATAT GCCCGTGTTT TGTTCTTCAG ACGGCAGCAG
          801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
          851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
          901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
          951 CGTGGCG.AA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTNACGAATC
              CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...
This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:
     m539.pep
                (partial)
              MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
           1
              LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAAVRAVIEV DADDAVCTQK
          101 LLFDQPDAGG AGDAAEH*NR LARAAVGFHK VGLDFGQVVQ ADLVEDFLGR
          151 QLGFLRVGGA LFVITAQARV NNALCDRLTA GAQGFAVFVF VTDSQVEVFG
          201 NIQTAVETGF FHGISVSSVF GAAAQDSAMA SRSASIPVFS ATEMRTAAIF
              PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA
              AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPTVSVRI MLHSG....
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from
N. gonorrhoeae:
     m539/g539
                          10
                                    20
                                             30
                                                       40
     m539.pep
                 MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA
                  MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLFAFFLVGGFDFLRVIGCGGVA
     g539
```

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815

	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADF					
g539	CLPDFQQNVGEADF				QPDAGGAGN	AAEHQHC
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAVGFHKVGLD					
	:: : :					
g539	FVRAIMGFHKVGLD	FGQVVQADLV	EDFLGRQFGF	FRVGGASFVI	TAQAGIDDAI	CDCLTA
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGFAVFVFVTDS	QVEVFGNIQT	AVETGFFHGI	SVSSVFGAAA	QDSAMASRSA	SIPVFS
		1::1111:1	111111111111111111111111111111111111111	1111111111		11111
g539	DAAGFAVFAFVADG	QMQVFGNVQP	AVET GFFHGI	SVSSVFGAAA	OYSAMASRSA	SIPVES
-	190	200	210	220	230	240
						240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAAS	RHMPVFCSSD	GSRSVLLYTL	MHGISPAWTS		
					111111111	
q539	ATEMRTAAIFPAAS	RHMPVFCSSD	GSRSVLLYTL	MHGTSWAWTS	CSTFSTSSTC	א מים. דים א
9	250	260	270	280	290	300
		200	2,70	250	230	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAV				~	
moos.pep					_	
g539	AASTTCSSTSACTVS					
goog	310					
	310	320	330	340	350	360
r.o.o						
g539	WSFAYMPDLVSRLN					
	370	380				

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1565>:

```
a539.seq
         ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
         TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
    101
         AGGCGGACGA TGTATTGTTT GCGTTCTTTT TGGTTGGCGG CTTCGATTTT
    151 TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
    201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
    251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
    301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
    351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
    401 ACTTCGGGCA GGTCGTACAG GCGGATTTGG TCGAGGATTT CTTGGGGCGG
    451 CAGCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTTGTAA TAACTGCCCA
    501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
    551 GTTTCGCGGT CTTCGTTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
    601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
         GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
         CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTTT
         CCCGCAGCGT CGCGCCATAT GCCCGTGTTT TGTTCTTCAG ACGGCAGCAG
    751
         GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
    801
    851
         CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
    901
         GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
    951
         CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CGGCAGATCG CTGACGAATC
         CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
   1001
         CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTCG CATATATGCC
   1051
         CGACTTGGTC AGCCGGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG
   1101
```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

a539.pep

MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

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816

51 101 151 201 251 301 351	LRVIGCGGVA Y LLFDQPDAGG A QLGFLRVGGA I NVQPAVETGF B PAASRHMPVF C AASTTCSSTS A RAVVSSVAKS W	AGDAAEH*NR LFVITAQARV FHGISVSSVF CSSDGSRSVL ACAVSSSVAE	LARAAVGFHK NNALCDCLTT GAAAQYSAMA LYTLMHGISP KAEISLCGRS	VGLDFGQVVQ GAAGFAVFVF SRSASIPVFS AWISCSTFST LTNPTVSVRI	ADLVEDFLGI VTDGQMQVFO ATEMRTAAII SSICCPLFGA	? :- :
m539/a539 97	'.1% identity ii	n 345 aa ov	erlap			
m539.pep a539	MEDLQEIGE MEDLQEIGE	FDVAAVKVGRÇ FDVAAVKVGRÇ	30 30 QREHHRLHHPQI REHHRLHHPQI 30 30	PGNGEADDVLF PGNGEADDVLF	AFFLVGGFDFI	 RVIGCGGVA
					50	60
m539.pep a539	YLPDFQQNV YLPDFQQNV	GKADFAVVPE 	30 90 DDAAAVRAVIEV 	/DADDAVCTQK /DADDAVCTQK	111111111111	
m539.pep a539	111111111	IKVGLDFGQVV IKVGLDFGQVV	'QADLVEDFLGF 'QADLVEDFLGF	RQLGFLRVGGA: 	1111111111	11111 11:
m539.pep a539	11 111111	FVTDSQVEVF : :: FVTDGQMQVF	GNIQTAVETGF : GNVQPAVETGF	FHGISVSSVFC FHGISVSSVFC	11111 11111	240 RSASIPVFS
m539.pep a539	111111111	FPAASRHMPV FPAASRHMPV	FCSSDGSRSVL	LYTLMHGISPA LYTLMHGISPA	1111111111	
m539.pep a539	11111111	SACAVSSSVA	0 330 XKAEISLCGRS EKAEISLCGRS	LTNPTVSVRIN	1LHSG	
a539	31 WSFAYMPDL 37	VSRLNRLDLP	TLVX	340	350	360
_	artial DNA sec	gegg caacg	gggtg tttta	tcaaa acggo	aaact	ID 1567>:

- 51 tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
- 101 tgccggtgcc gaacccgatg ccgtctgaac cttcagacgg catcgggtgt
- 151 ttatttgtcc actcggacgg gtgcaggttc gtattgtgtc gattcgtcgc
- 201 cgtaatacag cacgccgagt ttgacgggga tgcgtccctg cgatttgcgg
- 251 tgggcgttgg aatcgcgcaa ggaatacgcg cagccgcagt attcctqctq
- 301 gtagaagttt tegegtttge tgattteaat cataegegeg eegeegeege
- 351 ctttgcgcca gttgaagtcc caataggcca catcatcgta aggcgcggcg
- 401 gcacggtgtc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>: g540.pep

¹ MPPSRRGNGV FYQNGKLANA VSACRLPNRQ TFPVPVPNPM PSEPSDGIGC

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```
51 LFVHSDGCRF VLCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRAAAVFLL
          101 VEVFAFADFN HTRAAAAFAP VEVPIGHIIV RRGGTVSAVV DLRHIFPA *
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1569>:
              (partial)
     m540.seq
               ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
            1
                 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCGTC GCCGTAATAC
           51
          101
                 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTGC GGTGGGCATT
                 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
                 TTTCACGTTT GCTGATTTCA ATCATGCGCG CGCTGCCGCC GCCTTTGCGC
                 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
                 TCCGCAGTCG TTGATTTGCG CCATATTTTT CCAGCGTGA
This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:
     m540.pep
                (partial)
               ..PNPMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
            1
                 GIPQGIGTTA IFLLVEVFTF ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
           51
                 SAVVDLRHIF PA*
          101
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng)
from N. gonorrhoeae:
     m540/g540
                                                       10
                                                                20
     m540.pep
                                               PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                               GNGVFYQNGKLANAVSACRLPNRQTFPVPVPNPMPSEPSDGIGCLFVHSDGCRFVLCRFV
     q540
                    10
                             20
                                       30
                                                 40
                                                          50
                                                                    60
                                   50
                                             60
                                                      70
                                                                80
                                                                          90
     m540.pep \
                  AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHARAAAAFAPVEIPIH
                  AVIQHAEFDGDASLRFAVGVGIAQGIRAAAVFLLVEVFAFADFNHTRAAAAFAPVEVPIG
     q540
                             80
                    70
                                       90
                                                100
                                                         110
                        100
                                  110
                 HIIVRRGGAVSAVVDLRHIFPAX
     m540.pep
                  g540
                 HIIVRRGGTVSAVVDLRHIFPAX
                   130
                            140
     L' estremita' N-terminale di meningococco e' assente perche' interviene la
     fine del contig
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1571>:
     a540.seg
              ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAACT
           1
              TGCCAATGCG GTTTCCGATT GCAGATTGCC AAACCGGCAA ACCTTTCCCG
           51
          101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTCAGACGG CATCGGGTGT
          151 TTATTTGTCC ACCCGGATGG GTGCAGGTTC GTATTGTGTC GATTCGTCGC
          201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTTGCGG
          251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
          301 GTAGAAGTTT TCACGTTTGC TGATTTCAAT CATACGCGCG CTGCCGCCGC
          351 CTTTGCGCCA GTTGAAATCC CAATACACCA CATCATCGTA AGGCGCGGCG
          401 GCGCGGCGC CGCAGTCGTT AATCTGGTTC ATGTTTTTCC A
This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:
     a540.pep (partial)
           1 MPSSRRGNGV FYONGKLANA VSDCRLPNRO TFPVPMPNPM PSEPSDGIGC
              LFVHPDGCRF VLCRFVAVIQ HAEFDGDSAL *FAVGVGIPQ GIGTTAIFLL
          101 VEFTFADFN HTRAAAAFAP VEIPIHHIIV RRGGAAAAVV NLVHVFP
```

WO 99/57280 PCT/US99/09346

818

```
m540/a540 92.8% identity in 111 aa overlap
                                                      10
                                              PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
     m540.pep
                                              GNGVFYQNGKLANAVSDCRLPNRQTFPVPMPNPMPSEPSDGIGCLFVHPDGCRFVLCRFV
     a540
                                      30
                                                40
                                                         50
                                                      70
                         40
                                   50
                                            60
                                                               80
     m540.pep
                 AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHARAAAAFAPVEIPIH
                 AVIOHAEFDGDSALXFAVGVGIPQGIGTTAIFLLVEVFTFADFNHTRAAAAFAPVEIPIH
     a540
                                      90
                             80
                                               100
                                                        110
                        100
                                  110
                 HIIVRRGGAVSAVVDLRHIFPAX
     m540.pep
                 11111111::111:1 1:11
                 HIIVRRGGAAAAVVNLVHVFP
     a540
                            140
                  130
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1573>:
     g542.seq
      1 atgccgaaat ggtcgcgcat acggcgttgc agcgtccttt cgctgatgtt
      51 cagcgcggct gtcagccggt tgacttggtg tgcgccgccg tcgaacgcgg
     101 cattcagggt gcggctgaag tcttcagacg gcatagcgtc tgcttccgcc
     151 gtttgccccg ccgccggctc gatgccgtct gaaaccgtgt cccacaaatc
     201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatgtt tcgcccaaat
         gcccctttgg gacggtttgc aggcaggatg ccgccaagcc gcgcaggttt
        gggggcaaat cccatatcct gaccggttcg cggtaa
This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:
         MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFRVRLK SSDGIASASA
         VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
     101 GGKSHILTGS R*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1575>:
     m542.seq
      1 ATGCCGAAAT GGTCGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
        CAGCGCGTCT GTCAGCCGGT TGACTTGGTG TGCGCCGTCG GCAAACGCGG
        CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
        GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
        CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
        GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
     301 GGGGGCAAAT CCCATATCCT GACCGGTTCG CGGTAA
This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:
     m542.pep
        MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASA
         VCPAAGPMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF
     101 RQDAAKPRRF GGKSHILTGS R*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng)
from N. gonorrhoeae:
    m542/g542
                                    30
                 MPKWSRIRRCSVLSLMFSASVSRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
    m542.pep
                 MPKWSRIRRCSVLSLMFSAAVSRLTWCAPPSNAAFRVRLKSSDGIASASAVCPAAGSMPS
     g542
                         10
                                  20
                                            30
                                                     40
                                                               50
                         70
                                  80
                                            90
                                                    100
                                                              110
```

ETVSHKSDSSRNTSASXRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX

m542.pep

PCT/US99/09346 WO 99/57280

```
ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
     q542
                         70
                                  80
                                           90
                                                    100
                                                             110
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1577>:
     a542.seq
              ATGCCGAAAT GGTCGCGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
           1
              CAGCGTGTCT GCCAGCCGGT TGACTTGATG TGCGCCGCCG GCAAACGCGG
          51
         101
              CATTCAGGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
              GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
         151
              CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
         201
              GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
         251
              GGGGGCAAAT CCCATATCCT GACCGGTTCG CGGTAA
         301
This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:
     a542.pep
              MPKWSRIRRC SVLSLMFSVS ASRLT*CAPP ANAAFRMRLK SSDGIASASA
           1
              VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
          51
         101
              GGKSHILTGS R*
m542/a542 94.6% identity in 111 aa overlap
                                           30
                                                    40
    m542.pep
                 MPKWSRIRRCSVLSLMFSASVSRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
                 MPKWSRIRRCSVLSLMFSVSASRLTXCAPPANAAFRMRLKSSDGIASASAVCPAAGPMPS
     a542
                         10
                                  20
                                           30
                                                    40
                                                              50
                         70
                                  80
                                           90
                                                   100
                                                             110
                 ETVSHKSDSSRNTSASXRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
    m542.pep
                 ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
     a542
                        70
                                  RΛ
                                           90
                                                   100
                                                             110
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1579>:
    q543.seq
          atggtttgtc ggttatttgc cgccgttttt ggctttcaac tcggcaatca
          gcccgtcgat gcctttggct ttgatgattt cgccgaattg gttgcggtac
     101 acggtaacca ggctcgtgcc ttcgatggcg acgttgtagg tacggtattt
     151 geogeogett tggtaggtgg taaagtecat attgacggge ttetgaccgg
     201 ggatgccgac ttcggcacgg acgacgattt ccttgccgcc cttattgacg
     251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcaqcatcqt
     301 qccqqaataq gtgcggatca gcaggqtttq aaattctttq qccaacqctt
     351 qtttttqcqc qtcqqacqcq qtacqccaaq qqttqccqac cqccaatqcq
     401 gtcatacgtt ggaaatcgaa atagggaacc gcataggctt cqqcttttqq
     451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggtcaaa acctgtgtgg
         cqttttggcg gatttgtccc actgcgtcgg ccggggaggc aaatgccatg
     551 ccgatgctca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
         cacgatgtct ttcctgaaaa tggatgtgta tgtttattct gcggcttttt
         ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
     651
     701
          ccgatcaggt tttccagaac cattgcagaa ctggttacqg agatqqtqtc
          geoggeagea aggtttteeg tategeogee etgetgeage ecgatgtact
          gttcgcccaa aagtcccgaa gtcaggattt gcgcggaaac gtcactgctg
         aactgatact tgccgtccaa atcaaggcgc accctcgcct gataggattt
     901 cgggtcaagc ccgatagcgc cgacgcgccc gaccaatacg cctgcggatt
     951 tgacggggc attgaccttc aaaccgccga tgtcgccgaa atcggcataa
    1051 gaaagcgaga aaggcaaccg ccgccgcgcc gatcaagacg aacagtccga
    1101 cccaaaattc caatatgttc tttttcatta a
This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:
    q543.pep
        MVCRLFAAVF GFQLGNQPVD AFGFDDFAEL VAVHGNQARA FDGDVVGTVF
```

```
51 AAALVGGKVH IDGLLTGDAD FGTDDDFLAA LIDDGIVFDV DGRVFEFOHR
         AGIGADQQGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
     101
          ACRSRVAAFE DGQNLCGVLA DLSHCVGRGG KCHADAQNTD AQCADEGGFF
     151
          HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFQN HCRTGYGDGV
         AGSKVFRIAA LLQPDVLFAQ KSRSQDLRGN VTAELILAVQ IKAHPRLIGF
     301 RVKPDSADAP DQYACGFDGG IDLQTADVAE IGINGVSFVR TAERRAARHA
          ESEKGNRRRA DQDEQSDPKF QYVLFH*
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1581>:
     m543.seq
                ATGGTTTGTC GGTTATTTGC CGCCGTTTTT GGCTTTCAAC TCGGCAATCA
                GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
            51
                ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
           101
           151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
           201 GTACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
           251 ATGGGATTGT CTTTGACGTT GACGTTGGCG TTTTTTAATT TCAGCATCGT
           301
                GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATTCTTTG GCCAACGCTT
                GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTTGCCGAC CGCCAATGCG
           401
                GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
                GCGAGCGGTG TTGGCATCGC CGTTTTTTAA GATGCTCAAT ACTTGAGTGG
                CGTTTTGACG GATTTGGCTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
                CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGGG AGGATTTTTT
               CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
           651 CTTTTTCCGC ATTGCCGCCG TCGGCATTTT TCTCGGCAAA ACTCGTCATG
           701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
           751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
           801 TGTACTGCTC GCCCAAAAGT CCCGAAGTCA GGATTTGCGC GGAAACGTCG
           851 CTGCTGAACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
           901 GGATTTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
           951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
         1001 GCATAAACGG CGTAAGTTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
         1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
         1101 GTCCGACCCA AAATTCCAAT ATGTTCTTCT TCATTAA
This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:
     m543.pep
         MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
         TAALVGGEVH VDGFLPGYAD FGADDDFFAA FIDDGIVFDV DVGVFXFQHR
     101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
     151 ASGVGIAVFX DAQYLSGVLT DLAYRVGRGG KCHADAQNTD AQCADEGGFF
     201 HDXVSXFEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF ONHCRTGYGD
     251 GVAGSKVFRV AALLQPDVLL AQKSRSQDLR GNVAAELILA VQIEAHPRLI
         GFRVKSDSAD APDQYACGFD GGIDLQTADV AEIGINGVSF VRTAERRTAG
     351 HAESEKGNRR RANQDEQSDP KFQYVLLH*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng)
from N. gonorrhoeae:
    m543/g543
                         10
                                   20
                                             30
                                                      40
                                                                          60
    m543.pep
                 MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
                 {\tt MVCRLFAAVFGFQLGNQPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVGGKVH}
    q543
                         10
                                   20
                                             30
                                                      40
                                                                50
                                                                          60
                                   80
                                             90
                                                     100
                 \verb|VDGFLPGYADFGADDDFFAAFIDDGIVFDVDVGVFXFQHRAGIGADQQGLKFFGQRLFLR|
    m543.pep
                 IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEFQHRAGIGADQQGLKFFGORLFLR
    g543
                         70
                                   80
                                            90
                                                     100
                                                               110
                                                                         120
```

140

150

160

170

	821						
m543.pep g543	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRV	1111					
m543.pep	190 200 210 220 230 KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIAAVGIFLGKTRHEFA	239 ADKV : :					
g543	KCHADAQNTDAQCADEGGFFHDVFPENGCVCLFCGFFRIAALSVFLGEAGHEF	TDQV					
m543.pep	240 250 260 270 280 290 FQNHCRTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSQDLRGNVAAELILAVQIEAF	1111					
30.10	240 250 260 270 280 290	1PRL					
m543.pep	300 310 320 330 340 350 IGFRVKSDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRTAGHAESEK	359 KGNR					
g543	IGFRVKPDSADAPDQYACGFDGGIDLQTADVAEIGINGVSFVRTAERRAARHAESEK 300 310 320 330 340 350	KGNR					
m543.pep	360 370 379 RRANQDEQSDPKFQYVLLHX :						
g543	RRADODEOSDPKFQYVLFHX 360 370						
The following partial DNA sequence was identified in N. meningitidis <seq 1583="" id="">:</seq>							
a543.seq							
1	ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA						
51	GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC						
101	ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT						
151	ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG						
201	NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG						
251	ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTTTTAATT TCAGCATCGT						
301 351	GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATTCTTTG GCCAACGCTT						
401	GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTTGCCGAC CGCCAATGCG						
451	GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG						
501	GCGGGCGGTG TTGGCATCAC CGCTTTTTAA GATGCTCAAT ACTTGAGTGG CGTTTTGACG GATTTGGTTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG						
551	CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT						
601	CATGATTAAG TGTCCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG						
651	CTTTTTCCGC ATTGCCGCCG TCGGCATTTT TCTCGGCAAA ACTCGTCATG						
701	AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT						
751	GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA						
801	TGTACTGCTC GCCCAAAAGT CCCGAAGTCA GGATTTGCGC GGAAACGTCG						
851	CTGCTGAACT GATACTTGCC CTCCAAATCC ACCCGAACG TGCGCTGA						

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

1101 GTCCGACCCA AAATTCCAAT ATGTTCTTTT TCATTAA

a543.pep MAYGLLAAVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF 51 TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR 101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL 151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF 201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRTGYGD 251 GVAGSKVFRV AALLQPDVLL AQKSRSQDLR GNVAAELILA VQIEAHPRLI 301 GFRVKSDSAD APDQYACGFD GGIDLQTADV AEIGINGVSF VRTAERRTAG

851 CTGCTGAACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA 901 GGATTTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG 951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG 1001 GCATAAACGG CGTAAGTTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC 1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0%	% identity in 378 a	aa overlap				
	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQL	GNQSVHAFR	FDNFAELVAVI	HGNOARAFDGI		
a543	MAYGLLAAVXSLQL	XNQSVHAFR	FDNFAELVAVI	HGNOARAFDGI	OVVGTVFTAAI	LVGGEVH
	10	20	30	40	50	60
	70	80	90 .	100	110	120
m543.pep	VDGFLPGYADFGADI	DDFFAAFID	DGIVFDVDVGV	/FXFQHRAGI	SADQQGLKFF(GORLFLR
	1111111 11111	1111111	!			
a543	VDGFLPGXADFGADI			/FXFQHRAGI	GADQQGLKFF	GQRLFLR
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCG					
			[]]]]]]	::	111111111111	11111
a543	VGRGAPRVADRQCG	RTLEIEIGNE	RIGFGFLAGGV	/GITAFXDAQY	LSGVLTDLVY?	RVGRGG
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCA					
				441111111	111111111	
a543	KCHADAQNTDAQCAD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCRTGYGDGVAGS	SKVFRVAALI	LQPDVLLAQKS	RSQDLRGNVA	AELILAVQIE	AHPRLI
					1111111111	
a543	QNHCRTGYGDGVAGS					
	250	260	270	280	290	300
	212	200				
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQY	ACGFDGGIL	DLQTADVAEIG	INGVSFVRTA	ERRTAGHAES	EKGNRR
5.45			111111111			
a543	GFRVKSDSADAPDQY					
	310	320	330	340	350	360
	370	379				
m512						
m543.pep	RANQDEQSDPKFQYV					
o E 4 2	THE THE THE THE THE THE THE THE THE THE					
a543	RANQDEQSDPKFQYV	TL HX				

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1585>: 9544.seq

- 1 atgaaaaaaa tactcaccgc cgccgccgtc gcactgatcg gcatcctcct
- 51 cgccaccgtc ctcatccccg acagtaaaac cgcgcccgcc ttctccctgc
- 101 ccgacctgca cggaaaaacc gtttccaacg ccgacctgca aggcaaagtc
- 151 accctgatta atttttggtt tccctcctgt ccgggttgtg tgagcgaaat
- 201 gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
- 251 teetegeegt tgeccageee ategateega tagaaagegt eegecaatae
- 301 gtcaaagact acggactgcc gtttaccgtc atttatgatg cggacaaagc
- 351 cgtcggacag gcattcggca cacaggttta tccgacttcc gtccttatcg
- 401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcgaacc cgatttcggc
- 451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

370

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>: g544.pep

- 1 MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGKV
- 51 TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
- 101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

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823
     151 KLYOEIDTAL AO*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1587>:
     m544.seq
       1 ATGAWAAAAA TACTCACCGC CGCCGTCGTC GCACTGATCG GCATCCTCCT
         TGCCATCGTC CTCmTCCCCG ACAGCAAAAC CGCGCCCGCC TTCTCCmTGC
         CCGACCTGCA CGGAAAAACC GTTTCCAACG CCGACCTGCA AGGCAAAGTA
     151 ACCCTGATTA ATTTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAWAT
     201 GCCCAAAATC ATTAAAACGG CAAATGACTA TAAAAWCAAA AACTTCCAAG
         TACTTGCCGT CGCCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
     301 GTCAAAGACT ACGGTTTGCC GTTTACCGTC ATGTATGATG CGGACAAAGC
         TGTCGGACAG GCGTTCGGCA CACAGGTTTA TCCGACTTCC GTCCTTATCG
         GCAAATAAGG CGAAATCTTC AAAACCTACG TCGGCGAACC CGATTTCGGC
         AAACTCTACC AAGAAATCGA TACGCGCGTG GCGCAATAG
This corresponds to the amino acid sequence <SEQ ID 1588; ORF 544>:
     m544.pep
       1 MXKILTAAVV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGKV
         TLINFWFPSC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
         VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGK*GEIF KTYVGEPDFG
     151 KLYQEIDTRV AQ*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 544 shows 90.7% identity over a 162 as overlap with a predicted ORF (ORF 544.ng)
from N. gonorrhoeae:
     m544/g544
                                  20
                                            30
                                                      40
     m544.pep
                 MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLOGKVTLINFWFPSC
                 MKKILTAAAVALIGILLATVLIPDSKTAPAFSLPDLHGKTVSNADLQGKVTLINFWFPSC
     q544
                                  20
                                            30
                                                     40
                                                               50
                                                                        60
                                  80
                                            90
                                                    100
                                                              110
                 PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGO
     m544.pep
                 q544
                 PGCVSEMPKVTKTANDYKNKDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGO
                         70
                                  80
                                            90
                                                    100
                                                              110
                        130
                                 140
                                           150
                 AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX
     m544.pep
                 AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX
     g544
                        130
                                 140
                                           150
                                                    160
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1589>:
     a544.seg
           1
              ATGAAAAAA TACTCACCGC CGCCGTCGTC GCACTGATCG GCATCCTCCT
          51
              TGCCATCGTC CTCATCCCCG ACAGCAAAAC CGCGCCCGCT TTCTCCCTGT
              CCGANCTGCA CGGAAAAANC GTTTNCAACG CCGACCTGCA AGGCNAAGTT
         101
              ANCCTGATTA ANTTTTGGTT TCCCTCCTGT CCGGGTTGTG TGAGCGAAAT
         151
              GNCCANAATC ATTAAAACGG CAAATGACTA TAAAAACAAA AACTTCCAAG
         201
              TCCTTGCCGT CGCCCAGCCC ATCGATCCGA TAGAAAGCGT CCGCCAATAT
         251
             GTCAAAGACT ACGGTTTGCC GTTTACCGTC ATGTATGATG CGGACAAAGC
              TGTCGGACAG GCGTTCGGCA CACAGGTTTA TCCGACTTCC GTCCTTATCG
              GCAAAAAGG CGAAATCCTC AAAACTTATG TCGGCGAACC CGATTTCGGC
         451 AAACTCTACC AAGAAATCGA TACCGCGCTG GCACAATAG
```

This corresponds to the amino acid sequence <SEO ID 1590; ORF 544.a>:

a544.pep

```
MKKILTAAVV ALIGILLAIV LIPDSKTAPA FSLSXLHGKX VXNADLOGXV
XLIXFWFPSC PGCVSEMXXI IKTANDYKNK NFQVLAVAQP IDPIESVRQY
VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG
```

PCT/US99/09346 WO 99/57280

824

151 KLYQEIDTAL AQ*

```
m544/a544 88.9% identity in 162 aa overlap
```

```
30
          MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGKVTLINFWFPSC
m544.pep
          1111:1 11:11 1:11 1:11
a544
          MKKILTAAVVALIGILLAIVLIPDSKTAPAFSLSXLHGKXVXNADLQGXVXLIXFWFPSC
                         20
                                30
                                         40
                 70
                         80
                                 90
                                        100
                                                110
                                                        120
          PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ
m544.pep
          PGCVSEMXXIIKTANDYKNKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ
a544
                 70
                         80
                                90
                                        100
                                                110
                130
                        140
                                150
m544.pep
          AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX
          AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX
a544
                130
                        140
                                150
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1591>:

```
g547.seq
```

- 1 atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgcccaaat
- cqtcgaaact ttcgacgtat tcttctttag gaacgattgc gcctttttta
- cqcagatgaa acagcggtgc ggttgggtct gctcgttggt atatctcgtt
- gatatattta caagatgcgg cttcgagatt ccgaaccgct cctttaaaga
- gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
- 251 ccgaagtcga gatggatgcc cattacttcc ccttactcag aaaatattta
- 301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
- 351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaacggaa
- 401 aaaagcggtt tgttttttgt tgttaa

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547.pep

- 1 MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTOMKORC GWVCSLVYLV
- DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
- KFIMLHIVTN IRVFCVCVKE LLTILVKNLS PNGKKRFVFC C*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1593>:

m547.sea

- 1 ATGTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT
- CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTTTA
- CGCAGATGAA ACAGCGGTGC GGTTGGGTCT GCTCGTTGGT ATATCTCGTT
- GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCGCT CCTTTAAAGA
- GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTTT AGGACTAATG
- CCGAAGTCGA GATGGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
- AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTTGTGT
- GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTTG TCTCCAAACG
- GAAAAAGCG GTTTGTTTTT TGTTGTTAA

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

- m547.pep
 - 1 MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
 - DIFPROGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
- KFIMLHIFTN IKVFXCVCVK ELLTILVKNL SPNGKKRFVF CC*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from N. gonorrhoeae:

m547/g547

WO 99/57280

```
20
                                         30
                                                  40
                                                           50
                        3.0
                                                                    60
                MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI
    m547.pep
                MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI
    q547
                                20
                                         30
                                                  40
                                                           50
                        10
                                                                    60
                        70
                                80
                                         90
                                                 100
                                                          110
                PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRKYLKFIMLHIFTNIKVFXCVCVK
    m547.pep
                PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRKYLKFIMLHIVTNIRVF-CVCVK
    g547
                        70
                                80
                                         90
                                                 100
                       130
                               140
                ELLTILVKNLSPNGKKRFVFCCX
    m547.pep
                ELLTILVKNLSPNGKKRFVFCCX
    q547
              120
                       130
                                140
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1595>:
    a547.seq
             ATGTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT
           1
             CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACAATTGC ACCTTTTTTA
             CGCAGATGAA ACAGCGGTGC GGTTGGGTCT GCTCGTTGGT ATATCTCGTT
             GATATCTTTC CAAGATGCGG CTTCGAGATT CCGAACCGCT CCTTTAAAGA
             GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTTT AGGACTAATG
         201
             CCGAAGTCGA GATAGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
         251
         301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTT.TGTGT
             GTGCGTCAAG GAATTGTTGA CAATTTTAGT T
This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:
    a547.pep
             MFVDNGFNKT VASFAQIVET FDVFFFRNNC TFFTQMKQRC GWVCSLVYLV
             DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEIDA HYFPLLRKYL
             KFIMLHIFTN IKVFXCVCVK ELLTILV
         101
m547/a547 97.6% identity in 127 aa overlap
                                20
                                         30
                                                  40
                                                           50
                MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTOMKORCGWVCSLVYLVDIFPRCGFEI
    m547.pep
                MFVDNGFNKTVASFAQIVETFDVFFFRNNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI
    a547
                                20
                                         30
                                                  40
                                         90
                       70
                                80
                                                 100
                                                          110
                PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRKYLKFIMLHIFTNIKVFXCVCVK
    m547.pep
                PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRKYLKFIMLHIFTNIKVFXCVCVK
    a547
                       70
                                80
                                         90
                                                 100
                                                          110
                      130
                               140
                ELLTILVKNLSPNGKKRFVFCCX
    m547.pep
                111111
                ELLTILV
    a547
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1597>:
    q548.seq
```

```
1 atgttttccg taccgcgttc ctttttgccg ggcgttttcg tacttgccgc
```

- gettgeegee tgeaaacete aagacaacag tgeggegeaa geegettett
- caagtgcatc cgcgccggct gcggaaaatg cggcaaagcc gcaaacgcgc
- qqtacqqata tqcqtaaqqa agacatcggc ggcgatttca cactqaccqa
- cggcgaaggc aagcctttca gcctgagcga tttgaaaggc aaggtcgtga
- ttctqtcttt cggctttacg cactgtcccg atgtctgccc qacaqqqctt

g548

130

140

```
ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
           gaaagtggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
      351
           tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
      401
          acgggcggcc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
      451
          tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
          cttccggtgc gtatcttatc gataaaaacg gtgaggttgc cattttctcg
      601
           ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
      651
This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:
      g548.pep
          MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPOTR
          GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
         LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
          TGGONLPVIK QOYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
          PYGSEPETIA ADVRTLL*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1599>:
     m548.sea
               ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GGCGTTTTCG TACTTGCCGC
               GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
           51
              CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCA ANACACGCGC
          101
          151 GGTACGGATA TGCGTAAGGA AGACATCGGC GGCGATTTCA CGCTGACCGA
          201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
          251
               TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
          301 TTGACGTACA GCGACACGTT GAAGCAGTTG GGCGGCCAGG CTAAGGACGT
               GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
          351
               TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGS TCTGACGGCA
          401
               ACGGGCGGCC AAAACCTGCC GGTCATCAAG CAGCAATACC GCGTGGTTTC
               TGCCAAAGTC AATCAAAAMG ACGACAGCGA AAACTATTTG GTCGACCACT
               CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
               CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
          601
          651
This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:
     m548.pep
       1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
         GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTEL
         LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
          TGGQNLPVIK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
         PYGSEPETIA ADVRTLL*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng)
from N. gonorrhoeae:
     m548/g548
                                   20
                                             30
                                                      40
                                                                50
                                                                          60
                 MFSVPRSFLPGVFVLAALAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG
     m548.pep
                  MFSVPRSFLPGVFVLAALAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTDMRKEDIG
     q548
                         10
                                             30
                                                      40
                                                                50
                                                                          60
                         70
                                   80
                                             90
                                                     100
                 GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV
    m548.pep
                 GDFTLTDGEGKPFSLSDLKGKVVILSFGFTHCPDVCPTGLLTYSDTLKQLGGQAKDVKVV
    g548
                         70
                                   80
                                             90
                                                     100
                                                               110
                                                                         120
                        130
                                  140
                                            150
                                                     160
                 FVSIDPERDTPEIIGKYAKQFNPDFIXLTATGGQNLPVIKQQYRVVSAKVNQXDDSENYL
    m548.pep
```

160

170

180

200

190

VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLLX m548.pep 9548 VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLLX 190 200 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1601>: a548.seq ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GGCGTTTTCG TACTTGCCGC GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT 51 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC 101 151 GGTACGGATA TGCGTAAGGA AGACATCGGC GGCGATTTCA CGCTGACCGA CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT 251 301 TTGACGTACA GCGACACGTT GAAGCAGTTG GGCGGGCAGG CTAAGGACGT 351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA 401 ACGGGCGACC AAAACCTGCC GGTCATCAAG CAGCAATACC GCGTGGTTTC 451 501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACTATTTG GTCGACCACT CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG 551 601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT 651 CTGA This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>: a548.pep MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR 1 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTEL 51 101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA TGDQNLPVIK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS 151 201 PYGSEPETIA ADVRTLL* m548/a548 97.7% identity in 217 aa overlap 30 40 m548.pep MFSVPRSFLPGVFVLAALAACKPQDNSAAQVASSSASAAAENAAKQXTRGTDMRKEDIG 11111111111 ${\tt MFSVPRSFLPGVFVLAALAACKPQDNSAAQVASSSASAAENAAKPQTRGTDMRKEDIG}$ a548 10 20 30 40 60 70 80 90 100 110 120 GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV m548.pep a548 GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV 70 80 90 100 110 130 140 150 160 170 ${\tt FVSIDPERDTPEIIGKYAKQFNPDFIXLTATGGQNLPVIKQQYRVVSAKVNQXDDSENYL}$ m548.pep FVSIDPERDTPEIIGKYAKQFNPDFIGLTATGDQNLPVIKQQYRVVSAKVNQKDDSENYL a548 130 150 160 170 180 190 200 210 m548.pep VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLLX VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLLX a548 190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

- 1 atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
- 51 tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttaa
- 101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```
caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
     201 cggcagccgt agcgacgcga ggcagcaggc gggaatcgaa cggagtagga
     251 atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
     301 ttcttcggtt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
     351 cqcqtttcat ttcttcgttg atggtggttg cgccgacatc caacgcgccc
     401 cqqaaqatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
     451 ggagcgccg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
     501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
     551 tcgttcatcg tgttcaacat ttcaggcgtc agcaggtttg cgccggagag
     601 qcccaaqaaq atqtctttgc ctttaaccgc atcggcaagt acgcgccggc
     651 cqttgtcttc aacggcgtag aattttttgg attcgtccat gcggtctttg
     701 tcttcgcggg tttggtaaat cacgcctttg gagttgcaaa cggttacgtt
     751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcgg
     801 cggcacctgc gccggagcac accaaagtcg cttcttcgat tttacggccg
         gtataacgca gggcgttcaa tacggcggcg gcggtaatga tggccgtgcc
         gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa
This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:
     q550.pep
           1 MITDRFHLFH FPVSFIYQSD NKMPPENSSD GILTTNGLQL PFAQLGSVSF
           51 OICNRTGCHA AFHRCFGGSR SDARQQAGIE RSRNQVFRAE FEFLTVSGNH
         101 FFGYFFHROI COSIHAGAFH FFVDGGCADI QRAPEDEREA QYVVHLVREV
         151 GAAGTDNHVR TGFFRQRRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
         201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
         251 FTFOAOIOOL VOAGNRGGTC AGAHOSRFFD FTAGITOGVO YGGGGNDGRA
         301 VLVIMKYGDF AAFA*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1605>:
     m550.seq
              (partial)
               ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
                GTTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCACG
           51
                CCTTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCAAATCCAG
         101
                CAATTGGWTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
         151
                AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACGCAKGGC GTTCAATACG
         201
                GCGGCGGCGG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
         251
                GATTTTGCAG CGTTTGCGTA A
         301
This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:
    m550.pep (partial)
         ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
           OLXOAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
      51
            DFAAFA*
     101
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 550 shows
                 % identity over a aa overlap with a predicted ORF (ORF 550.ng)
from N. gonorrhoeae:
    m550/g550
                                                              20
                                             DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN
    m550.pep
                                               DGFFVHRVOHFRROOVCAGEAQEDVFAFNRIGKYAPAVVFNGVEFFGFVHAVFVFAGLVN
    g550
                        190
                                  200
                                            210
                                                     220
                                                               230
                                                                         240
                        40
                                 50
                                           60
                                                     70
                                                              80
                                                                        90
                 HAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA
    m550.pep
                  HAFGVANGYVFTFQAQIQQLVQAGNRGGTCAGAHQSRFFDFTAGITQGVQYGGGGNDGRA
    g550
                        250
                                  260
                                            270
                                                     280
                                                               290
                      100
                 VLVVVEYGDFAAFAX
    m550.pep
                  111:::||11||1
                 VLVIMKYGDFAAFAX
    q550
```

PCT/US99/09346 WO 99/57280

829

310

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1607>:
```

```
a550.seq
         CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
     51
         TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
         GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
    151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
    201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
    251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
    301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
    351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTCAC TTGGTTCGGG
    401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTCGC
    451 CAGCGGCGC AGGATTTCCG GATTCGGGTT GGCCATAGCG AACACGATGG
    501 GTTTTTCGTT CATGGTGTTC AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
    551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
    601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
    651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
    701 ACGTTTTCGC GTTTCAAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
    751 CGCGGCCGCA CCTGCGCCGG AACACCCAA AGTCGCTTCT TCGATTTTAC
    801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
    851 GTGCCGTGCT GGTCGTCGTG GAATACGGGG ATTTTGCAGC GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEO ID 1608; ORF 550.a>:

```
a550.pep
         LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
      51 FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
    101 AGAFHFFVDG RRADIQRTAE DEREAQYIVH LVREVGAAGT DNHVRTGFFR
    151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
    201 LAVVFNGVEL FGLVHTVFVF AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
    251 RGRTCAGTHQ SRFFDFTAGK TQGVQYGSGG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

290

				10	20	30
m550.pep			I	GIGKHALAVVI	FNGVELFGLV	HTVFVFAGL
			1			
a550	EHDGFFVHGVQ	YFRRQQVRAGI	EAQEDVFAFI	GIGKHALAVVI	FNGVELFGLV	HTVFVFAGL
	170	180	190	200	210	220
	40	5.0	50	7.0	0.0	• •
		50	60	70	80	90
m550.pep	VNHAFGVANGH	VFAFQAQIQQI	LXQAGNRGRI	CAGTHQSRFF!	OFTAGKTXGVQ	QYGGGGNDG
						11:11:11
a550	VNHAFGVANGH	VFAFQAQIQQI	LVQAGNRGRT	CAGTHQSRFFI	OFTAGKTQGVQ	YGSGGNDG
	230	240	250	260	270	280
	100					
m550.pep	RAVLVVVEYGD	FAAFAX				
	11111111111	11111				
a550	RAVLVVVEYGD	FAAFAX				

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1609>: g552.seq

```
1 atgaagctga aaaccttgtt attgcccttc gccgcactgg cattgtgtgc
 51 caacgcattt geegeeeege eeggegaege gtegttggea egttggetgg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggtca gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaaa tagcggtatc ttggactgca
```

```
ttgtcaggga aaatcgcgcg acatcatctg cccgagttta cqqaaqagtt
             acggcgcatc atctgcggcg gtatagtgga ttaa
 This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:
      q552.pep
           1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
         51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
         101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
         151 LSGKIARHHL PEFTEELRRI ICGGIVD*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1611>:
      m552.seq
               (partial)
                ..ATTAAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
            1
                 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
           51
                 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
                 AATGCCGGAT TTAAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA
                 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
                 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
          301
                 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
          351
                 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
          401
                 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
          451
                 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
          501
                 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAAACAAG
                 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA
This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:
     m552.pep
                (partial)
            .. IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
               NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKOAVRNT
        101
               LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
               LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*
        151
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng)
from N. gonorrhoeae:
     m552/g552
                         10
                                   20
                                            30
                                                      40
                                                                50
                                                                          60
                 {\tt IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK}
     m552.pep
                  MKLKTLLLPFAALALCANAFAAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK
     g552
                                            30
                                                      40
                                                               50
                                   80
                                            90
                                                     100
                                                               110
                 ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
     m552.pep
                 g552
                 ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
                         70
                                   80
                                            90
                                                     100
                                                              110
                                                                        120
                        130
                                           150
                                                     160
                                                              170
                                                                        180
                 YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
     m552.pep
                 q552
                 YGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX
                        130
                                  140
                                           150
                                                    160
                        190
     m552.pep
                 CKQAGQVGKRHQKX
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1613>:
     a552.seq
              ATTAAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
           1
              CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
          51
         101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
              AATGCCGGAT TTAAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA
         151
```

```
201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAAATCC CGATGCGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

a552.pep

- 1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
- 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
- 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
- 151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

m552/a552 100.0% identity in 193 aa overlap

	-					
	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLAI	CTNAFAAPI	SDASLARWLD	TONFORDIER	NMIEGFNAGE	KPYADK
					1111111111	
a552	IKLKTLLLPFATLAI	CTNAFAAPI	SDASLARWLD	TQNFDRDIE	NMIEGFNAGE	KPYADK
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAE	AFNRYRENV	LKDLITPEVK	QAVRNTLLKN	AREIYTQEEI	DGMIAF
		11111111	111111111	111111111	111111111	111111
a552	ALAEMPEAKKDQAAE	AFNRYRENV	LKDLITPEVK	QAVRNTLLKN	AREIYTQEEI	DGMIAF
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPR	LIKKSMSEI	AVSWTALSGK	IAQHHLPEFT	EELRRIICGG	KNPDAG
		111111111		111111111	111111111	111111
a552	YGSPVGQSVVAKNPR			IAQHHLPEFT	EELRRIICGG	KNPDAG
	130	140	150	160	170	180
	190					
m552.pep	CKQAGQVGKRHQKX					
a552	CKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1615>: m552-1.seq

```
TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT

51 GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGGCTCG TTGGCGCGTT

101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG

151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT

201 GCCGGAAGCG AAAAAAAGATC AGCGGCAGA AGCCTTTAAC CGTTATCGTG

251 AGAATGTTTT GAAAGATTTG ATTACGCCCA AAGTGAAACA GGCTGTCCGC

301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA

551 CGGCATGATT GCCTTTTACG GTTCGCCTG CGGTCAGTCC GTCGTTGCCA

401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG

451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA

501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGCTGTA

551 AACAAGCCGG ACAGGTTGGG AAAAGGCCATC AGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>: m552-1.pep

- 1 LNIKLKTLLL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
- 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
- 101 NTLLKNAREI YTQEEIDGMI AFYGSPVGQS VVAKNPRLIK KSMSEIAVSW
- 151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1617>: a552-1.seq

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```
1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
    GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
    GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
201
251 AGAATGTTTT GAAAGATTTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
    CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
```

351 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG 401

451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA 501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA

AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>: a552-1.pep

```
LNIKLKTLLL PFATLALCTN AFAAPPSDAS LARWLDTQNF DRDIEKNMIE
1
   GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
51
```

NTLLKNAREI YTQEEIDGMI AFYGSPVGQS VVAKNPRLIK KSMSEIAVSW 101

TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

a552-1/m552-1 100.0% identity in 195 aa overlap

```
40
         LNIKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYA
a552-1.pep
          LNIKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYA
m552-1
                       20
                               30
                                      40
                                              50
                                     100
                70
                       80
                               90
                                             110
         DKALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMI
a552-1.pep
          DKALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMI
m552-1
                                     100
               70
                       80
                               90
                                             110
                      140
                              150
                                     160
                                             170
               130
         AFYGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD
a552-1.pep
         AFYGSPVGQSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD
m552-1
                      140
                              150
                                     160
```

190

AGCKQAGQVGKRHQKX a552-1.pep 111111111111

AGCKQAGQVGKRHQKX m552-1190

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1619>: q553.seq

```
1 atqqattatc tgcaaaacct gtctttgggc ttgacaaaaa agctgcccgt
    tatactgcaa acagaagtag cggagtgtgg cttggcatgt ctagcggctg
    tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
    tactqtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
151
    tqatqatatq gggctgacgg gacgggcgtt gaggctggat ttaqacgaat
201
```

- tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt qtqqtqctqq aatcggtatc ttcggacggg gctgccgtca tggatccggc
- ttcqqqacqa cqcaaaqtca aqacqqaqqa aatatcqcqc aaqtttacgg
- 401 qaattqcttt qqaactgtgg ccaaacacgc gtttcgaggc aggggaagaa aagcaggaaa toogcatoot accoatgttg cgcgggattt ctgggctggg 451
- 501 qcqqacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
- 551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
- 601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
- 651 cqqcaatcta cctcccgaat caggcaaagt catgataaat gggcacgaca 701 tttacagctt accgccacct tttattccgc aatttgagtg cgatggtcaa
- 751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>: g553.pep

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833

- 1 MDYLQNLSLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK 51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDLNHF
- 101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
- 151 KQEIRILPML RGISGLGRTL FQLLALAAAM EVFAFLQNVS FKIGRGESLA
- 201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDGQ
- 251 GRTMFYSGLN LNR*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1621>:

m553.seg (partial)

- 1 ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
- 51 CATTCTGCAA ACAGAAGTTG CTGAATGTGG TTTAGCATGC CTGACATCCA
- 101 TCTTGTCCTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
- 151 TACACCCTGT CATTAAAGGG CGCAAATCTT GCAGACATCA TGAGATTTGG 201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
- 251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAACTT AAACCATTTT
- 301 GTTGTACTTT GTTCCATTTC CAAAGACAGT ATCGTCATTA TGGACCCTGC
- 351 TGTCGGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
- 401 GGATTGCCCT AGAATTATTC CCCAATACCC ATTTTGAAGA GAAAAAAGAA
- 451 ACAAAGAAAA TCAAAATATT ATCTCTATTA AGGGGGGG.T CAGGCTTAAA
- 501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTTCTTTG GAAGTCTTTG
- 551 CATTG...

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

- m553.pep (partial)
 - 1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYYGF HTDLRTLRQK
- 51 YTLSLKGANL ADIMRFGNEM NLTPRALRLE LDELSNLQLP CILHWNLNHF
- 101 VVLCSISKDS IVIMDPAVGM RKIKMDEVSQ KFTGIALELF PNTHFEEKKE
- 151 TKKIKILSLL RGXSGLKRSL IQMLILAISL EVFAL...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from N. gonorrhoeae:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLSLGLTKK	LPVILQTEVA	AECGLACLAAV	/AGFYGFYTDL	RALRSKYCLS	SLKGENL
_			:::	::: :	1:11:11	
m553	MDYLSRLSFGFNKK	LPVILQTEVA	AECGLACLTS I	LSYYGFHTDL	RTLROKYTLS	SLKGANL
	10	20	30	40	50	60
	70	80	90	100	110	120
g553.pep	ADIVRFADDMGLTG	RALRLDLDEI	LGSLRLPCIL	WDLNHFVVLE	SVSSDGAAVN	MDPASGR
		11111:111	:: :		: : : ::	
m553	ADIMRFGNEMNLTP	RALRLELDEI	SNLQLPCILE	WNLNHFVVLC	SISKOSIVI	MDPAVGM
	70	80	90	100	110	120
	130	140	150	160	170	180
g553.pep	RKVKTEEISRKFTG				-	
		1 : :	: : ::	: :	: : :	::
m553	RKIKMDEVSQKFTG	IALELFPNTH	IFEEKKETKKI	KILSLLRGXS	GLKRSLIQMI	LILAISL
	130	140	150	160	170	180
	190	200	210	220	230	240
g553.pep	EVFAFLQNVSFKIG	RGESLALIGE	RSGCGKSTLLI	DILSGNLPPES	GKVMINGHD	YSLPPP
	:					
m553	EVFAL					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1623>:

a553.seq

- ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT 1
- 51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT CTGGCGGCTG
- 101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
- 151 TAC

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This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:
     a553.pep
               MPHLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
           51
m553/a553 62.7% identity in 51 aa overlap
                                              30
                                                        40
                  MDYLSRLSFGFNKKLPVILQTEVAECGLACLTSILSYYGFHTDLRTLRQKYTLSLKGANL
     m553.pep
                  MPHLQNLSLGLKKKLPVILQTEISECGLACLAAVAGFHGFHTNLRALRSKY
     a553
                                    20
                                              30
                          70
                                    80
                                             90
                                                      100
                                                                110
                                                                          120
                  ADIMRFGNEMNLTPRALRLELDELSNLQLPCILHWNLNHFVVLCSISKDSIVIMDPAVGM
     m553.pep
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1625>:
q554.seq..
       1 atgacageac ataaaateet geegteett etteecatea tettaggegt
      51 ttctcacgca acggctgcat cgcccgcgcc caacagaccg acggtacacq
     101 ccgcccccac gctccaaaca cccgaaaccc tcacggcggc acacatcgtt
     151 atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
     201 tgtcgaaccg gcggcactaa cccaactgat gaccgcatat ttggttttca
     251 aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaataccc
         gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccggcga
         tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
     401 acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
         aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
     501 caccgtattc aaaaacccga caggcttggg tagagaagga caggtttcca
     551 ccgccaaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
     601 gaatattacc cgctgttttc catcaaatcg ttcaagtttg aaaacataga
     651 acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
     701 tgaaagccgg gcacacagaa agcggcggct acaaccttgc cgtgtcatac
     751 tccggcaacg gcaggcacat ccttgtcatc acactaggtt cggaatcggc
     801 ggaaacccgc gcatcggaca acagcaagct gctgaaccgg gcattgcagg
     851 ccttcgatac gcccaaaata tatccgaaag gcaaaaccgt tgcccaaatc
     901 caaatttccg gaggcagcaa aaaaaccgtc cgcgcaggct tcctcaaaga
     951 agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
    1001 tggaaaccat acagccgatt cccgcccgg taaaaaaaqg qcagatttta
    1051 ggaaaaatca aaatcaggca aaacggacat accattgccg aaaaaqaaat
    1101 cgtcgcactg gaaaacgtag aaaaaagaag ccggtggcaa aggctttgga
    1151 cgcgtctgac agggcagtaa
This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:
g554.pep..
      1 MTAHKILPVL LPIILGVSHA TAASPAPNRP TVHAAPTLQT PETLTAAHIV
     51 IDLQSRQTLS AKNTNTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
     101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LCANDAALTL ADRLGNGSIE
     151 NFVQQMNKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
     201 EYYPLFSIKS FKFENIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
     251 SGNGRHILVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
     301 QISGGSKKTV RAGFLKEAYI TLPHKEAKMA EQILETIQPI PAPVKKGQIL
     351 GKIKIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1627>:
m554.seq..
      1 ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
     51 TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
     101 CCGCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
     151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
```

201 TGTTGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTCA
251 AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACTT AAAAATACCC

```
GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
     TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
 351
     ACGATGCCGC CCTAACCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
     AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
     CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
     CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
     GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
     ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
 701
     TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
     TCCGGCAACG GCAGGCACAT CCTTGTCATC ACATTGGGTT CGGAATCGGC
751
801
     GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
     CCTTCGATAC GCCCAAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
851
901
     CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>: m554.pep..

- MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFQT PETLTAAHIV 1
 - 51 IDLOSKOILS AKNINTPVEP AALTOLMTAY LVFKNMKSGN IOSEENLKIP
- ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALTL AGRLGNGSIE
- 151 NFVQQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
- 201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
- 251 SGNGRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
- 301 QISGGSKKTV RAGFLKEAYI TLPHKEAKMA EQILETIQPI PAPVKKGQIL
- GKIKIRONGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from N. gonorrhoeae: m554/g554

10 20 30 40 60 MTAHKILPVLLSIILGVSHATAASPAPNRPTVHAAPTFOTPETLTAAHIVIDLOSKOILS m554.pep MTAHKILPVLLPIILGVSHATAASPAPNRPTVHAAPTLOTPETLTAAHIVIDLOSROTLS g554 10 20 30 40 50 60 70 80 90 100 110 120 AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS m554.pep q554 AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTVS 70 80 90 100 110 140 150 160 130 170 180 TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLGMKNTVFKNPTGLSREG m554.pep TDKLLKGMIALCANDAALTLADRLGNGSIENFVQQMNKEARRLGMKNTVFKNPTGLGREG g554 130 140 150 160 170 180 190 200 210 220 QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE m554.pep QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE g554 200 190 210 220 230 240 250 260 270 280 290 300 SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI m554.pep

-554	COCUMIT AMOVO		IGDG3 PMD3 GD			
g554	SGGYNLAVSYS					
•	250	260	270	280	290	300
	210	220	222			
	310	320	330	340	350	360
m554.pep	QISGSKKTVRA	AGE DKEAY LIDE	HKEAKMAEQII	LETIOPIPAPVI	KKGQILGKIKI	RONGY
-554			111111111			:
g554	QISGSKKTVRA					
	310	320	330	340	350	360
	350	200	200			
	370	380	390			
m554.pep	TIAEKEIVALEN					
~554						
g554	TIAEKEIVALEN	=				
	370	380	390			
m1 C 11 '	17557.4	•			•	
The following		sequence wa	s identified	ın N. mening	ritidis <seq< td=""><td>ID 1629>:</td></seq<>	ID 1629>:
a554.sed						
	L ATGACAGCAC	ATAAAATCCT	GCCCGTCCT	G CTTTCCATCA	TCTTAGGCGT	ŗ
51	L TTCTCACGCA	ACGGCTGCAT	CGCCCGCGC	C CAACAGACCG	ACGGCACAC	3
101	CCGCCCCCAC	GTTCCAAACA	CCCGAAACC	TCACAGCGGC	ACACATCGT'	
151	ATCGACCTTC	AAAGCAAACA	GATTTTATCO	GCCAAAAACA	TCAATACCCC	
201	TGTCGAACCG	GCGGCACTAA	CCCAACTGAT	GACCGCATAT	' CTGGTTTTC	1
251	. AAAACATGAA	ATCGGGAAAT	ATCCGATCTC	AAGAAAACTI	' AAAAATACCO	;
301	GAATCCGCAT	GGGCTTCAGA	AGGAAGCAGA	ATGTTTGTAC	GTCCCGGCGA	1
351	. TACGGTCAGC	ACCGACAAAC	TCTTAAAAGG	CATGATTGCA	CTATCCGCA	1
401	. ACGATGCCGC	CCTAACCCTT	GCCGGCCGGC	TGGGCAACGG	CTCGATTGA	1
451	. AATTTTGTGC	AACAAATGAA	CAAAGAAGCC	CGACGCTTGG	GCATGAAGAA	L
501 551	. CACTGTATTC	AAAAATCCGA	CAGGCTTGAG	TAGAGAAGGA	CAGGTTTCCA	
601	COUCHAAGA	CCTCGCCCAG	CIGICIGAAG	CATTGATGCG	CGACTTTCCC	i
651	CCANANCANC	CGCTGTTTTC CGCAATATCC	UATCAAATC1	TTCAAATTCA	AAAATATAGA	
701	TCANACCCCC	ACACACAGAA	ACCCCCCCCCC	GGACAACAAT	GTAAACGGTC	
751	TCCCCCAACC	GCAGGCACAT	CCTTCTCATA	ACAMUCTIGU	CCCAARCCCC	
801	CGAAACACGC	GCAGGCACAT	ACAGCAAGCT	CCTCAACTCC	CCATTCCAAAC	
851	ССТТССАТАС	GCCCAAAATA	TATCCGAAACI	CCANANCCCT	TCCCCA A A TO	
901		GAGGCAGCAA				
951	AGCCTACATC	ACTCTGCCAC	ATAAGGAAGC	CADADATECEN	CAACAAAGA	
1001	TAGAAACCAT	ACAGCCGATT	CCCGCCCCAG	TAAAAAAAAA	CCD D D TTTTTD	
1051	GGAAAAATCA	AAATCAGACA	AAACGGATAC	ACCATTGCCG	AAAAAAAAAA	
. 1101		GAAAATGTAA				
1151		AGGGCAGTAA		00001000/21	11000111000	
This correspon	ds to the amir	o acid seque	nce <seo i<="" td=""><td>D 1630: OR1</td><td>F 554 a>·</td><td></td></seo>	D 1630: OR1	F 554 a>·	
a554.pep		1				
1		LSIILGVSHA	TAASPAPNRP	ТАНААРТЕОТ	PETI.TAAHTU	
51	IDLOSKOILS	AKNINTPVEP	AALTOLMTAY	LVFKNMKSGN	TRSFFNIKID	
101	ESAWASEGSR	MFVRPGDTVS	TDKLLKGMIA	LSANDAALTL	AGRIGNGSTE	
151	NFVQQMNKEA	RRLGMKNTVF	KNPTGLSREG	OVSTAKDLAO	LSEALMRDEP	
201	EYYPLFSIKS	FKFKNIEQNN	RNILLYRDNN	VNGLKAGHTE	SGGYNLAVSY	
251	SGNGRHILVI	TLGSESAETR	ASDNSKLLNW	ALQAFDTPKI	YPKGKTVAOI	
301	QISGGSKKTV	RAGFLKEAYI	TLPHKEAKMA	EQILETIOPI	PAPVKKGOIL	
351	GKIKIRQNGY	TIAEKEIVAL	ENVKKRSRWQ	RLWACLTGQ*		
m554/a554 9	9.2% identity	in 389 aa ov	erlap			
	•		20 3	0 40	50	60
m554.pep	MTAHKILI	PVLLSIILGVSE				71.0580115
* 1	111111			<u></u>		501/5111
a554	MTAHKILI	PVLLSIILGVSH	ATAASPAPNR	PTAHAAPTFOTI	PETLTAAHTVTI	DLOSKOTIS
			.0 3		50	60
						00
			0 90		110	120
m554.pep	AKNINTP	/EPAALTQLMTA	YLVFKNMKSGI	NIQSEENLKIPE	ESAWASEGSRMI	EVRPGDTVS
.				11:11111111		
a554	AKNINTP	/EPAALTQLMTA	YLVFKNMKSGI	VIRSEENLKIPE	SAWASEGSRMI	VRPGDTVS

##
a554 TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLGMKNTVFKNPTGLSREG 130 140 150 160 170 180 190 200 210 220 230 240 m554.pep QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE
a554 TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLGMKNTVFKNPTGLSREG 130 140 150 160 170 180 190 200 210 220 230 240 m554.pep QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE
130 140 150 160 · 170 180 190 200 210 220 230 240 m554.pep QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE
190 200 210 220 230 240 m554.pep QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE
m554.pep QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE
a554 QVSTAKDLAQLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE
190 200 210 220 230 240
250 260 270 280 290 300
m554.pep SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI
a554 SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI
250 260 270 280 290 300
310 320 330 340 350 360
m554.pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIPAPVKKGQILGKIKIRQNGY
a554 QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIPAPVKKGQILGKIKIRQNGY
310 320 330 340 350 360
370 380 390
m554.pep TIAEKEIVALENVKKRSRWQRLWACLTGQX
a554 TIAEKEIVALENVKKRSRWQRLWACLTGQX
370 380 390

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1631>: g556.seq..

```
1 atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51 cgccgtttta agcctcatta tcgtattgat tgtcgattcc tggccgcttg
101 ccatcctgct tgccgccgtc atcgtcgccg ccgctgcggg cggctttgtt
```

- 151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt 201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
- 251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
- 301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg 351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
- 401 agaaacgtcc gcaccgttaa

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>: g556.pep.

- MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAAV IVAAAAGGFV
- WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
- 101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1633>: m556.seq..

- 1 ATGGACAATA AGACCAAACT GCGCTTGGGC GGCCTGATTT TACTGACCAC
- 51 CGCCGTTTTA AGCCTCATTA TCGTATTGAT TGTCGATTCC TGGCCGCTTG
- 101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
- 151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
- 201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
- 251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
- 301 CTGTCGCAAA AATGTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
- CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
- 401 AGAAACGTCC GCACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>: m556.pep..

- 1 MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAAV IVAAAAGGFV
- 51 WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

WO 99/57280

838

101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from N. gonorrhoeae:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKTKLRLGGLILI	TTAVLSLI	IVLIVDSWPLA	ILLAAVIVA	AAAGGFVWTSI	RRQQRQF
-	11111111111111	111111				
g556	MDNKTKLRLGGLILI	TTAVLSLI	IVLIVDSWPLA	ILLAAVIVA	AAAGGFVWTSI	RRQQRQF
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGF	RINEANLRR	MYHSGGQHQKD.	AITLICLSQE	(CSVDEAHAM)	FKKRPTR
		1111111		1111111111		
g556	IERLKKFDIDPEKGF	RINEANLRR	MYHSGGQHQKD	AITLICLSQF	CSVDEAHAMI	FKKRPTR
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQK	RPHRX				
	111111111111	11111				
q556	QEINQMAAKQSRGQK	RPHRX				
,	130	140				

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1635>:

a556.seq

```
1 ATGGACATA AGACCAAACT GCGCTTGGGC GGCCTGATTT TACTGACCAC
51 CGCCGTTTTA AGCCTCATTA TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCCGCCGTC ATCGTCGCCG CCGCTGCGGG CGGCTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGTC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAAAAAG ATGCGATTAC CCTGATCTGC
301 CTGTCGCAAA AATGTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

- MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAAV IVAAAAGGFV WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGO HOKDAITLIC
- LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKTKLRLGGLIL:	LTTAVLSLIIV	/LIVDSWPLA	ILLAAVIVAA	AAGGFVWTSR	RQQRQF
		[[]]	11111111	1111111111	1111111111	111111
a556	MDNKTKLRLGGLIL:	LTTAVLSLIIV	/LIVDSWPLA	ILLAAVIVAA	AAGGFVWTSR	RQQRQF
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKG	RINEANLRRMY	HSGGQHQKD	AITLICLSOK	CSVDEAHAMF	
• •	111111111111111	1111111111		111111111	1111111111	НПП
a556	IERLKKFDIDPEKG	RINEANLRRMY	/HSGGQHQKD	AITLICLSQK	CSVDEAHAMF	KKRPTR
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQ	KRPHRX				
1 -1		HIIII				
a556	QEINQMAAKQSRGQI	KRPHRX				
	130	140				

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1637>:

```
g557.seq
       1 atgaacaaaa tattccttac tgccgcagcc ttggtgctgg gcgcgtgcgg
      51 tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
      101 gctggcacat cgaaggcgga caggcattgc aatttccttt ggaaaccgcq
      151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
      201 cctgcgtata gacagcgttt cccaaaacaa ggaaacctat accgttaccc
      251 gtgcggcagt catcaacgaa tatcttttga tattgacggt tgaagcgcag
          gtattgaaac gcggcgagcc ggtcggcaaa ccgatgaccg tgtccgtccg
     351 ccgcattttg gattatgccg acaacgaaat tttgggcaaa caggaagaag
     401 aagaaaccct gtgggcggaa atgcggcagg atgttgccga acagattgtc
          cgccgcctga cctttctgaa ggcggaatga
 This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:
 g557.pep..
       1 MNKIFLTAAA LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
      51 LYQASGRVDD AAGAQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
     101 VLKRGEPVGK PMTVSVRRIL DYADNEILGK QEEEETLWAE MRQDVAEQIV
     151 RRLTFLKAE*
 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1639>:
m557.seq..
       1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
      51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
     101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTTCCTTT GGAAACCGCG
     151 CTGTATCAGG CTTCGGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
     201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
     251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
     301 GTATTGAAAC GCGGCGAGCC GGTCGGTAAA CCGATGACCG TGTCCGTCCG
     351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
     401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
     451 CGCCGCCTGA CCTTTCTGAA GGCGGAATGA
This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:
m557.pep..
       1 MNKLFLTAAV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
      51 LYQASGRVDD AAGAQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
     101 VLKRGEPVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
     151 RRLTFLKAE*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng)
from N. gonorrhoeae:
m557/g557
                              20
                                                 40
                                                          50
            {\tt MNKLFLTAAVLMLGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETALYQASGRVDD}
m557.pep
            g557
            MNKIFLTAAALVLGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETALYQASGRVDD
                    10
                              20
                                       30
                                                40
                                                          50
                              80
                                                100
                                                         110
                                                                   120
            AAGAQMTLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEPVGKPMTVSVRRVL
m557.pep
            g557
            AAGAQMTLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEPVGKPMTVSVRRIL
                    70
                              80
                                       90
                                               100
                                                         110
                   130
                             140
                                      150
                                               160
m557.pep
            AYADNEILGKQEEEAALWAEMRQDAAEQIVRRLTFLKAEX
             q557
            DYADNEILGKQEEEETLWAEMRQDVAEQIVRRLTFLKAEX
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1641>:

150

160

140

```
a557.seq
            1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
            51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
           101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
           151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
           201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
               GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
           301 GTATTGAAAC GCGGCGAGCC GGTCGGCAAA CCGATGACCG TGTCCGTCCG
           351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
           401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
          451 CGCCGCCTGA CCTTTCTGAA GGCGGAATGA
 This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:
      a557.pep
               MNKLFLTAAV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
           51
               LYQASGRVDD AAGAQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
          101
               VLKRGEPVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
               RRLTFLKAE*
          151
m557/a557 99.4% identity in 159 aa overlap
                          10
                                   20
                                             30
                                                      40
                                                                50
                                                                         60
                  {\tt MNKLFLTAAVLMLGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETALYQASGRVDD}
     m557.pep
                  MNKLFLTAAVLMLGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETALYQASGRVDD
     a557
                          10
                                   20
                                             30
                                                                50
                                   80
                                            90
                                                     100
     m557.pep
                  {\tt AAGAQMTLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEPVGKPMTVSVRRVL}
                  a557
                  AAGAQMTLRIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEPVGKPMTVSVRRVL
                         70
                                   80
                                            90
                                                     100
                                  140
                         130
                                           150
     m557.pep
                  AYADNEILGKQEEEAALWAEMRQDAAEQIVRRLTFLKAEX
                  a557
                  AYADNEILGKQEEEAALWAEMRQDAAEQIVRRLTFLKAEX
                        130
                                  140
                                           150
                                                     160
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1643>:
g558.seq..
      1 ATGGATGCTT GTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
      51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
     101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
     151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
     201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
     251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
     301 CTTTCAGACG GCATTGTTTA G
This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:
g558.pep..
         MDACFFVIPA QAGIRRFGIV FKRSGRILAG AGMMPLYTFS ELYMLQQGTA
        HQAPHCVLPE RGCPPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
      51
        LSDGIV*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1645>:
m558.seq..
      1 ATGAATGCTT GTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT
     51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
     101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
     151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
     201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
    251 AGTCCATTTC CGACATCTST CGGGCGATGC CGTCTGAAAA CCAATCTCCA
         CTTTCAGACG GCATTGTTTA G
This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:
```

```
841
m558.pep..
         MNACFFVIPT QAGIRRFGIV FKRSGRILAG AGMMPLYTFS ELYMFQQGTA
         HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP
      51
     101 LSDGIV*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng)
from N. gonorrhoeae:
m558/g558
                    10
                             20
                                       30
                                                40
            MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLYTFSELYMFQQGTAHQAPHCVLPE
m558.pep
            MDACFFVIPAQAGIRRFGIVFKRSGRILAGAGMMPLYTFSELYMLQQGTAHQAPHCVLPE
a558
                             20
                                       30
                                                40
                    70
                             80
                                       90
                                               100
            RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPLSDGIVX
m558.pep
               RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPLSDGIVX
g558
                    70
                             80
                                       90
                                               100
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1647>:
     a558.seq
              ATGAATGCTT GTTTTTTCGT CATTCCCACA CAGGCGGGAA TTCGGAGATT
           1
          51
              CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
         101
              TGCCCTTATA TATAGTGGAT TAAATTTAAA TCAGGACAAG GCGACGAAGC
         151 CGCAGACAGT ACAAATAGTA CGGCAAGGCG AGGCAACGCC GTACTGGTTT
         201 AAATTTAATC CACTATACTT TCTCCGAGCT TTATATGTTT CAACAGAGGA
         251 CGGCACATCA AGCACCGCAC TGCGTGTTGC CCGAACGAGA CTGCCCTCCG
         301 ATTAGATTCT ATCGCTATAA ACAGACGGGT TTCAACCGAA AAGGAATGGG
              AATGAAGTCC GTTTCCGACA CCTCTCGGGC GATGCCGTCT GAAAACCAAT
              CTCCACTTTC AGACGGCATT GTTTAG
This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:
     a558.pep
              MNACFFVIPT QAGIRRFGIV FKRSGRILAG AGMMPLYIVD *I*IRTRRRS
          51
              RRQYK*YGKA RQRRTGLNLI HYTFSELYMF QQRTAHQAPH CVLPERDCPP
              IRFYRYKQTG FNRKGMGMKS VSDTSRAMPS ENQSPLSDGI V*
         101
          70.2% identity in 141 aa overlap
m558/a558
                 MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLY-----
    m558.pep
                 **************************
                 MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLYIVDXIXIRTRRRSRRQYKXYGKA
    a558
                                  20
                                           30
                                                    40
                             40
                                      50
                                                60
                                                         70
                        ----TFSELYMFQQGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS
    m558.pep
                            a558
                 RQRRTGLNLIHYTFSELYMFQQRTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS
                                  80
```

The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 1649>: g560.seq

140

90

100

100

ISDIXRAMPSENQSPLSDGIVX

VSDTSRAMPSENQSPLSDGIVX 130

90

m558.pep

a558

atgctcatca tccgcaacct gatttactgg ctgatactct gttccagcct

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```
qattttcctc tttcccttta tgctgctcgc ctcgcctttc cgggacgggg
         cqcacaagat ggcgcgggtc tgggtcggca tcctcaactg gtcgctcaaa
         cacatcqtcg ggctcaaata ccgcatcatc ggcgcggaac acattccgqa
         ccgccctcc gtcatctgcg ccaaacacca aagcggctgg gaaacgctcg
     251 cqctccaaga gatttttccg ccgcaggttt acgttgccaa gcgcgagttg
     301 ttcaaaatcc cctttttcgg ctggggcttg aaactggtca aaaccatagg
     351 catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
     401 gtttggcgcg caaaaacgaa ggttattgga ttaccatttt ccccgaaggc
     451 acgcgccttg cgcccggaaa acgcggcaaa tacaaactcg gcggcgcgcg
     501 catggcgaaa atgtttgaga tggacatcgt ccccgtcgcc ctcaacagcg
     551 gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
     601 gtcatcatct gtccgaccat cccgcacgca agcggcagcg aagccgaatt
     651 gatggaaaaa tgcgaacacc tcattgaaac gcaacaaccg cttatttccg
     701 gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga
This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:
q560.pep..
         MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
         HIVGLKYRII GAEHIPDRPS VICAKHQSGW ETLALQEIFP PQVYVAKREL
         FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
         TRLAPGKRGK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
         VIICPTIPHA SGSEAELMEK CEHLIETQQP LISGAGPFAA EMPSET*
The following partial DNA sequence was identified in N.meningitidis <SEQ ID 1651>:
m560.seq
         ATGCTCATCA TCCGCAACCT GATTTACTGG CTGATACTCT GTTCCACCCT
      1
         GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
      51
         CGCACAAGAT GGCGCGGTC TGGGTCGGCA TTCTCAACTG GTCGCTCAAA
         CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
         CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
         CCCTTCAGGA CATTTTCCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
     301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAACTGGTCA AAACCATAGG
     351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
     401 GGTTGGTGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCGAAGGC
     451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAAACTCG GCGGCGCGCG
    501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCGTCGCC CTCAACAGCG
     551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
     601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
     651 GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTTCCG
     701 GCGCAGGCCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA
This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:
m560.pep
         MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
      1
     51 HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
     101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
     151 TRLAPGKRGK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
         VVICPTIPHA SGSEAELMEK CEHLIETQQP LISGAGPFAA KMPSETA*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N.gonorrhoeae
ORF 560 shows 97.2% identity over a 246 as overlap with a predicted ORF (ORF 560.ng)
from N. gonorrhoeae:
m560/q560
                                        30
            MLIIRNLIYWLILCSTLIFLFPFMLLASPFRDGAHKMARVWVGILNWSLKHIVGLKYRII
m560.pep
            MLIIRNLIYWLILCSSLIFLFPFMLLASPFRDGAHKMARVWVGILNWSLKHIVGLKYRII
g560
                    10
                              20
                                       30
                                                 40
                                                           50
                                        90
                                                100
m560.pep
            GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
            q560
            GAEHIPDRPSVICAKHQSGWETLALQEIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
```

	70	80	90	100	110	120
m560.pep	130 NNRREANEQLIK	140	150	160	170	180
msev.pep					GARMAKMFEMD.	IVPVA
g560	NNRREANEQLIK		ITIFPEGTRL	APGKRGKYKLO		!!!!! IVPVA
	130	140	150	160	170	180
mF(0 non	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSF					
g560	LNSGEFWPKNSFI	LKYPGEITVII	CPTIPHASGS)	::::::::::::::::::::::::::::::::::::::	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	 PPAA
	190	200	210	220	230	240
m5.60 man	MAD CEMA V					
m560.pep	KMPSETAX :					
g560	EMPSETX					
-						
The following	partial DNA s	equence was	s identified	in N. menin	gitidis <seq< td=""><td>ID 1653>:</td></seq<>	ID 1653>:
a560.sec						
1	ATGCTCATCA	TCCGCAACCT	GATTTACTG	G CTGATACTC	T GTTCCACCC	
51 10 1					C CGAGACGGGG T CTCGCTCAA	
151					T CTCGCTCAAA A ACATCCCCGA	
201	CCGCCCCGCC	GTCATCTGCG	CCAAACACCA	A AAGCGGCTG	G GAAACGCTCG	·
251	CCCTTCAGGA	CATTTTTCCG	CCGCAGGTTT	r ACGTTGCCA	A ACGCGAGTTO	;
301	TTCAAAATCC	CCTTTTTCGG	CTGGGGCTTC	AAACTGGTC	A AAACCATAGO	;
351 401	CATAGACCGC	AACAACCGCC	GCGAAGCCAA	A CGAGCAGCT	C ATAAAACAGG	,
451					T CCCCGAAGGC G GCGGCGCGCG	
501	CATGGCGAAA	ATGTTTGAGA	TGGACATCGT	CCCCGTCGC	C CTCAACAGCG	' !
551	GCGAATTTTG	GCCGAAAAAC	TCCTTTCTGA	AATATCCGG	G GGAAATCACC	
601	GTCGTCATCT	GTCCGACCAT	CCCGCACGC	AGCGGCAGC	G AAGCCGAATT	ı
651 701		TGCGAACACC	TCATCGAAAC	C GCAGCAGCC	G CTCATTTCCG	ı
701	GCGCAGGCCC	GIIIGCCGCC	AAAATGCCGT	. CIGAAACCG	CAIGA	
This correspon	ds to the amin	o acid seque	nce <seo 1<="" td=""><td>D 1654: OF</td><td>RF 560.a>:</td><td></td></seo>	D 1654: OF	RF 560.a>:	
a560.pep				- 100 1, 01	a 500.a .	
1	MLIIRNLIYW				V WVKILNLSLK	
51	HIVGLKYRII	GAENIPDRPA	VICAKHQSGW	ETLALQDIF	P PQVYVAKREL	
101 151	FKIPFFGWGL	KLVKTIGIDR	NNRREANEQI	IKQGLARKN	E GYWITIFPEG	
201		SGSEAELMGK	CEHLIETOOF	LNSGEFWPKI	N SFLKYPGEIT	
	***************************************		02	DIDGIGI IN	A MILDELA	
m560/a560 9	8.4% identity	in 247 aa ov	erlap			
		10 2	20 3	0 40	50	60
m560.pep	MLIIRNLI	YWLILCSTLIE	TLFPFMLLASF	FRDGAHKMAR	JWVGILNWSLKH	IVGLKYRII
5.60		1111111111	111111111	111111111	H	
a560	MLIIRNLI			FRDGAHKMARV 0 40	WVKILNLSLKH	
		10 2	.0 3	0 40	50	60
		70 8	9 9	0 100	110	120
m560.pep	GAENIPDR	PAVICAKHQS	WETLALQDIF	PPQVYVAKREI	LFKIPFFGWGLK	LVKTIGIDR
- " - "	1111111	111111111111	1111111111	11111111111		
a560					LFKIPFFGWGLK	
		, 0	10 9	0 100) 110	120
		30 14				180
m560.pep	NNRREANE	QLIKQGLVRKN	EGYWITIFPE	GTRLAPGKRG	YKLGGARMAKM:	FEMDIVPVA
- 5.60		1111111:11	111111111	1111111111111	1111111111	11111111
a560	NNRREANE	OTTKÖGTAKKN	EGYWITIFPE	GTRLAPGKRGE	YKLGGARMAKM	FEMDIVPVA

	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFL	KYPGEITVVIO	CPTIPHASGSE	EAELMEKCEHI	LIETQQPLISC	SAGPFAA
		{			111111111	
a560	LNSGEFWPKNSFL	KYPGEITVVIC	CPTIPHASGSE	EAELMGKCEHI	JIETQQPLISC	SAGPFAA
	190	200	210	220	230	240
m560.pep	KMPSETAX					
F L						
a560	KMPSETAX					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1655>:

```
m561.seq.
          ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
       1
          GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
      51
          TGACACTGCT GCTCTCTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
          GAGGCGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
          TGAAGGCTCG CCCCGTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
          AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
     251
          TCGGACACCC CTCTTGCTTA TGATTTGATA CAATCCATGC TGATTATAGA
     301
          TTGGCAGGCA CACATCCTCC CCCCGCTCCA GTCCTACCGG CGACCGACTC
     351
         AGGTCGATCT CTACCGCTTT GCCGGAAACA TCGAACTGTT TTTGCAGGCA
     401
         TTGGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
     451
         GGCAATTATG TTGATGACGC TGGTGTCGTC TGTACTGATG CTGTTTTGGC
     501
     551 ACCAGATTTG GGTTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
          CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
         GGAATTCAAA CAGGTCGGC GTTGTTTCAA TCAAATGGGC GGCAGGTTGA
     701 AAATTTTATA TGATGATTTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
     751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAAA CTACACGGGA
     801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
     851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
     901 GGATCCGATG TTTATGTTTC CATTCATCAT GCGGATTGCG GCACAGCAGC
          TTCGGATTTG GGGAAGTACC ATGAGGAAAT CTTCCCCATT GAGTACCAGA
          ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTTCTCTT
          GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
         ATCGCTTGCC GGCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
    1101
         TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
    1151
         GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
    1201
         CGAAAACAAA CGGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAAACAG
    1251
         GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTTCCGT
         ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCGC
         CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
         GTTCGTTCCT GCCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
    1451
         CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCGCGCCA CCCATGTAAA
    1501
         ATTCACCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
    1551
         ACGGACAAGG TTTCGACACG GAGAAAATAG GAGAACCCAC GGGCAGCCAT
          GTCGGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
    1651
          AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
    1701
          CATCTGAAGA AAGCTTGAAA TGA
    1751
```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

m5

61.pep					
1	MILPARFSDG	ISLSLRLKLL	TGLWVGLAAL	SVVLTLLLSL	RLENAASVIE
51	EAGNLRMQAY	RLAYMAGEGS	PRAQIDNQVA	EFEKSLKRIA	QSDAIHPLIP
101	SDTPLAYDLI	QSMLIIDWQA	HILPPLQSYR	RPTQVDLYRF	AGNIELFLQA
151	LENANEKNTW	WLRRFQWAIM	LMTLVSSVLM	LFWHQIWVIR	PLQALREGAE
201	RIGRRCFDIP	VPEGGTPEFK	QVGRCFNQMG	GRLKILYDDL	EGQVAEQTRS
251	LEKQNQNLTL	LYQTTRDLHQ	SYIPQQAAEH	FLNRILPAVG	ADSGRVCLDG
301	GSDVYVSIHH	ADCGTAASDL	GKYHEEIFPI	EYQNETLGRL	LLSFPNGISL
351	DEDDRILLQT	LGRQLGVSLA	GAKQEEEKRL	LAVLQERNLI	AQGLHDSIAQ
401	ALTFLNLQVQ	MLETAFAENK	REEAAENISF	IKTGVQECYE	DVRELLLNFR
451	TKISNKEFPE	AVADLFARFT	QQTGITVETA	WENGSFLPPQ	EAQLQMIFIL

501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFDT EKIGEPTGSH 551 VGLHIMQERA KRIHAVLEIR SQAQQGTTVS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

```
m561/q561
                89.7% identity in 223 aa overlap
                                            30
                                                     40
                                                              50
                                                                        60
                 MILPARFSDGISLSLRLKLLTGLWVGLAALSVVLTLLLSLRLENAASVIEEAGNLRMQAY
     m561.pep
                 MILPTRFSDGIPLSLRLKLLTGLWVGLAALSVVLTLLLSFRLENAASVIEEAGNLKMQAY
     g561
                         10
                                  20
                                           30
                                                     40
                         70
                                  80
                                           90
                                                    100
                                                             110
                 RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
     m561.pep
                 RLAYMAGEGSPRAQIDNQIAEFEKSLKRISQSDAIHPLIPSDNPLAYDLIQSMLIIDWQA
     q561
                         70
                                  80
                                           90
                                                    100
                                                             110
                        130
                                 140
                                          150
                                                    160
                                                             170
                                                                       180
                 HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
     m561.pep
                 q561
                 NILPPLQAYRRPTQIELYRFAGNIELFLQALENAGEKNTWWLRRFQWVIMLMTLVSSVLM
                        130
                                 140
                                          150
                                                    160
                                                             170
                                                                       180
                        190
                                 200
                                          210
                                                    220
                                                             230
                                                                       240
                 LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLKILYDDL
    m561.pep
                 1: :: 1
                 LFWHQIWVIRPLQALREGAERIGQRHFDIPVPEDVRPNSNRSGGVSTKWRSGX
     g561
                        190
                                 200
                                          210
                                                    220
                                                             230
                        250
                                 260
                                          270
                                                    280
                                                                       300
                 EGQVAEQTRSLEKQNQNLTLLYQTTRDLHQSYIPQQAAEHFLNRILPAVGADSGRVCLDG
    m561.pep
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1657>:
    a561.seq
              ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
              GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
          51
              TGACACTGCT GCTCTTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
         101
             GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
         151
              TGAAGGCTCG CCCCGTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
              AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
              TCGGACACCC CTCTTGCTTA TGATTTGATA CAATCCATGC TGATTATAGA
              TTGGCAGGCA CACATCCTCC CCCCGCTCCA GTCCTACCGG CGACCGACTC
              AGGTCGATCT CTACCGCTTT GCCGGAAACA TCGAACTGTT TTTGCAGGCA
              TTGGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
              GGCAATTATG TTGATGACGC TGGTGTCGTC TGTACTGATG CTGTTTTGGC
         501
             ACCAGATTTG GGTTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
         551
             CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
         601
              GGAATTCAAA CAGGTCGGGC GTTGTTTCAA TCAAATGGGC GGCAGGTTGA
         651
             AAATTTTATA TGATGATTTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
         701
             CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAAA CTACACGGGA
         751
             TCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
         801
             GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
         851
             GGATCCGATG TTTATGTTTC CATTCATCAT GCGGATTGCG GCACAGCAGC
         901
             TTCGGATTTG GGGAAGTACC ATGAGGAAAT CTTCCCCATT GAGTACCAGA
         951
        1001
             ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTTCTCTT
        1051
             GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
        1101
             ATCGCTTGCC GGCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
        1151
             TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
        1201
             GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
             CGAAAACAAA CGGGAGGAAG CCGCAGAAAA CATCGGCTTC ATCAAAACAG
        1251
```

GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTTCCGT

ACCAAAATCA GTAATAAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCTC

1401 1451 1501 1551 1601 1651 1701	GCGCTTTACG C. GCACGCACCT G CAAGAAAGCT T. ATTCAGACTG C. ACGGACAGGG T. GTCGGACTGC A. AGAAATCCGT T. CATCTGAAGA A.	CCTACACAG GTCCAACAT TCAAACAGG TTTGACACG TATCATGCA CCCAAGCTC	GACGAGCAGC CCGAAAACAT ATGGAAGTTT GAAAACATTG GGAGCGTGCC AACAGGGAAC	TCCAAATGAT GCCCACGCCA TACAATGACC GAGAACCATC AAACGCATCC	TTTCATCCTG CCCATATCAA ATTCAAGACA GGGCAGCCAT ATGCCGTTTT	
This correspond	s to the amino	acid seque	nce <seq ii<="" td=""><td>O 1658; ORF</td><td>561.a>:</td><td></td></seq>	O 1658; ORF	561.a>:	
a561.pep		01 01 01 1/11	mor fattor a a r	OTTE MITTOI	D.T. TILLIA DILITO	
1 51	MILPARFSDG IS EAGNLRMQAY R					
101	SDTPLAYDLI Q					
151	LENANEKNTW W					
201	RIGRRCFDIP V					
251	LEKQNQNLTL L	YQTTRDLHQ	SYIPQQAAEH	FLNRILPAVG	ADSGRVCLDG	
301	GSDVYVSIHH A					
351	DEDDRILLQT L					
401	ALTFLNLQVQ MITKISNKEFPE A					
451 501	QESLSNIRKH A					
551	VGLHIMQERA KI					
331	, OZIII Z.I.					
m561/a561	96.9% ide	ntity in 5	90 aa overl	ap		
	1.		0 30		50	60
m561.pep					LENAASVIEEAGNI	~
a561	MILPARESDO		TELWAGEWAT 0 30		LENAASVIEEAGNI 50	RMQAY 60
	1,	U 2	.0 30	, 40	30	80
	7(0 8	0 90	100	110	120
m561.pep			AEFEKSLKRIA	AQSDAIHPLIPS	DTPLAYDLIQSMLI	IDWQA
					11111111111111	
a561					DTPLAYDLIQSMLI	
	70	0 8	0 90	100	110	120
	130	0 14	0 150	160	170	180
m561.pep					LRRFQWAIMLMTLV	
moor.pep					111111111111	
a561					LRRFQWAIMLMTLV	
	130	0 14	0 150	160	170	180
	190				230	240
m561.pep					VGRCFNQMGGRLKI	
a561					VGRCFNQMGGRLKI	
8501	190				230	240
	250				290	300
m561.pep					LNRILPAVGADSGR	
a561	EGQVAEQTR:				LNRILPAVGADSGR 290	300
	2.50	20	270	, 200	230	300
	310	0 32	0 330	340	350	360
m561.pep					LSFPNGISLDEDDR	
• •					1111111111111111	
a561 _.					LSFPNGISLDEDDR	
	310	32	0 330	340	350	360
	370	0 38	0 390	400	410	420
m561.pep					LTFLNLQVQMLETA	
a561					LTFLNLQVQMLETA	

WO 99/57280

847

	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTO	SVQECYEDVRE	ELLLNFRTKIS	NKEFPEAVAD	LFARFTQQT	GITVETA
				1111111111	11:111111	
a561	REEAAENIGFIKTO	SVQECYEDVRE	ELLLNFRTKIS	NKEFPEAVAD	LFSRFTQQT	STTVETA
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENGSFLPPQEAQI	LQMIFILQESI	SNIRKHARAT	HVKFTLSEHG	GRFTMTIQDN	4GQGFDT
				1:11 1 ::	1 11111111	
a561	WENGTHLPTQDEQI	LQMIFILQESI	SNIRKHAHAT	HIKFRLLKQD	GSFTMTIQDN	NGQGFDT
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGL	HIMQERAKRIH	HAVLEIRSQAÇ	QGTTVSLTVA	SEESLKX	
	1:1111:111111	1111111111		1111111111		
a561	ENIGEPSGSHVGLE	HIMQERAKRIH	HAVLEIRSQAÇ	QGTTVSLTVA	SEESLKX	
	550	560	570	580	590	

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1659>: q562.seq..

```
atggcaagee egtegagtet geettteaat tegggeaaga eeaaacegae
 1
    ggcttttgcc gcgccggttt tggtcggaat catgttttcc acgccgctgc
51
    gggcgcggcg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
101
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tqqaaacqac qqtcatqtcq qcqqtcaqqa cqctqtcqtt cacqccqtac
301 acqacqqttq catcgacatc gtcgccgccc ggtgcggaaa tgaggacttt
351 tttcgcgccg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggt tgcgggtcga gaagaagggg attttgtcgc cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcgttg
601 acggcgacga tttggagttg gtcttga
```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRTLSFTPY TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS SAGLRVEKKG ILSPLTMRLP PSWDTSASKR PCTVSNLVRW ALVSRLPLAL 201 TATIWSWS*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1661>:

m562.seq

ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC 1 51 GGCTTTTGCC GCGCCGGTTT TGGTCGGAAT CATGTTTTCC ACGCCGCTGC 101 GGGCGCGGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG 151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT 251 TGGAAACGAC GGTCATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC 301 ACGACGGTTG CATCGACATC GTCGCCGCCC GGTGCGGAAA TGAGGACTTT 351 TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTTCTTTG CTGGTGAACG 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT 451 TCGGCAGGGT TGCGGGTCGA GAAGAAGGGG ATTTTGTCGC CGTTGACGAT 501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG TGTCGAATTT GGTCAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG 601 ACGGCGACGA GTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

- MASPSSLPFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
- 51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRTLSFTPY

- 101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
- 151 SAGLRVEKKG ILSPLTMRLP PSWDTSASKR PCTVSNLVRW ALVSRLPLAL

201 TATSWSWS*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m562/g562 99.0% identity in 208 aa overlap 40 50 MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP m562.pep MASPSSLPFNSGKTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP q562 10 20 30 40 70 8Ò 90 100 110 LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP m562.pep LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP q562 70 80 90 100 110 120 130 140 150 160 170 LSRWILAFSLLVNAPVHSMTKSTPSSFHGSSAGLRVEKKGILSPLTMRLPPSWDTSASKR m562.pep LSRWILAFSLLVNAPVHSMTKSTPSSFHGSSAGLRVEKKGILSPLTMRLPPSWDTSASKR g562 130 140 150 160 170 180 190 200 209 PCTVSNLVRWALVSRLPLALTATSWSWSX m562.pep PCTVSNLVRWALVSRLPLALTATIWSWSX q562 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1663>: a562.seg ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC 1 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTTCC ACGCCGCTGC 51 GGGCGCGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG 101 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC 151 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT 201 TGGAAACGAC GGTCATGTCG GCGGTCAGGA TGCTGTCGTT CACGCCGTAC 251 ACGACGGTTG CATCGACATC GTCGCCGCCC GGTGCGGAAA TGAGGACTTT 301 TTTCGCGCCG CTTTCCAGAT GAACTTTGGC TTTTTCTTTG CTGGTGAACG 351 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT 401 451 TCGGCAGGT TGCGGGTCNA GAAGAANGGG ATTTTGTCGC CGTTGACGAT GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGCACGG 501 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG ACGGCGACGA TTTGGAGTTG GTCTTGA This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>: a562.pep MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL 1 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRMLSFTPY 51 101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSMT KSTPSSFHGS SAGLRVXKXG ILSPLTMRLP PSWDTSASKR PCTVSNLVRW ALVSRLPLAL 151 201 TATIWSWS* 96.6% identity in 208 aa overlap m562/a562 10 20 30 40 50 MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP m562.pep MASPSSLSFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP a562 10 20 30 40 50

m562.pep	70 LTMPTLSLNTLATG	80 ERQLVVQEAI	90 LETTVMSAVR	100 TLSFTPYTTVA	110 STSSPPGAE	120 MRTFFAP	
a562	LTMPTLSLNTLATG	ERQLVVQEAI 80	ETTVMSAVRI 90	MLSFTPYTTVA 100	STSSPPGAE	MRTFFAP 120	
	130	140	150	160	170	180	
m562.pep	LSRWILAFSLLVNA	PVHSMTKST	PSSFHGSSAGI	LRVEKKGILSP	LTMRLPPSW	DTSASKR	
a562	LSRXTLAFSLLVNA	PVHSMTKSTE	PSSFHGSSAGI	LRVXKXGILSP	LTMRLPPSW:	DTSASKR 180	
	130	140	150	160	. 170	100	
	190	200	209				
m562.pep	PCTVSNLVRWALVS	RLPLALTATS	SWSWSX				
a562.	PCTVSNLVRWALVS		WSWSX				
	190	200					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>: 9563.seq

```
ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
   1
     GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
 51
     GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
101
     TCCAAAGCCT TTTGTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
     GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
     CTCCTAAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
     CAAGTCAATA TTCAAACCcc tACTTCGGCa ggGGTTTCTG TTAATCAATA
     TGCCCAGTTT GATGTGGGTA ATCGCGGGGC GATTTTAAAC AACAGTCGCA
     GCAACACCCA AACACAGCTA GGCGGTTGGA TTCAAGGCAA TCCTTGGTTG
     ACAAGGGGCG AAGCACGTGT GGTTGTAAAC CAAATCAACA GCAGCCATCC
    TTCACAACTG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
     TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
    GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
    CTTTAGCGGC TTTAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
    GTTTGGATGC CCGTGATACC GATTTCACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTC GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCACGATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
    TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
     AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1051
     TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1101
     TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
     GGCACACTTG CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATTT
     TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
     GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGCATTCGG
     ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1351
     CGGTACGACA GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA
     TTGACGGACA ACAAACCAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
     ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
     CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
     TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
    AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1651
     CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1701
     CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1751
     TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1801
     AGCATTTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
     GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1901
     GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
1951
     AACTCAAGTA ACCGGAACTG CGCCTGCTAA AATCATTGCA GGTAGCGATT
2001
     TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC
2051
```

2101	GGCGGCCAAT	TGCTTGTGCA	AACAGAAAAA	GACGGTTTGC	ATAACGAGCA
2151	AACCTTTGGC	GAGAAGAAAG	TCTTCAGCGA	AAATGGTAAG	TTGCACAACT
2201	ACTGGCGTGC		GGACATGATG		
2251	AATTATACTT	TGCCGGAGGA	AATCACACGC	GACATTTCAC	TGGGTTCATT
2301	TGCCTATGAA	TCGCATAGCA	AAGCATTAAG	CCGTCATGCG	CCCAGCCAAG
2351	GCACTGAGTT		AACCGGGATA		
2401	AACGGTATTT	CGCTACCCTA		TCTTTTACCC	
2451	CAGCAGCTTA		ATCCTGCCAA		
2501		CTTTGCCAAC		GGTTGGGTAG	
2551	CTGGGCAGCC	TCAAACTAGA		ACAAATCGCA	GTTTGGGTGA
2601	TGGTTATTAC	GAGCAACGTT		ACGAAGAACA	
2651	GGCATCGTCG TTAATGGATA		TGCGGCACGT	TCGATGAATC	
2701			AAGCAGCGCA		
2751	CATIGCATIA	AGIGCCGACT	AAACTTCCTG	ATGGCGGCAC	ACAAACCGTA
2801 2851	TTCATCCCAC	AGGTTTATGT	ACGCGTTAAA	AATGGCGGCA	TAGACGGTAA
2901	AGGTGCATTG	TTGTCAGGCA	GCAATACACA	AATCAATGTT	TCAGGCAGCC
2951			GCAGGGCGCA		TATCAATACC
3001		ACAATATCGG		CATGCGCAAA	AATCAGCGGT
3051			ATAATATTGG	CGGCATTCTT	TCTGCCGAAC
3101	AGACATTATT	GCTCAATGCG		TCAACAACCA	AAGCACGGCC
3151	AAGAGCAGTC	AAAATGCACA		ACCTACCTAG	ACCGAATGGC
3201		ATCACAGGCA	AAGAAAAAGG	${\tt TGTTTTAGCA}$	GCGCAGGCAG
3251	GCAAAGACAT		GCCGGTCAAA		
3301	GGGCAAACCC	GGCTGCAGGC	AGGACGCGAC	ATTAACCTGG	ATACGGTACA
3351		TATCAAGAAA		TGCCGATAAC	
3401			GGCAGCAGCA		
3451			TCTCAATGCC		
3501	CGCAAAAGGC	ACACTTGCCG	TGTATGCTAA	AAATGACATT	ACTATCAGCT
3551	CAGGCATCCA		GTTGATGATG		
3601		GTAATAAATT	AGTCATTACC	GATAAAGCCC	AAAGTCATCA
3651	CGAAACTGCT		CCTTTGAAGG		
3701	CAGGAAACGA		CTTGGCAGTA TCATGTTCGC		
3751	ACCCGGATTC		ATCAAACCCA		
3801	AAGCCAAAGC	CTTCACTATC	GGCAGCAAGA	CAAACACACA	AGAAAACCAA
3851			AGGCAGTACC		TGAAAGGCGA
3901			AACACTACGA		
3951 4001			CTTATCAGCA		GGATATTGGC
4051	GCAGCACAAA	ACCAATTAAA	CAGCAAAACC	ACCCAAACCT	ACGAACAAAA
4101	AGGCTTAACG	GTGGGCATTC	AGTTCGCCCG	TTACCGATTT	GGCACAACAA
4151	GCGATTGCCG	TAGCACACAA	AGCAGCAAAC	AAGTCGGACA	AAGCAAAAAC
4201	GACCGCGTTA	ATGCCATGGC	GGCTGCCAAT	GCAGGTTGGC	AGGCCTATCA
4251	AACAGGCAAA	GGCGCACAAA	ACTTAGCCAA	TGGTACAACC	AATGCCAAAC
4301	AAGTCAGCAT	CTCCATAACC	TACGGCGAAC	AGCAAAACCG	ACAAACCACC
4351	CAAGTTCAAG	CCAATCAAGC	CCAAGCGAGT	CAAATTCAAG	CAGGCGGCAA
4401	AACTACCCTT	TATTGCCGAA	GGTGCGGCGA	ACAATCCAAT	ATCAACATCA
4451	CAGGCTCAGG	TGTTTCAGGC	AGAGCAGGAA	CCGGCCTGAT	TGCCGATAAG
4501	CAAATCCATC	TGCAATCAGC	CGAGCAAAGC	AATACCGAAC	GCAGCCAAAA
4551	CAAATCAGCA	GGCTGGAACG	CAGGTGCTGC	CGTATCATTC	GGACAAGGAG
4601	GCTGGTCATT	AGGCGTTGCC	GCAGGCGGCA	ATGTCGGCAA	AGGCTACGGC
4651	TATGGCGATA	GCGTAACCCA	CCGCCATAGC	CATATTGGCG	ACAAAGGCAG
4701	CCAAACCCTT	ATCCAAAGTG	GTGGCGATAC	CATCATCAAA	GGCGCGCAAG
4751	TACGCGGCAA	AGGCGTACAA	GTCAATGCCA	CAACAAACCTAAG	CATICAAAGT
4801	GTACAAGATA	GAGAAACTTA	TCAAAGCAAA	TCCCCATTA	CCGGTGCACA
4851	AGTTACCGTA	GGTTATGGCT	TCAGTGCCAG	ACCANACCCC	AGCCAAAGCA
4901	AAATCCGAGC	CONCLATGUT	ADDUMINED A CO	AGCMANGCGG	GCCTCAAAGG
4951					AAAAACCGAT
5001			GGCAGTGATA		
5051					GCGGCAAAAC
5101 5151					CTGACAAGCA
2121	AC I GOGACAG	CCCCCI D D D D D			

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TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
         GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
    5251
         TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
    5301
         CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
    5351
         CGACATTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
    5401
         TGAACTGGAT TTACAAAgaA CCGTCAGCCA AGATTTTAGT AAAAATGTTC
    5451
         AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
    5501
    5551
         AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
         GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
         CAGATAATTG GCAACAAGGC AAAGTCATTC TCAACATGTT AGCCTCAGGT
    5651
    5701
         TTAGCTGAGC CGACCCAAAG CGGAGCqqqc ATCGCTGCGG CTACCGCATC
         GCCaqaCGTA TCGTATGCGA TTGGACAGCA CTTTAAaqaT TTAGCCGGTC
    5751
         AAAACGCGAA TGGCAAACTA ACCGCCAGTC AagaAACCGC TCACGTTCTT
         GCCCACGCGG TATTAGGAGC AGCGGTTGCC GCAGCATGAG GCAACAATGC
    5851
    5901 CCCGCAGGA GCATTGGGTG CGGGCGGGTC qqAaqcqqCC GCCCCAATCA
   5951 TCGGCAAATG GCTGTACGGC AAAGGAGACg gcggcagccT GAATgcggag
   6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggta cGgctGCCGG
   6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGGT TGTTTTcaaa
         cggctTCaga TTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA
This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>;
q563.pep..
      1 MNKTLYRVIF NRKRGAVVAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
         SKAFCFSALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNGIP
         QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
         TRGEARVVVN QINSSHPSQL NGYIEVGGRR AEVVIANPAG IAVNGGGFIN
         ASRATLTTGQ PQYQAGDFSG FKIRQGNAVI AGHGLDARDT DFTRILLYAN
    251 KITLISTAEQ AGIRNQGQLF ASSGNVAIDA NGRLVNSGTM AAANVODMNN
         TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
         SLNNQNGEIA TNQQLIIHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLSNN
         GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLOAGKRIR
         IKANNLDNAV QGNIQSGGTT DIGTQHNLTN RGLIDGOOTK IOAGOMNNIG
         TGRIYGDNIA IAATRLDNQD ENGTGAAIAA RENLNLGIEQ LNNRENSLIY
         SGNDMAVGGA LDTNDQATGK AQRIHNAGAI IEAAGKMRLG VEKLHNTNEH
         LKTQLVETGR ERIVDYEAFG RHELLREGTQ HELGWFVYNN ESDHLRTPDG
         VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
         GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHNYWRARRK GHDETGHREO
    751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSOGTELPOS NRDNIRTAKS
         NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YROWLGSDYM
         LGSLKLDPNN LHKRLGDGYY EORLINEOIA ELTGHRRLDG YONDEEOFKA
         LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVWLVOKEV KLPDGGTOTV
    951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
   1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTLLLNA GNNINNQSTA
   1051 KSSQNAQGSS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSDQ
   1101 GQTRLQAGRD INLDTVQTGK YQEIHFDADN HTIRGSTNEV GSSIOTKGDV
   1151 TLLSGNNLNA KAAEVGSAKG TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
   1201 SGGGNKLVIT DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVISDNG
   1251 TRIQAGNHVR IGTTQTQSQS ETYHQTQKSG LMSAGIGFTI GSKTNTOENO
   1301 SQSNEHTGST VGSLKGDTTI VASKHYEQTG SNVSSPEGNN LISTQSMDIG
   1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYRF GTTSDCRSTO SSKOVGOSKN
   1401 DRVNAMAAAN AGWQAYQTGK GAQNLANGTT NAKQVSISIT YGEQQNRQTT
   1451 QVQANQAQAS QIQAGGKTTL YCRRCGEQSN INITGSGVSG RAGTGLIADK
   1501 QIHLQSAEQS NTERSQNKSA GWNAGAAVSF GQGGWSLGVA AGGNVGKGYG
   1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTIIK GAQVRGKGVQ VNAKNLSIQS
   1601 VQDRETYQSK QQNAGAQVTV GYGFSASGDY SQSKIRADHA SVTEQSGIYA
   1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFSTGTLA GSDIONYSOY
        EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH LTSIADKNGA SSSVGYGSDS
   1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVTTDTAE
        RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQTNTEI NQHLDKLKAD
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KEAAETAAAE ALANGDMETA KRKAHEAQDA AAKADNWQQG KVILNMLASG

1901 LAEPTQSGAG IAAATASPDV SYAIGQHFKD LAGQNANGKL TASQETAHVL 1951 <u>AHAVLGAAVA AAXGNNAPAG ALGAGGSEAA APIIGKWLYG KGDGGSLNAE</u> 2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM* The following partial DNA sequence was identified in N.meningitidis <SEQ ID 1667>: m563.seq

.seq.	,				
1	ATGAATAAAA	CTCTCTATCG	TGTAATTTTC	AACCGCAAAC	
51		GCTGAAACTA			TGTGCCGATA
101		CAGCGCTCAT			TACTACTCAT
151		GTCGTTCAAA		TTTTCTTTAT	TGGGCTTTTC
201		GCTGTAGGTA			
251	TTGCTGATAA	AGCTGCTCCT	AAAACTCAAC	AAGCCACGAT	TCTGCAAACA
301	GGTAACGGCA	TACCGCAAGT	CAATATTCAA	ACCCCTACTT	CGGCAGGGGT
351	TTCTGTTAAT	CAATACGCCC	AGTTTGATGT	GGGTAATCGC	GGGGCGATTT
401	TAAACAACAG	CCGCAGCAAC	ACCCAAACAC	AGCTAGGCGG	
451	GGTAATCCTT	GGTTGGCAAG	GGGCGAAGCA	CGTGTGGTTG	TAAACCAAAT
501	CAACAGCAGC	CATTCTTCAC	AAATGAATGG	CTATATTGAA	GTGGGCGGAC
551	GACGTGCAGA	AGTCGTTATT	GCCAATCCGG	CAGGGATTGC	AGTCAATGGT
601	GGTGGTTTTA	TCAATGCTTC	CCGTGCCACT	TTGACGACAG	GCCAACCGCA
651	ATATCAAGCA	GGAGACCTTA	GCGGCTTTAA	GATAAGGCAA	GGCAATGTTG
701	TAATCGCCGG	ACACGGTTTG	GATGCCCGTG	ATACCGATTT	CACACGTATT
751	CTCAGTTATC			GTATGGGGAC	
801	TGTCGTCGCG	GGACAAAACG	ATGTGGTCGC	AACAGGTAAT	GCACATTCGC
851		TAATGCTGCT			
901	GGCACACATA	TCCCTTTATT	TGCGATTGAT	ACAGGCAAAT	TAGGAGGTAT
951	GTATGCCAAC	AAAATCACCT	TGATCAGTAC	GGCCGAGCAA	GCAGGCATTC
1001	GTAATCAAGG	GCAGTTGTTT	GCTTCTTCCG	GTAATGTGGC	GATTGATGCA
1051		TAGTCAATAG			
1101	TACGGATAAT	ACAGCGGAAC			
1151	AAAACAGCGG			GCACTCAAAT	
1201	TCGATTCAAA	ACACTGGCAC	ATTATTGTCC	TCAGGCGAAA	TATTGATTCA
1251	CAATTCGGGC	AGCCTGAAAA	ATGAAACATC	AGGCACCATT	GAAGCCGCTC
1301	GTTTGGCTAT			ATCAAGGCAA	
1351	ACAGGTTCAC	AAAAACTCCA	TATTGATGCA	CAAGGCAAAA	TGGATAACCG
1401	TGGCCGCATG	GGTTTACAAG	ATACCGCACC	AACCGCGTCA	AATGGTTCAA
1451	GCAATCAAAC	CGGCAATAGT	TACAATGCAT	CTTTCCATTC	
1501	ACACCAACAA	CGGCAACAGG	TACGGGTACT	GCAACCGTTT	CTATATCAAA
1551	CATAACTGCG	CCTACCTTTG	CTGATGGGAC	AATTCGCACT	
1601	TGGATAATTC			GTCAAACAGA	
1651	CAACAAGGTT	TAAATAATGC	AGGACAAATA	GACATTCATC	AGTTAAATGC
1701	AAAAGGTTCG	GCGTTTGACA	ATCACAATGG	AACAATTATC	AGTGATGCGG
1751	TCCACATTCA	AGCCGGCAGC	CTGAATAATC	AAAATGGCAA	CATCACAACA
1801	CGCCAACAGT	TAGAGATTGA	AACCGATCAA	CTGGATAACG	CTCATGGCAA
1851		GCAGAAATAG			AGCCTGAACA
1901		CGAAATAGCG			TCACGATGGT
1951	CAGCAATCTA	CCGCTGTCAT	TGATAATACG	AATGGCACGA	TACAATCAGG
2001	CCGTGATGTT	GCTATTCAGG	CAAAATCGTT	ATCCAACAAC	GGCACACTTG
2051	CCGCTGATAA	TAAACTGGAT	ATTGCGTTAC	AAGATGATTT	TTATGTAGAA
2101	CGCAATATCG	TGGCGGGCAA	TGAATTGTCG	CTCAGTACAC	GAGGCAGCCT
2151	GAAAAATTCA	CATACTTTGC	AAGCAGGAAA	ACGCATTCGG	ATTAAAGCAA
2201	ATAACCTTGA	TAATGCAGCA	CAAGGCAACA	TTCAATCCGG	CGGTACGACA
2251	GACATTGGCA	CGCAGCACAA	TTTAACCAAT	AGAGGCTTGA	TTGACGGACA
2301	ACAAACCAAA	ATCCAAGCCG	GGCAAATGAA	TAATATCGGT	ACAGGTCGGA
2351	TTTATGGCGA	CAATATCGCT	ATTGCGGCTA	CCCGCTTAGA	CAATCAAGAT
2401	GAAAACGGTA	CAGGTGCCGC	CATTGCGGCA	CGTGAAAACC	TGAATTTAGG
2451	CATCGGACAA	TTAAACAACC	GTGAAAACAG	TCTGATTTAC	AGCGGTAACG
2501	ATATGGCGGT	TGGCGGCGCA	TTAGATACCA	ATGGCCAAGC	CACAGGCAAA
2551	GCCCAAAGGA	TACACAATGC	CGGCGCAACC	ATTGAAGCTG	CAGGCAAAAT
2601	GCGTTTAGGT	GTAGAAAAGC	TGCACAATAC	CAATGAGCAT	TTGAAAACGC
2651	AGTTGGTAGA	AACAGGGCGC	GAGCATATTG	TTGATTACGA	AGCATTTGGA
2701	CGACACGAAT	TATTGCGAGA	AGGCACGCAA	CATGAATTAG	GCTGGTCTGT
2751	CTATAACGAT	GAATCAGACC	ACTTACGCAC	CCCTGATGGA	GCGGCGCATG
2801	AAAATTGGCA	TAAATACGAT	TATGAAAAAG	TCACCCAAAA	AACCCAAGTT
2851	ACCCAAACTG	CGCCAGCCAA	AATCATTTCA	GGTAATGATT	TAACCATTGA
2901	TGGTAAAGAA	GTATTTAATA	CCGATAGCCA	AATCATTGCT	GGTGGCAATC
2951	TCATTGTACA	AACAGAAAAA	GACGGTTTGC	ATAACGAGCA	AACCTTTGGC

GAAAAGAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA 3001 GAAACATAAA GGACGAGACT CAACGGGACA TAGCGAACAA AATTACACTT TGCCGGAGGA AATCACACGC AACATTTCAC TGGGTTCATT TGCCTATGAA 3101 TCGCATCGCA AAGCATTAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT 3151 GCCGCAAAGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC 3201 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT 3251 CTTGTTGAAA CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTTGGGTAG 3301 TGACTATATG CTGGACAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC 3351 GTTTGGGTGA TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA 3401 GAGCTGACAG GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA 3451 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC 3501 TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC 3551 GATATTGTTT GGTTGGTACA AAAAGAAGTT AAGCTTCCTG ATGGCGGCAC 3601 ACAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA TAGACGGTAA AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC TGAAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT 3751 TATCAATACC GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT 3901 TCTGCCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCAACAGCCA AAGCACCACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG 3951 ACCGAATGGC AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA 4001 GCGCAGGCAG GAAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA 4051 ATCAGAGCAA GGGCAAACCC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG 4101 ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC CATGTTATTC GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG AAGTCAGCAG CGCAAACGGT ACACTCGCTG TGTCTGCCAA AAATGACATC AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG CAGGAAACGA TGCCAACATC CTTGGCAGCA ATGTTATTTC 4501 CGATAATGGC ACCCAGATTC AAGCAGGCAA TCATGTTCGC ATTGGTACAA 4551 CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA TTGATGAGTG CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA 4651 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT 4701 TGAAAGGCGA TACCACCATT GTTGCAGGCA AACACTACGA ACAAATCGGC AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT AGACATTCAA GCGGCACACA ACAAATTAAA CAGTAATACC ACCCAAACCT ATGAACAAAA AGGCCTAACG GTGGCATTCA GTTCGCCCGT TACCGATTTG GCACAACAAG CGATTGCCGT AGCACAAAGC AGCAAACAAG TCGGACAAAG 4951 CAAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG 5001 CCTATCAAAC AGGTAAGAGT GCACAAAACT TAGCCAATGG TACAACCAAT 5051 GCCAAACAAG TCAGCATCTC CATAACCTAC GGCGAACAGC AAAACCGACA 5101 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAAGCAG 5151 GTGGTAAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC 5201 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC 5251 CGATAACGAC ATCACACTCC AATCAGCCGA GCAAAGCAAT ACCGAACGCG 5301 GCCAAAACAA ATCGGCAGGC TGGAACGCAG GTGCTGCCGT ATCATTCGGA CAAGGAGGCT GGTCATTAGG CGTTACCGCA GGCGGCAATG TCGGCAAAGG CTACGGCAAT GGCGACAGCA TCACCCACCG CCATAGCCAT ATCGGCGACA 5451 AAGGCAGCCA AACCCTTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC 5501 GCGCAAGTAC GCGGCAAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT 5551 TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACAA CAAAACGCCA 5601 GTGCACAAGT TACCGTAGGT TATGGCTTCA GTGCCGGTGG CGATTACAGC 5651 CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT TTATGCCGGA GAAGACGGCT ATCAAATCAA GGTCGGAAAC CATACAGACC TCAAAGGCGG CATCATCACC AGTACCCAAA GCGCAGAAGA CAAGGGTAAA AACCGCTTTC AGACGGCCAC CCTCACCCAT AGCGACATCA AAAACCACAG 5851 CCAATACAAA GGCGAAAGTT TTGGATTGGG CGCAAGTGCG TCCATAAGCG 5901 GCAAAACACT GGGACAGGGC GCACAAAATA AACCTCAAAA CAAACACCTG ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA 6051

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
     GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
     CGAACGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
     AAAGTGAACT GGATTTACAA AGAACCGTCA GCCAAGATTT TAGTAAAAAT
      GTTCAACAAG CCAATACCGA GATTAACCAA CATTTAGACA AACTCAAAGC
     AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
     ATATGGAAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
     AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
6451
     AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
     CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
     GGTCAAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
     TCTTGCCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
6701 ATGCTCTAGC AGGAGCATTG AGTGCGGGCG GGTCGGAAGC GGCTGCGCCT
6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
6901 AATGCGCAAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
7001 ATCCTGGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
7051 CAATTAAATT TATTTCCTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
7301 ATAGGTTAAA CACAAAGAG TTAGTTGGAT TAATTCTGGA AACTTATAAA
7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAATACA AGCAATATAT
7451 TGATTCACTT AGATAATACT GGTGCCGGAT TTAAAATTCA GCAGAGGAGA
7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA
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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>: m563.pep..

1 MNKTLYRVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVPFGTTH 51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTOOATILOT 101 GNGIPOVNIO TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TOTOLGGWIO GNPWLARGEA RVVVNOINSS HSSOMNGYIE VGGRRAEVVI ANPAGIAVNG 201 GGFINASRAT LTTGQPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI LSYHSKIDAP VWGQDVRVVA GQNDVVATGN AHSPILNNAA ANTSNNTANN GTHIPLFAID TGKLGGMYAN KITLISTAEQ AGIRNQGQLF ASSGNVAIDA NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVENSGTAV SQQGTQIHSQ SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQGKLSQ TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSSTT TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA QQGLNNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT ROOLEIETDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIIHDG QOSTAVIDNT NGTIQSGRDV AIQAKSLSNN GTLAADNKLD IALQDDFYVE RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT 751 DIGTOHNLTN RGLIDGOOTK IQAGOMNNIG TGRIYGDNIA IAATRLDNOD ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDTNGQATGK AQRIHNAGAT IEAAGKMRLG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG 851 RHELLREGTO HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV TOTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE SHRKALSHHA PSQGTELPQS NGISLPYTSN SFTPLPSSSL YIINPVNKGY 1101 LVETDPRFAN YRQWLGSDYM LDSLKLDPNN LHKRLGDGYY EORLINEOIA ELTGHRRLDG YQNDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS 1151 DIVWLVQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTOINV 1201 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML SAEQTLLLNA GNNINSQSTT ASSQNTQGSS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSEQ GQTRLQAGRD INLDTVQTSK HQATHFDADN HVIRGSTNEV GSSIQTKGDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI 1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA OSSTFEGKOV 1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTTQTQSQS ETYHOTOKSG

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LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGSLKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNSNT TQTYEQKGLT VAFSSPVTDL
     AQQAIAVAQS SKQVGQSKND RVNAMAAANA GWQAYQTGKS AQNLANGTTN
1651
     AKQVSISITY GEQQNRQTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
     NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKSAG WNAGAAVSFG
     QGGWSLGVTA GGNVGKGYGN GDSITHRHSH IGDKGSQTLI QSGGDTTIKG
     AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901
     QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKGK
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPQNKHL
2001
     TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051
     AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
     VOOANTEINO HLDKLKADKE AAETAAAEAL ANGDMETAKR KAHEAODAAA
2101
     KADNWOOGKV ILNMLASGLA APTOSGAGIA AATASPAVSY AIGOHFKDLA
2151
2201 GQNANGKLTA SQETAHVLAH AVLGAAVAAV GDNNALAGAL SAGGSEAAAP
2251
     YISKWLYGKE KGSDLTAEEK ETVTAITNVL GTATGAAVGN SATDAAOGSL
2301 NAQSAVENND TVEQVKFALR HPRIAIAIGS VHKDPGSTLE PNISTIASTF
2351 OLNLFPNSEF GGEGGVGNAF RHVLWOATIT REFGKDIAVK VGNSHESGEK
2401 INYSIRRNLS LDKADEMIDQ LNNEIGREIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILIHLDNT GAGFKIQQRR
2501 KQIRAQISAR QWRR*
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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N.gonorrhoeae

ORF 563 shows 79.1% identity over a 2316 as overlap with a predicted ORF (ORF 563.ng) from N. gonorrhoeae: m563/g563

10 20 30 40 50 MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTHg563.pep ---SKAFC - 1 1 MNKTLYRVI FNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNI FS m563.pep 20 10 30 40 50 60 70 80 90 60 100 ${\tt FSALGFSLCLALGTVNIAFADGIITDKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN}$ g563.pep FSLLGFSLCLAVGTANIAFADGIIADKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN m563.pep 70 80 90 100 120 120 130 140 150 160 9563.pep QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE m563.pep OYAOFDVGNRGAILNNSRSNTOTOLGGWIOGNPWLARGEARVVVNOINSSHSSOMNGYIE 130 140 150 160 170 180 190 200 180 210 220 VGGRRAEVVIANPAGIAVNGGGFINASRATLTTGQPQYQAGDFSGFKIRQGNAVIAGHGL g563.pep m563.pep VGGRRAEVVIANPAGIAVNGGGFINASRATLTTGQPQYQAGDLSGFKIRQGNVVIAGHGL 190 200 210 220 230 q563.pep DARDTDFTRIL----DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNAAANTSNNTANN m563.pep 250 260 270 280 290 300 250 260 270 280 g563.pep ---LYANKITLISTAEQAGIRNQGQLFASSGNVAIDANGRLVNSGTM m563.pep GTHIPLFAIDTGKLGGMYANKITLISTAEQAGIRNQGQLFASSGNVAIDANGRLVNSGTM 330 340

320

350

	300	310	320	330	340	
g563.pep	AAANVQDMNNTAEHK	VNIRSQAFEN 	SGTAVSQQGT(DIHSQSIQNT	GKLLSAGT	
m563.pep	AAANAKDTDNTAEHK	VNIRSQGVEN	SGTAVSQQGT	ZIHSQSIQNT	GTLLSSGEII	
	370	380	390	400	410	420
. 5.63						- -
g563.pep						
m563.pep	SLKNETSGTIEAAR 430	LAIDTDTLNN 440	QGKLSQTGSQI 450	CLHIDAQGKM 460	DNRGRMGLQI 470	480
g563.pep						-
m563.pep	NGSSNQTGNSYNAS	FHSSTTTPTT	'ATGTGTATVS	SNITAPTFA	DGTIRTHGA	LDNSGSI
moos.pcp	490	500	510	520	530	540
g563.pep						
m563.pep	IANGQTDVSAQQGL					
	550	560	570	580	590	600
			350	360 MGET ATMOOT	370 TTHDGOOST	380 TMTDNT
g563.pep		ļ		[:
m563.pep	RQQLEIETDQLDNAH 610	GKLLSAEIAD 620	LAVSGSLNNQ1 630	NGEIATNQQL 640	IIHDGQQST) 650	AVIDNT 660
			410	420	430	440
g563.pep	390 NGTIQSGRDVAIQAK	400 SLSNNGTLAA	410 DNKLDIALQDI	OFYVERKIVA	GNELSLSTR	GSLKNS
_		SI SNNGTI A	DNKI DTALODI	: OFYVERNIVA	 .GNELSLSTR(GSLKNS
m563.pep	670	680	690	700	710	720
	450	460	470	480	490	500
g563.pep	HTLQAGKRIRIKANN	LDNAVQGNIC	SGGTTDIGTQ	HNLTNRGLIC	GQQTKIQAG	QMNNIG
m563.pep		: LDNAAQGNIC		HNLTNRGLIC		QMNNIG
	730	740	750	760	770	780
	510	520	530	540	550	560
g563.pep	TGRIYGDNIAIAATR				1111111	
m563.pep	TGRIYGDNIAIAAT	RLDNQDENGT 800	GAAIAARENLI 810	NLGIGQLNNR 820	RENSLIYSGN 830	DMAVGGA 840
g563.pep	570 LDTNDQATGKAQRIH	580 NAGAIIEAAC	590 KMRLGVEKLH	600 NTNEHLKTQI	610 VETGRERIV	620 DYEAFG
				111111111		
m563.pep	LDTNGQATGKAQRI 850	HNAGATTEAA 860	870	880	890	900
	630	640	650	660	670	680
g563.pep	RHELLREGTQHELGW	FVYNNESDHI	LRTPDGVAHEN	WHKYDYEKVI	TOETOVTGTA	PAKIIA
m563.pep		: SVYNDESDHI			: 	: PAKIIS
sos.pep	910	920	930	940	950	960
	690	700	710	720	730	740

g563.pep	GSDLIIDSKAVFNSDSI : : : GNDLTIDGKEVFNTDS(970	: : :			1111111:11	::
g563.pep	GRDSTGHSEQNYTLPE	H :	11111 11		111111	
g563.pep	-GISLPYTSNSFTPLPS	:				
g563.pep	870 LHKRLGDGYYEQRLING LHKRLGDGYYEQRLING					
g563.pep	930 SAEQAAQLTSDIVWLV(: SAEQVAQLTSDIVWLV(1200	[[]]]]]]	1111:111			11111
g563.pep	SGSLKNSGTIAGRNAL SGSLKNSGTIAGRNAL	[1111111111		:	
g563.pep	GNNINNQSTAKSSQNA(: : : GNNINSQSTTASSQNT([11][1][1][1]			1111111111	:
g563.pep	GQTRLQAGRDINLDTV(GQTRLQAGRDINLDTV(: :				
g563.pep	KAAEVGSAKGTLAVYAI : : KAAEVSSANGTLAVSAI	: :	:: :			
g563.pep	QSSTFEGKQVVLQAGNI 			[11111
g563.pep	1290 : LMSAGIGFTIGSKTNT(!					

m563.pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGSLKGDTTIVAGKHYEQIGSTVSSPEGNN 1560 1570 1580 1590 1600 1610
g563.pep m563.pep	1350 1360 1370 1380 1390 1400 LISTQSMDIGAAQNQLNSKTTQTYEQKGLTVGIQFARYRFGTTSDCRSTQSSKQVGQSKN : :
g563.pep	1410 1420 1430 1440 1450 1460 DRVNAMAAANAGWQAYQTGKGAQNLANGTTNAKQVSISITYGEQQNRQTTQVQANQAQAS
g563.pep m563.pep	1470 1480 1490 1500 1510 1520 QIQAGGKTTLYCRRCGEQSNINITGSGVSGRAGTGLIADKQIHLQSAEQSNTERSQNKSA :
g563.pep	1530 1540 1550 1560 1570 1580 GWNAGAAVSFGQGGWSLGVAAGGNVGKGYGYGDSVTHRHSHIGDKGSQTLIQSGGDTIIK
g563.pep	1590 1600 1610 1620 1630 1640 GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQQNAGAQVTVGYGFSASGDYSQSKIRADHA
g563.pep	1650 1660 1670 1680 1690 1700 SVTEQSGIYAGEDGYQIKVGNHTGLKGGIITSSQSAKDKGKNRFSTGTLAGSDIQNYSQY
g563.pep	1710 1720 1730 1740 1750 1760 EGKSFGLGASVAVSGKTLGQGAKNKPQDKHLTSIADKNGASSSVGYGSDSDSQSSITKSG : : ::: : : : :
g563.pep	1770 1780 1790 1800 1810 1820 INTPKNIQITDEAAQIRLTGKIAAQTKADIDTNVTTDTAERHSGSLKNIFDKDRVQSELD :
g563.pep	1830 1840 1850 1860 1870 1880 LQRTVSQDFSKNVQQTNTEINQHLDKLKADKEAAETAAAEALANGDMETAKRKAHEAQDA
g563.pep	1890 1900 1910 1920 1930 1940 AAKADNWQQGKVILNMLASGLAEPTQSGAGIAAATASPDVSYAIGQHFKDLAGQNANGKL

WO 99/57280

859

		1950	1960	1970	1980	1990	2000
g563.pep	TASQE	TAHVLAHAV				IGKWLYGKGDO	
		11111111					:: :
m563.pep	TASQE	TAHVLAHAV	LGAAVAAVGE	NNALAGALSA	GGSEAAAPY.	ISKWLYGKEKO	SDLTAE
	2210	2220	2230	2240	2250	2260	
		2010	2020	2030	2040	2049	
q563.pep	EKETV	SAITRMLGT.	AAGAAEGNSS	SADAVWGCFQT	ASDFASSFS	YPINMX	
5	11111	:111:111	1:111 111:	: : :::			
m563.pep	EKETV	TAITNVLGT	ATGAAVGNSA	TDAAQGSLNA	QSAVENNDT	VEQVKFALRHI	PRIAIAI
	2270	2280	2290	2300	2310	2320	
m563.pep	GSVH	KDPGSTLEP	NISTIASTFO	LNLFPNSEFG	GEGGVGNAFI	RHVLWQATITI	(EFGKD1A
		2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1669>:

m564.seq ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA CCCAAGCTGT AGGTATTTTG CCAAATGATA TTGCGGGCTT TGCGGGTTTT 101 151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTC TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA 401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT CCTTGGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAAACC AAATCAACAG CAGCCATTCT TCACAACTGA ATGGCTATAT TGAAGTGGGC GGACGACGTG CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAATCG CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACACG TATTCTCAGT 701 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCGT 751 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC 801 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA 851 CATATCCCTT TATTTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC 901 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGGC ATTCGTAATC 951 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT 1001 AAACTGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT TTCACTTCAT GCCCGCAATG TTCATAATAG CGGTACGGTT GCCTCACAGG ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA 1151 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA 1201 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG 1251 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA 1301 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTAA GTGACGTTCC 1351 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA 1401 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA 1451 AACAATCCCG TTTCACCTAC AGCACCTGCA AAAAACTACG CCGTAGGACG 1501 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG 1551 GGCAAATTGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG 1601 1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA 1701 AGGCAAACTC CAGGCACACG ATCTGGCTGT TAACACTCAA ACTGCTAAAA 1751 ACAGCGGTCA CTTATTAACT CAAACCGGCA AGATTGATAA CCGTGAACTG CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTCGGG CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC TTGATACCGC CGGTTTACAT AATGCAGGTA ACATTCTTGC CGATAGTGGA ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC 2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG AGGCTGAAAC GGTTAACATC CAAAGTCAGC AACTGACTAA CCAAAGCGGC 2051 2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA CCAAAACGGC AAACTCCTAT CTGCAAACCA AGCACAATTA GCTGTTTCAG 2151 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

2251	ATTCACGATA	AAAATCAAAA	CACTTTGGCG	TTAAACAATG	CGGATGGCAC
2301	GATTCAATCT	GCCGGTAATG	TATCGCTACA	AGCCAAATCA	CTCGCCAACA
2351	ATGGCACATT	AACAGCCGGT	AACAAACTGG	ATATTGCTTT	GACGGACGAT
2401	TTCGTCGTAG	AGCGCGACCT	CACTGCAGGC	AAACAATTAA	ATCTAAGCAT
2451	AAAAGGCCGT	CTGAAAAATA	CCCATACCCT	ACAAGCAGGC	CATACGCTCA
2501	AACTCAATGC	CGGCAATATA	GATAACCAAG	TTACAGGCAA	
2551	GGAGAACAAA	CGGACATCAC	ATCCGAACAG		ACAGGGGCTT
2601	GATCAACAGC	GACGGTTTGA	CCCACATCGG	TGCAGGTCAA	
2651	ACACCGGGAC	AGGCAAAATC	TATGGCAACC	ATATTGCCCT	GGACGCGCAA
2701	ATACTGCTTA	ACCGGGAAGA	AACGACGGAA	•••	AAGCGGGGC
2751	AATAGCTGCA	AGGAAACGTT	TGGATATTGG	AGCGAAAGAG	ATTCATAACC
2801	AAGAAGGTGC	CCTACTATCC	AGCGAAGGTA	TTTTTGCCGT	AgGTAATCGA
2851	CTGGATGAAC	AACATCATGC	GGCAGGCATG	GCCGATACCT	TTGTTAATGG
2901	CAGTGCCGGT	TTGGAAGTAC	AAGGTGATGC	ATTGATGTCC	GTTCGGAATA
2951	TGCAGAATAT	CAATAATCAC	TTTAAAACAG	AGACATACTT	AGCCAAAGCG
3001	GAAAAGCAAG	TCCGCGACTA	CACCGTACTG	GGGCAAAATA	CCTACTATCA
3051	GGCGGGAAAA	GACGGTTTAT	TCGACAACTC		AAAGACCAAA
3101	CTACTGCTAC		AAAAATGGTT		GGCCAACCAA
3151	TGGCATGTCC	GAGACTACCA	CATCGAGACT	TATAAAGAAC	GCATCATCGA
3201	AAACCGGCCG		CTGTGGGCGG	TGATTTGACT	GCCTCAGGTC
3251	AAAATTGGCT	0.2.0	AGCCGGATTG	TAGTAGGCGG	GCGTATTATC
3301	ACTGATGATT		AGAAATTACC	AATCAAAGTA	CAACAGGCAA
3351	AGGTCGCACA	GATGCTGTCG	GCACACAGTG	GGATTCAGTT	ACAAAAAAAG
3401	GATGGTACAG	-	AGACAACGCC	-	AAACCATACT
3451	CCTTACCATG	ATACCCAACT	ATTTACCCAC		CGCCTGTATC
3501	CGTCATCCAA	CAGAATGCCG	CCTCCCCTTC		GCCGCATCTG
3551	CAATCAAACT	GATTGACGGA	GTATCCACGG	CAGCCGTCAA	TGGTCAGCGC
3601	ATCCATACCG	GTAATGTGGT	CTCGTTAAAT	AACGCTACTG	TTACTCTGCC
3651	TAACAGCAGC	CTCTATACCA	CCCATCCTGA	CAATAAAGGC	TGGTTGGTTG
3701	AAACCGATCC	TCAATTTGCA	GACTACCGCC	GCTGGTTGGG	CAGCGACTAC
3751	ATGTTGCAAC	AACTGCAATT	GGACACCAAT		AACGGCTTGG
3801	CGACGGCTAC	TACGAACAAA	AACTTGTTAA		CATCAGTTAA
3851	CAGGCTACCG	CCGACTCGAC	GGCTACAGGA	GTGATGAAGA	
3901	GCTCTGATGG	ACAACGGCCT	TACTGCTGCC	AAAACATTCG	GTCTCACCCC
3951	AGGTATCGCC	TTGAGTGCAG	AGCAAGTTGC	CCGCTTAACT	TCAGATATCG
4001	TTTGGATGGA	AAATCAAACC	GTCACCCTGT	CTGACGGTTC	GACTCAAACC
4051	GTACTGGTTC	CTAAAGTCTA	TGCCCTGGCG	CGCAAAGGTG	ATCTCAATAC
4101	CTCCGGTGGC	CTGATTAGTG	CCGAACAAGT		CTGCAAAACG
4151	GCAACCTGAC	TAACAGCGGT	ACCATTGCGG	GGCGACAGGC	CGTACTCATC
4201	CAGGCACGGA	ATATTAACAG	CAACGGTAAC		ACCAAATCGG
4251	CTTAAAAGCT		TCAATATCGA	CGGCGGGCAG	GTACAAGCAG
4301	GCAGACTGCT		GCGCAAAATA	TCAACCTTAA	CGGTACAACC
4351	CAAACTTCCG	GTAATGAACG	TAACGGCAAT		ATCGTATGGC
4401		GTGGTCGGAA	GCCATACTGA	ACAAGTAGAT	AACAGAACTT
4451	CAGACGGCAT	CCTATCCCTG	CATGCCAGCA	ACGATATCAA	CCTCAATGCG
4501	GCCACCGTCT	CTAACCAAGT	TAAAGACGGC	ACTACCCAAA	TTACCGCCGG
4551		AACCTCGGCA	CCATCCGTAC	CGAACATCGC	GAAGCCTATG
4601	GTACATTAGA	TGACGAGAAC	CATCGCCATG	TUUGUUAAAG	TACCGAAGTC
4651		TCCGCACGCA	AAACGGCGCA		CCGGTAACGA
4701	CTTAAAAATC		AACTGGAGGC		AAAACCGTCC AATAACCGAA
4751	TTGCCGCAGG	ACGTGATGTC	ACTATCAGCG		
4801	CTGGATACCT	CGGTAAGCGG	AAAAAGCAAA	GGCATCCTTT	CCAGTACCAA
4851	AACACACGAC	CGCTACCGCT	TCAGTCATGA		GGCAGCAACA
4901			GTTGCAGCCG	COUNTRY	CAATGTACGC
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5001	CATCGATATT		ATAATCGCTA		GAATACCACG
5051	AGAGCAAAAA	ATCAGGCGTC	ATGGGTACTG		CTTTACTATC TTGTCCATAC
5101			TGACACTGAT		
5151	AGGCAGCATT		TGAATGGAGA		GTTGCAGGAA
5201	ACCGCTACCG	ACAAACCGGC	AGTACCGTCT	TUAGCUCUGA	GGGGCGCAAT
5251			AGATGTAGAG	1 TUGUAAACA	ACCGGTATGC
5301	CACTGACTAC				GTCGCCCTCA
5351	ATGTCCCGGT	TGTCCAAGCT	GCACAAAACT	COCATACAAGC	AGCCCAAAAT
5401	GTGGGCAAAA	GTAAAAATAA	ACGCGTTAAT	GCCATGGCTG	CAGCCAATGC
5451			CAACCCAACA	AATGCAACAA	TTTGCTCCAA
5501	GCAGCAGTGC	GGGACAAGGT	CAAAACAACA	ATCAAAGCCC	CAGTATCAGT

			•		
5551	GTGTCCATTA	CCTACGGCGA	ACAGAAAAGT	CGTAACGAGC	AAAAAAGACA
5601	TTACACCGAA	GCGGCAGCAA	GTCAAATTAT	CGGCAAAGGG	CAAACCACAC
5651	TTGCGGCAAC	AGGAAGTGGG	GAGCAGTCCA	ATATCAATAT	TACAGGTTCC
5701	GATGTCATCG	GCCATGCAGG	TACTGCCCTC	ATTGCCGACA	ACCATATCAG
5751	ACTCCAATCT	GCCAAACAGG	ACGGCAGCGA	GCAAAGCAAA	AACAAAAGCA
5801	GTGGTTGGAA	TGCAGGCGTA	GCCGTCAAAA	TAGGCAACGG	CATCAGGTTT
5851	GGAATTACCG	CCGGAGGAAA	TATCGGTAAA	GGTAAAGAGC	AAGGGGGAAG
5901	TACTACCCAC	CGCCACACCC	ATGTCGGCAG	CACAACCGGC	AAAACTACCA
5951	TCCGAAGCGG	CGGGGATACC	ACCCTCAAAG	GTGTGCAGCT	CATCGGCAAA
6001	GGCATACAGG	CAGATACGCG	CAACCTGCAT	ATAGAAAGTG	TTCAAGATAC
6051	TGAAACCTAT	CAGAGCAAAC	AGCAAAACGG	CAATGTCCAA	GTTACTGTCG
6101	GTTACGGATT	CAGTGCAAGC	GGCAGTTACC	GCCAAAGCAA	AGTCAAAGCA
6151	GACCATGCCT	CCGTAACCGG	GCAAAGCGGT	ATTTATGCCG	GAGAAGACGG
6201	CTATCAAATC	AAAGTCAGAG	ACAACACAGA	CCTCAAGGGC	GGTATCATCA
6251	CGTCTAGCCA	AAGCGCAGAA	GATAAGGGCA	AAAACCTTTT	TCAGACGGCC
6301	ACCCTTACTG	CCAGCGACAT	TCAAAACCAC	AGCCGCTACG	AAGGCAGAAG
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6401	TTACCGACAA	ACAAGGCAGG	CCTACCGACA	GGATAAGCCC	GGCAGCCGGC
6451	TACGGCAGCG	ACGGAGACAG	CAAAAACAGC	ACCACCCGCA	GCGGCGTCAA
6501 .	CACCCACAAC	ATACACATCA	CCGACGAAGC	GGGACAACTT	GCCCGAACAG
6551	GCAGGACTGC	AAAAGAAACC	GAAGCGCGTA	TCTACACCGG	CATCGACACC
6601	GAAACTGCGG	ATCAACACTC	AGGCCATCTG	AAAAACAGCT	TCGACAAAGA
6651	CGCGGTCGCC	AAAGAGATCA	ACCTGCAAAG	GGAAGTAACG	AAGGAGTTCG
6701	GCAGAAACGC	CGCCCAAGCC	GTAGCGGCCG	TTGCCGACAA	ACTCGGCAAT
6751	ACCCAAAGTT	ACGAACGGTA	TCAGGAAGCC	CGAACCCTGC	TGGAGGCCGA
6801	ACTGCAAAAC	ACGGACAGCG	AAGCCGAAAA	AGCCGCCTTC	CGCGCATCCC
6851	TCGGCCAAGT	AAACGCCTAT	CTTGCCGAAA	ACCAAAGCCG	CTACGACACC
6901	TGGAAAGAAG	GCGGCATAGG	CAGGAGCATA	CTGCACGGGG	CGGCAGGCGG
6951	ACTGACGACC	GGCAGCCTCG	GCGGCATACT	GGCCGGCGGC	GGCACTTCCC
7001	TTGCCGCACC	GTATTTGGAC	AAAGCGGCGG	AAAACCTCGG	TCCGGCGGGC
7051	AAAGCGGCGG	TCAACGCACT	GGGCGGTGCG	GCCATCGGCT	ATGCAACTGG
7101	TGGTAGTGGT	GGTGCTGTGG	TGGGTGCGAA	TGTAGATTGG	AACAATAGGC
7151	AGCTGCATCC	GAAAGAAATG	GCGTTGGCCG	ACAAATATGC	CGAAGCCCTC
7201	AAGCGCGAAG	TTGAAAAACG	CGAAGGCAGA	AAAATCAGCA	GCCAAGAAGC
7251	GGCAATGAGA	ATCCGCAGGC	AGATACTGCG	TTGGGTGGAC	AAAGGTTCCC
7301	AAGACGGCTA	TACCGACCAA	AGCGTCATAT	CCCTTATCGG	AATGAAAGGC
7351	GAAGACAAAG	CCTTGGGTTA	TACTTGGGAC	TACCGCGACT	ACGGCGCAAG
7401	AAATCCGCAA	ACCTACAACG	ATCCGAAGCT	GTTTGAGGAA	TACCGCCGAC
7451	AGGACAAACC	CGAATACCGC	AACCTGACCT	GGCTGCACAG	CGGGACGAAA
7501	GACACCAAAA	TCAGGCAGGG	AGAGCGGAAA	AACGAAGAGT	TTGCACTGAA
7551	CGTTGCCGAA	GGACTGACGA	GCCTTGTCAA	CCCCAATCCG	AGGATAAAAG
7601	TCCCGATTCT	TGCAGGCATC	CGCAACCTGA	AAAACATCAA	GCCGACAGTT
7651	ACCGGCAGCG	ATCCCTTATT	GGCGGGTGCG	GGGAATATCC	GTATCCCTGC
7701	AAACGGCAAT	GTTGCGAAGG	GGGACAGGAT	TCCGGATACG	GCATTGGCTA
7751	GCAAGGGAAT	CAAACATAAA	GATCGTAAAG	ATCAACTGGA	GAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep MNRTLYKVVF NKHRNCMIAV AENAKREGKN TADTQAVGIL PNDIAGFAGF 1 51 IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QQPTILQTGN 101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN 151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG 201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS 251 YHSKIDAPVW GQDVRVVAGQ NDVAATGDAH SPILNNAAAN TSNNTANNGT 301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGQWFAS AGNVAVNAEG 351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL 401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV SAGKFDNSGK IGVSDVPQTG LNPNPSVIPQ IPSTATGSGS STVSVSKPGS NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL NAAKLRVSGD SFNNTVKGKL QAHDLAVNTQ TAKNSGHLLT QTGKIDNREL HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG TVTTKNNLRN TGKVSVARLN TEGQTLDNTR GRIEAETVNI QSQQLTNQSG HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS IHDKNONTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG 801 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

			•		
901	ILLNREETTE	GSTKAGAIAA	RKRLDIGAKE	IHNQEGALLS	SEGIFAVGNR
951	LDEOHHAAGM	ADTFVNGSAG	LEVQGDALMS	VRNMQNINNH	FKTETYLAKA
1001	EKOVRDYTVL	GONTYYQAGK	DGLFDNSQGQ	KDQTTATFHL	KNGSRIEANQ
1051	WHVRDYHIET	YKERIIENRP	AHITVGGDLT	ASGQNWLNKD	SRIVVGGRII
1101	TDDLNOKEIT	NOSTTGKGRT	DAVGTQWDSV	TKKGWYSGRK	RQRRTERNHT
1151	PYHDTOLFTH	DFDTPVSVIQ	QNAASPSFQP	AASAIKLIDG	VSTAAVNGQR
1201	IHTGNVVSLN	NATVTLPNSS	LYTTHPDNKG	WLVETDPQFA	DYRRWLGSDY
1251	MLOOLOLDTN	HLHKRLGDGY	YEQKLVNEQI	HQLTGYRRLD	GYRSDEEQFK
1301	ALMDNGLTAA	KTFGLTPGIA	LSAEQVARLT	SDIVWMENQT	VTLSDGSTQT
1351	VLVPKVYALA	RKGDLNTSGG	LISAEQVLLK	LQNGNLTNSG	TIAGRQAVLI
1401	QARNINSNGN	IQADQIGLKA	EKSINIDGGQ	VQAGRLLTAQ	AQNINLNGTT
1451	QTSGNERNGN	TAIDRMAGIN	VVGSHTEQVD	NRTSDGILSL	HASNDINLNA
1501	ATVSNQVKDG	TTQITAGNNL	NLGTIRTEHR	EAYGTLDDEN	HRHVRQSTEV
1551	GSSIRTQNGA	LLRAGNDLKI	RQGELEAEEG	KTVLAAGRDV	TISEGRQITE
1601	LDTSVSGKSK	GILSSTKTHD	RYRFSHDEAV	GSNIGGGKMI	VAAGQDINVR
1651	GSNLISDKGI	VLKAGHDIDI	STAHNRYTGN	EYHESKKSGV	MGTGGLGFTI
1701	GNRKTTDDTD	RTNIVHTGSI	IGSLNGDTVT	VAGNRYRQTG	STVSSPEGRN
1751	TVTAKSIDVE	FANNRYATDY	AHTQEQKGLT	VALNVPVVQA	AQNFIQAAQN
1801	VGKSKNKRVN	AMAAANAAWQ	SYQATQQMQQ	FAPSSSAGQG	QNNNQSPSIS
1851	VSITYGEQKS	RNEQKRHYTE	AAASQIIGKG	QTTLAATGSG	EQSNINITGS
1901	DVIGHAGTAL	IADNHIRLQS	AKQDGSEQSK	NKSSGWNAGV	AVKIGNGIRF
1951	GITAGGNIGK	GKEQGGSTTH	RHTHVGSTTG	KTTIRSGGDT	TLKGVQLIGK
2001	GIQADTRNLH	IESVQDTETY	QSKQQNGNVQ	VTVGYGFSAS	GSYRQSKVKA
2051	DHASVTGQSG	IYAGEDGYQI	KVRDNTDLKG	GIITSSQSAE	DKGKNLFQTA
2101	TLTASDIQNH	SRYEGRSFGI	GGSFDLNGGW	DGTVTDKQGR	PTDRISPAAG
2151	YGSDGDSKNS	TTRSGVNTHN	IHITDEAGQL	ARTGRTAKET	EARIYTGIDT
2201	ETADQHSGHL	KNSFDKDAVA	KEINLQREVT	KEFGRNAAQA	VAAVADKLGN
2251	TQSYERYQEA	RTLLEAELQN	TDSEAEKAAF	RASLGQVNAY	LAENQSRYDT
2301	WKEGGIGRSI	LHGAAGGLTT	GSLGGILAGG	GTSLAAPYLD	KAAENLGPAG
2351	KAAVNALGGA	AIGYATGGSG	GAVVGANVDW	NNRQLHPKEM	ALADKYAEAL
2401	KREVEKREGR	KISSQEAAMR	IRRQILRWVD	KGSQDGYTDQ	SVISLIGMKG
2451	EDKALGYTWD	YRDYGARNPQ	TYNDPKLFEE	YRRQDKPEYR	NLTWLHSGTK
2501	DTKIRQGERK		GLTSLVNPNP	RIKVPILAGI	RNLKNIKPTV
2551	TGSDPLLAGA	GNIRIPANGN	VAKGDRIPDT	ALASKGIKHK	DRKDQLEKK*

Computer analysis of this amino acid sequence gave the following results: Homology with fha

```
m564/fha
                                PRT;
                                    3591 AA.
                  STANDARD;
    FHAB BORPE
ID
    P12255;
AC
    01-OCT-1989 (REL. 12, CREATED)
    01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
    01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
    FILAMENTOUS HEMAGGLUTININ. . . .
DE
                               524 Opt:
                                         594
                   190 Initn:
           Init1:
                            21.7% identity in 2427 aa overlap
Smith-Waterman score: 866;
                                                        50
                                               40
                   10
                            20
                                      30
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m564
            MNTNLYRLVFSHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
fhab borpe
                                                    40
                                                             50
                             20
                                        30
                   10
                                                        110
                                                                119
                                               100
                    70
                              80
                                       90
            LSLLLG-SALILTSSSATAQGIVADKSAPAQQQPTILQTGNGIPQVNIQTPTSAGVSVNQ
m564
       .pep
                                     1 | 1 | :1| | 1| :1 | 1| | | | :1:1| | 1:
                            111:1
             :1:1: ::1 1::
            WALMLACTGLPLVTH---AQGLV----P-QGQTQVLQGGNKVPVVNIADPNSGGVSHNK
fhab borpe
                                                           100
                                                   90
                        70
                                         80
               60
                                               160
                                      150
                             140
                    130
          120
            YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQLNGYIEV
m564
       .pep
            FQQFNVANPGVVFNNGLTDGVSRIGGALTKNPNLTR-QASAILAEVTDTSPSRLAGTLEV
fhab borpe
                                         140
                                                   150
                                                            160
                      120
                                130
             110
```

	80 190 200 210 220 230 239 GGRRAEVVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLSGFKIRQGNVVIAGHGLD : ::: :: :: : :: : : :: !: : :: YGKGADLIIANPNGISVNGLSTLNASNLTLTTGRPSVNGGRI-GLDVQQGTVTIERGGVN 170 180 190 200 210 220
	40 250 260 270 280 290 ARDTDYTRILSYHSKIDAPVWGQDVRVVAGQNDVAATGDAHSPILNNAAANTSN
m564 .pep	300 310 320 330 340 350 NTANNGTHIPLFAIDTGKLGGMYANKITLISTVEQAGIRNQGQWFASAGNVAVNAEGKLV : : : : : : : : : :: AAAGAYAIDGTAAGAMYGKHITLVSSDSGLGVRQLGS-LSSPSAITVSSQGEIA 290 300 310 320 330
m564 .pep	360 370 380 390 400 410 NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDNSGTVLSSGRLTVRNLGRL : :: : : ::: : LGDATVQRGPLSLKGAGVVSAGKLASGGGAVNVAGGGAVKIASASSVGNL 340 350 360 370 380
m564 .pep	420 430 440 450 460 470 KNQNNGTIQAARLDMSTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNP :: : : :::::::::::::::::::::::::::::
m564 .pep	480 490 500 510 520 530 NPSV-IPQIPSTATGSGSSTVSVSKPGSNNPVSPTAPAKNYAVGRIQTTGAFD-NAGSIN : : :: : :: : : : :: : TRRVDVDGKQAVALGSASSNALSVRAGGALKAGKLSATGRLDVDGKQAVTLGSVA 440 450 460 470 480 490
m564 .pep	
m564 pep	80 590 600 610 620 630 QTAKNSGHLLTQTGKIDNRELHNAGEIAANNLTLIHSGRLSNDKKGNIRAAHLQLDTA ::: :::::!:::! ::: :::! :::! AIGVQGGEAVSVANANSDAELRVRGRGQVDLHDLSAARGADISGEGRVNIGRARSDSDVK 560 570 580 590 600 610
m564 .pep	640 650 660 670 680 690 GLHNAGNILADSGTVTTKNNLRNTGKVSVARLNTEGQTLDNTRGRIEAETVNIQSQQLTN : : : :: : : : : :
m564 .pep	700 710 720 730 740 750 QSGHITATEQLTINSRNVDNQNGKLLSANQAQLAVSDGLYNQHGEIATNRQLSIHDKNQN :: :: ::: : : : :::::::

	760 770 780 790 800 810
m564 .pep	TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDDFVVERDLTAGKQL-NLS
fhab borpe	: ::: :: :: : : :: : : : : : RLDGA-HAGGQLRVSSDGQAALGSLAAKGELTVSAARAATVA-ELKSLDNIS
za	720 730 740 750 760
	820 830 840 850 860 870
m564 .pep	IKGRLK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLINSDGLT
moo! .pop	: : :::::: : :: : : : :: : :
fhab_borpe	
	770 780 790 800 810
	880 890 900 910 920 930
m564 .pep	HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETTEGSTKAGAIAARKRLDI-GAKEIHN
fhab borpe	: :::: :: : : : :: : :: :: : : : : : : : : : : : : : : : : :
Indb_bolps	820 830 840 850 860
	940 950 960 970 980 990
m564 .pep	
fhab_borpe	AANSLHANRDVRVSGKDAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV 870 880 890 900 910 920
	870 880 890 900 910 920
	1000 1010 1020 1030 1040 1050
m564 .pep	ETYLAKAEKQVRDYTVLGQNTYYQAGKDGLFDNSQGQKDQTTATFHLKNGSRIEANQ-
fhab borpe	ALQSAKASGTLHVQGGEHLDLGTLAAVGAVDVNGTGDVRVAKLVSDAGADLQAGRS
	930 940 950 960 970
	1060 1070 1080 1090 1100
m564 .pep	WHVRDYHIETYKERIIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRIITDDLNQKE
	: : : : : : :: : : : : : :
fhab_borpe	MTLGIVDTTGDLQARAQQKLELGSVKSDGGLQAAAGGALSLAAAEVAGALELSGQGV 980 990 1000 1010 1020 1030
	300 330 1000 1010 1020 1000
	110 1120 1130 1140 1150 1160
m564 .pep	ITNQSTTGKGRTDAVGTQWDSVTKKGWYSGRKRQRRTERNHTPYHDTQLFTHDFDTPV ::::::::: :: : : ::: : :: :
fhab borpe	TVDRASASRARIDSTGSVGIGALKAGAVEAASPRRARRALRQDFFTPG
_	1040 1050 1060 1070 1080
	1170 1180 1190 1200 1210 1220
m564 .pep	SVIQQNAASPSFQPAASAIKLIDGVSTAAVNGQRIHTGNVVSLNNATVTLPNSSLYT
61 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	: :: : ::: : : : : : : SVVVRAQGNVTVGRGDPHQGVLAQGDIMDAKGGTLLLRNDALTENGTVTISADSAVL
fhab_borpe	1090 1100 1110 1120 1130 1140
F.C.A	1230 1240 1250 1260 1270 1280 THPDNKGWLVETD-PQFADYRRWLGSDYMLQQLQLDTNHLHKRLGDGYYEQKLVNEQIHQ
m564 .pep	:::::: ::: ::: :::
fhab_borpe	EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFLNGTLRAVNDNNETMSGRQIDV
	1150 1160 1170 1180 1190
	1290 1300 1310 1320 1330 1340
m564 .pep	$\verb LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFGLTPG-IALSAEQVARLTSDIVWMENQTV \\$
fhab borpe	
	VDGRPQITDAVTGEARKDESVVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK

	1350	1360	1370	1380	1390	1400
m564 .pep	TLSDGSTQTVLVPKV	1:1	:: ::::	: :: :	111 :::	: 1:
fhab_borpe	ENGASVTVRTT 1260	GNI		QGVLEV-GGA 1280	LTNEFLVGSI 1290	OGTQRIE 1300
m564 .pep	1410 ARNINSNGNIQ	ADQIGI	120 143 LKAEKSINIDGO	GQVQAGRLLT.	AQAQN]	1450 NLNGTT
fhab borpe	: :: :: AQRIENRGTFQSQAE	PAGTAGALV	/KAAEAIVHDG\	VMATKGEMQI.	AGKGGGSPTV	TAGAKA
	1310	1320	1330	1340	1350	1360
m564 .pep	OTSGNERNGNTAI-	ORMAGINVV-	1480 -GSHTEQVDNR	TSD-GILSLH	ASNDINLNA	VQKZVTA
fhab borpe	: : :: TTSANKLSVDVASWI	NAGSLDIK	KGGAQVTVAGR'	YAEHGEVSIQ	GDYTVSADA]	ALAAQV
11100_20250	1370	1380	1390	1400	1410	1420
m564 .pep	1510 1520 KDGTTQITAGNNI	NLGT-IRT	EHREAYGT	LDDENHRHVR	QST	EVGS
fhab borpe	: :::: : :: TORGGAANLTSRHD	::: 11	:: 1	::: :: :	:::	1:1:
mab_borpe	1430	1440	1450	1460	1470	1480
m564 .pep	1560 1 SIRTQNGALLRAGNI	OLKIRQGELI	EAEEGKTVLAA	GRDVTISE	GRQITELDTS	SVSG
fhab borpe	: ::::: :1	: 1::	::::::::::	: : ::	1::11 : :	: [
IMAD_DOIPE	1490	1500	1510	1520	1530	
-564 non	1610 162 KSKGILSSTKTE	20 HDRYRF:	1630 SHDEAV-GSNI	1640 GGGKMIVAAG	1650 ODINVRGSNI	1660 LISDKGI
	1 11::1:	: 1	: : : :	: :: : 11	: :: :::	: ::
61 1- 1- a	PMECNICOTUTECTO	ESNGRVI.DAI	KHDLTVTASGO	ADNRGSLKAG	HDFTVOAOR	DNSG
fhab_borpe 1	KMESNKDIVIKTEQI 540 1550	FSNGRVLDA	KHDLTVTASGQ	ADNRGSLKAG	HDFTVQAQR:	DNSG
_ 1	KMESNKDIVIKTEQI 540 1550	FSNGRVLDA 1560	KHDLTVTASGQ 1570 80 169	ADNRGSLKAG 1580 0 170	1590 1590	IDNSG
1 m564 .pep	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: :::	FSNGRVLDAI 1560 16 16 NRYTG	KHDLTVTASGQ 1570 80 169 -NEYHESKKSG ::: :::	ADNRGSLKAG 1580 0 170 VMGTGGLGFT : : :	HDFTVQAQRI 1590 0 17: GIGNRKTTDD:	IDNSG LO PDRTNIV
_ 1	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI	FSNGRVLDAI 1560 16 16 NRYTG LRNTGQVVA	KHDLTVTASGQ 1570 80 169 -NEYHESKKSG ::: :::	ADNRGSLKAG 1580 0 170 VMGTGGLGFT : : : LENTGRVD	HDFTVQAQRI 1590 0 171 FIGNRKTTDD 1	IDNSG IO PORTNIV II
m564 .pep	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610	FSNGRVLDAI 1560 16 16 NRYTG I LRNTGQVVAI 162	KHDLTVTASGQ 1570 80 169 -NEYHESKKSG :: ::: GHDIHIINSAK 0 1630	ADNRGSLKAG 1580 0 170 VMGTGGLGFT : : : LENTGRVD 16	HDFTVQAQRI 1590 0 173 FIGNRKTTDD 1 PARNDIALDV 40 16	IDNSG IO PDRTNIV I ADFTN 550 1770
m564 .pep fhab_borpe m564 .pep	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: :	FSNGRVLDAJ 1560 16 16 NRYTG LRNTGQVVA 162 0 1 IVAGNRYRQ	KHDLTVTASGQ 1570 80 169 -NEYHESKKSG :: ::: GHDIHIINSAK 0 1630 1740 TGSTVSS	ADNRGSLKAG 1580 0 170 VMGTGGLGFT : : : LENTGRVD 16 1750 PEGRNTVTAK	HDFTVQAQRI 1590 0 173 FIGNRKTTDD 1 PARNDIALDV 40 16 1760 SSIDVEFANNI	IDNSG IO PDRTNIV I ADFTN 550 1770 RYATDYA ::
m564 .pep	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: :	FSNGRVLDAJ 1560 16 16 NRYTG LRNTGQVVA 162 0 1 IVAGNRYRQ	1570 1570 1570 1570 1570 169	ADNRGSLKAG 1580 0 170 VMGTGGLGFT : : : LENTGRVD 16 1750 PEGRNTVTAK	HDFTVQAQRI 1590 0 173 FIGNRKTTDD 1 PARNDIALDV 40 16 1760 SSIDVEFANNI	IDNSG IO PDRTNIV I ADFTN 550 1770 RYATDYA ::
m564 .pep fhab_borpe m564 .pep fhab_borpe	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: : -TGSLYAEHDA-TL 1660 1780	FSNGRVLDAJ 1560 16 16 NRYTG LRNTGQVVA 162 0 1 TVAGNRYRQ : : : TLAQGTQRD 1670	KHDLTVTASGQ 1570 80 169 -NEYHESKKSG :: ::: GHDIHIINSAK 0 1630 1740 TGSTVSS : LVVDQDHILPV 1680 1800	ADNRGSLKAG	1590 0 173 IGNRKTTDD 1 : : PARNDIALDV 40 16 1760 SIDVEFANNI : : : :: SLTTEIETGI 1700 1820	IDNSG IO PDRTNIV I ADFTN 550 1770 RYATDYA :: NPGSLIA 1710 1830
m564 .pep fhab_borpe m564 .pep fhab_borpe m564 .pep	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: : -TGSLYAEHDA-TL 1660 1780 HTQEQKGLTVALNV :: :	FSNGRVLDAI 1560 16 16 NRYTG LRNTGQVVA 162 0 1 TVAGNRYRQ : : : TLAQGTQRD 1670 1790 PVVQAAQNF	KHDLTVTASGQ 1570 80 169 -NEYHESKKSG :: ::: GHDIHIINSAK 0 1630 1740 TGSTVSS : LVVDQDHILPV 1680 1800 IQAAQNVGKSK :::::	ADNRGSLKAG	HDFTVQAQRI 1590 0 173 FIGNRKTTDD 1 PARNDIALDV 40 16 1760 SIDVEFANN : : : :: SLTTEIETGI 1700 1820 NAA-WQSYQ	IDNSG IO PDRTNIV I ADFTN 550 1770 RYATDYA :: NPGSLIA 1710 1830 ATQQMQQ : :
m564 .pep fhab_borpe m564 .pep fhab_borpe	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: : -TGSLYAEHDA-TL 1660 1780 HTQEQKGLTVALNV :: : EVQENI	FSNGRVLDAI 1560 16 16 NRYTG LRNTGQVVA 162 0 1 TVAGNRYRQ : : : TLAQGTQRD 1670 1790 PVVQAAQNF	KHDLTVTASGQ 1570 80 169 -NEYHESKKSG :: ::: GHDIHIINSAK 0 1630 1740 TGSTVSS : LVVDQDHILPV 1680 1800 IQAAQNVGKSK :::::	ADNRGSLKAG	HDFTVQAQRI 1590 0 173 FIGNRKTTDD 1 PARNDIALDV 40 16 1760 SIDVEFANN : : : :: SLTTEIETGI 1700 1820 NAA-WQSYQ	IDNSG IO PDRTNIV I ADFTN 550 1770 RYATDYA :: NPGSLIA 1710 1830 ATQQMQQ : :
m564 .pep fhab_borpe m564 .pep fhab_borpe m564 .pep fhab_borpe	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: : -TGSLYAEHDA-TL 1660 1780 HTQEQKGLTVALNV :: : EVQENI	FSNGRVLDAI 1560 16 16 NRYTG LRNTGQVVAI 162 0 1 TVAGNRYRQ : : : TLAQGTQRD 1670 1790 PVVQAAQNF DNKQA 1720 1850	KHDLTVTASGQ: 1570 80 169 -NEYHESKKSG:: ::: GHDIHIINSAK 0 1630 1740 TGSTVSS: LVVDQDHILPV: 1680 1800 IQAAQNVGKSK ::::: IVVGKDLTLS- 1730 1860	ADNRGSLKAG	1590 0 173 1590 0 173 1GNRKTTDD 1 ARNDIALDV 40 16 1760 SIDVEFANNI : : : :: SLTTEIETGI 1700 1820 NAA-WQSYQ : : NALLWAAGE: 1750 1880	IDNSG IO PDRTNIV I ADFTN 550 1770 RYATDYA :: NPGSLIA 1710 1830 ATQQMQQ : : LTVKAQN
m564 .pep fhab_borpe m564 .pep fhab_borpe m564 .pep fhab_borpe m564 .pep	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: : -TGSLYAEHDA-TL 1660 1780 HTQEQKGLTVALNV :: : EVQENI	FSNGRVLDAI	KHDLTVTASGQ: 1570 80 169 -NEYHESKKSG:: ::: GHDIHIINSAK 0 1630 1740 TGSTVSS: LVVDQDHILPV: 1680 1800 IQAAQNVGKSK ::::: IVVGKDLTLS- 1730 1860 TYGEQKSRNEQ : ::	ADNRGSLKAG	HDFTVQAQRI 1590 0 173 FIGNRKTTDD 1 PARNDIALDV 40 16 1760 SIDVEFANN : : : :: SLTTEIETG 1700 1820 NAA-WQSYQ : : NALLWAAGE 1750 1880 SQIIGKGQTT : : :	IDNSG IO PDRTNIV I ADFTN 550 1770 RYATDYA :: NPGSLIA 1710 1830 ATQQMQQ : : LTVKAQN 1890 LAATGSG :
m564 .pep fhab_borpe m564 .pep fhab_borpe m564 .pep fhab_borpe m564 .pep	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: : -TGSLYAEHDA-TL 1660 1780 HTQEQKGLTVALNV :: : EVQENI 1840 FAPSSSAGQGQNNN :: : :: ITNKRAALIEAGGN	FSNGRVLDAI	1570	ADNRGSLKAG	HDFTVQAQRI 1590 0 173 FIGNRKTTDD 1 PARNDIALDV 40 16 1760 SIDVEFANN : : : :: SLTTEIETG 1700 1820 NAA-WQSYQ : : NALLWAAGE 1750 1880 SQIIGKGQTT : : :	IDNSG IO PDRTNIV I ADFTN 550 1770 RYATDYA :: NPGSLIA 1710 1830 ATQQMQQ : : LTVKAQN 1890 LAATGSG :
m564 pep fhab_borpe m564 pep fhab_borpe m564 pep fhab_borpe m564 pep fhab_borpe	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: : -TGSLYAEHDA-TL 1660 1780 HTQEQKGLTVALNV :: : EVQENI 1840 FAPSSSAGQGQNNN :: : :: ITNKRAALIEAGGN 1760 1770	FSNGRVLDAI	KHDLTVTASGQ: 1570 80 169 -NEYHESKKSG:: ::: GHDIHIINSAK: 0 1630 1740 TGSTVSS: LVVDQDHILPV: 1680 1800 IQAAQNVGKSK ::::: IVVGKDLTLS- 1730 1860 TYGEQKSRNEQ: : : LNKLGRIRAGE 1790 1920	ADNRGSLKAG	1590 0 173 IGNRKTTDD 1 PARNDIALDV 40 16 1760 SIDVEFANN : : : :: SITTEIETG 1700 1820 NAA-WQSYQ : : NALLWAAGE 1750 1880 GQIIGKGQTT : :: PRIENT	IDNSG IO FDRTNIV III ADFTN 550 1770 RYATDYA III NPGSLIA 1710 1830 ATQQMQQ IIII LTVKAQN 1890 LAATGSG II AKLSGEV 1810
m564 pep fhab_borpe m564 pep fhab_borpe m564 pep fhab_borpe m564 pep fhab_borpe	KMESNKDIVIKTEQI 540 1550 1670 VLKAGHDIDISTAHI :: ::: TMAAGHDATLKAPHI 1600 1610 1720 1730 HTGSIIGSLNGDTV : :: : -TGSLYAEHDA-TL 1660 1780 HTQEQKGLTVALNV :: : EVQENI 1840 FAPSSSAGQGQNNN :: : :: ITNKRAALIEAGGN 1760 1770	FSNGRVLDAI	### HTML REPORT NAME	ADNRGSLKAG	1590 0 17: 1590 0 17: 1590 0 17: 1590 0 17: 1590 160 1760 1760 1810 1760 1820 1820 1820 1820 1840 1750 1880 1890 1880 1940 1940 1940 1940 1940 1940 1940 194	IDNSG IO FDRTNIV I ADFTN 550 1770 RYATDYA II NPGSLIA 1710 1830 ATQQMQQ I I I LTVKAQN 1890 LAATGSG I AKLSGEV 1810 1950 IGNGIRF I I

	1960 1970 1980 1990 2000 2010 GITAGGNIGKGKEQGGSTTHRHTHVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH
m564 .pep	:: :: : :: : :: :: ::
fhab borpe	GKDLYLNAGARKDEHRHLLNEGVIQAGGHGHIGGDVDNRSV-
	1870 1880 1890 1900
	2020 2030 2040 2050 2060
m564 .pep	IESVODTETYOSKOONGNVQVTVGYGFSASGSYRQSKVKADHASVTGQSGIYAGE
	::: : ::: : : : : : : : : URTVSAMEYFKTPLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY
fhab_borpe	1910 1920 1930 1940 1950 1960
	2070 2080 2090 2100 2110 2120 DGYQIKVRDNTDLKGGIITSSQSAEDKGKNLFQTATLTASDIQNHSRYEGRSFGIGGS
m564 .pep	DGYQIKVRDNTDLKGGIIT35Q5AEDAGANLFQIAILIA3DIQNA3AIEGASIGIGGS
fhab borpe	TEWSVNTLKNLDL-GYQAKPAPTAPPMPKAPELDLRGHTLESAEGRKI-FGEY
	1970 1980 1990 2000 2010
	2130 2140 2150 2160 2170
m564 .pep	FDLNGGWDGTVTDKQGRPTDRISPAAGYGSDGDSKNSTTRSGVNTHNIHITDEAG
fhab_borpe	KKLQGEYEKAKMAVQAVEAYGEATRRVHDQLGQRYGKALGGMDAETKEVDGIIQ 2020 2030 2040 2050 2060 2070
2	2180 2190 2200 2210 2220 2230
m564 .pep	QLARTGRTAKETEARIYTGIDTETADQHSGHLKNSFDKDAVAKEINLQREVTKEFGRNAA :: : : :::: : :::: : ::::: :
fhab borpe	
IMAD_DOIPE	2080 2090 2100 2110 2120
	2240 2250 2260 2270 2280 2290
m564 nen	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL
	1::1 11::1 ::1::: : : : : : : : : : : :
fhab_borpe	AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKEQTVLAAGAGLTLSNGAIHNGENA
	2130 2140 2150 2160 2170 2180
	2300 2310 2320 2330 2340 2350
m564 .pep	AENQSRYDTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK
fhah harna	: :: : : : : : : AONRGRPEGLKIGAHSATSVSGSFDALRDVGLEKRLDIDDALAAVLVNPHIFTRIGAAQT
fhab_borpe	2190 2200 2210 2220 2230 2240
The following part	ial DNA sequence was identified in N. gonorrhoeae <seq 1671="" id="">:</seq>
q565.seq	
1 at	tggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51 cg 101 cd	gtaaccacc accattttcg coogtoccag accggogget tocaatactt cctgogttt ogcatogoog aacgacacog gotogootge acttotgget
151 ac	cctgcacgc gtgcgatgtc caagtcgagc gcgaaatacg gaatatcctc
201 tt	ttgggcgaa gacgcgtccg accgtctgcc cgccctgcc gaagccgaca
251 at	tcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgcag
301 at	tcgagcgac ttcatgtccc agcttga
This corresponds to	o the amino acid sequence <seq 1672;="" 565.ng="" id="" orf="">:</seq>
q565.pep	1
1 MI	DSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
	CTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 II	ERLHVPA*
The following part	tial DNA sequence was identified in N. meningitidis <seq 1673="" id="">:</seq>
m565.sea	
1 A	TGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51 C	GTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT CCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCGC ACTTCTGGCA
	CCTGCGTTT CGCATCGCCG AACGACACCG GIICGCCCGC ACIICIGGCA CCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC

151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC 201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

PCT/US99/09346

251	TCAGCACATG	GTCGGACTTG	CTCATGGTTT	CTACCAGCAT	ACTGTGCAGA
301	TCGAGCGACT	TCATGTCCCA	GCTTGACTTG	ACCAAACGCC	CGACCAGCGC
351	ATCGCTGCCG	CCCAAGAGGA	AGGGCGCGAT	AATCATCGAC	AGCAGAACCG
401	CCGCCGTCGC	CGCCTGTTCC	CATTCTGGCG	AAACCATATC	AAGCTGCCCG
451	GCAATGGCCA	GCATCACGAA	GCCGAACTCG	CCGCCCTGCG	CGAGATACAA
501	AGCCGTTTTG	AGGCTGTCGC	CGACCGAATG	TTTCATTTTG	AAGGCAATGG
551	CAAACACAAC	CAGTGCCTTC	AACACCAGCA	GCATTGCCAA	CAGCATCAAT
601	ACCTGCCGCC	AGCCGCCGAT	CAATGCCTGA		

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```
m565.pep

1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTECFIL KAMANTTSAF NTSSIANSIN
201 TCRQPPINA*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

```
m565/g565 100.0% identity in 67 aa overlap
                                20
                                         30
                                                  40
                MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
    m565.pep
                \verb|MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS|
    g565
                                20
                                         30
                                                  40
                                80
                                         90
                                                  100
                AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
    m565.pep
                AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX
    q565
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1675>:
    a565.seq
```

1	ATGGACAGCA	CATTGTCTAA	AACGTGTTGC	GTTTCGTGCA	TATTGTTGAG
51	CGTAACCACC	ACCATTTTCG	CCCGTCCCAG	ACCGGCGGCT	TCCAATACTT
101	CCCTGCGTTT	CGCATCGCCG	AACGACACCG	GTTCGCCCGC	ACTTCTGGCA
151	ACCTGCACCC	GCGCAATGTC	CAAGTCGAGC	GCGAAATACG	GAATATCCTC
201	TTGGGCAAGG	ACGCGTCCGA	CCGTCTGCCC	GCCCCTGCCG	AAGCCGACAA
251	TCAGCACATG	GTCGGACTTG	CTCATGGTTT	CTACCAGCAT	ACTGTGCAGA
301	TCGAGCGACT	TCATGTCCCA	GCTTGACTTG	ACCAAACGCC	CGACCAGTGC
351	ATCGCTGCCG	CCCAAGAGGA	AGGGCGCGAT	AATCATCGAC	AGCAGAACCG
401	CCGCCGTCGC	CGCCTGTTCC	CATTCTAGCG	AAACCATATC	AAGCTGCCCG
451	GCAATGGCCA	GCATCACGAA	GCCGAACTCG	CCGCCCTGCG	CGAGATACAA
501	AGCCGTTTTG	AGGCTGTCGC	CGACCGAATG	TTTCATTTTG	AAGGCAATGG
551	CAAACACAAC	CAGTGCCTTC	AACACCAGCA	GCATTGCCAA	CAGCATCAAT
601	ACCTGCCGCC	AGCCGCCGAT	TAATGCCTGA		

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```
a565.pep

1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTECFIL KAMANTTSAF NTSSIANSIN
201 TCRQPPINA*

m565/a565

99.5% identity in 209 aa overlap

10 20 30 40 50 60

m565.pep

MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
```

a565	MDSTLSKTCCVSCI	LLSVTTTIFA	ARPRPAASNTS	LRFASPNDTO	SPALLATCT	RAMSKSS
4041	10	20	30	40	50	60
		2.0	0.0	100	110	120
	70	80	90			
m565.pep	AKYGISSWARTRPT	VCPPLPKPT:	ISTWSDLLMVS	TSILCRSSDE	MSQLDLTKR.	PTSASLP
		111111111				111111
a565	AKYGISSWARTRPT	VCPPLPKPT:	ISTWSDLLMVS	TSILCRSSDE	MSQLDLTKR	PTSASLP
4000	70	80	90	100	110	120
	130	140	150	160	170	180
m565.pep	PKRKGAIIIDSRTA	AVAACSHSG	ETISSCPAMAS	SITKPNSPPCA	RYKAVLRLS:	PTECFIL
mooo.pep		111111111	11111111111	1111111111		111111
F. C. F.	PKRKGAIIIDSRTA	AMANCEHEE	ETISSCPAMAS	TTKPNSPPCZ	RYKAVI.RI.S	PTECETL
a565					170	180
	130	140	150	160	170	180
	190	200	210			
m565.pep	KAMANTTSAFNTSS	IANSINTCR	SPLINAX			
	1111111111		[
a 5 65	KAMANTTSAFNTSS	IANSINTCR	ZANIGG			
222	190	200	210			

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1677>:

g566.seq..

```
1 atgccgtctg aacaatatct tttcagacgg cattttgtat gggggttaac
51 ggttgttcag cccgagtacg tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgc gacggcaccg gcggcaaagg tcatgcggct
151 gccggctttg tgggtgattt ccacgcgttc gccgtcggtg gcgaagaggg
201 cggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcccggc gatgacttcg cccattcgta
```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

g566.pep..

1 MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA 51 AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA

51 AGFVGDFHAF AVGGEEG 101 LFEVAAERAG DDFAHS*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1679>:

m566.seq..

1 ATGCCGTCTG AACAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51 GGTTGTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTGCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACCG GCGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGGCGTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCCCGC GATGACTTCG CCCATGCGTA

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

m566.pep..

- 1 MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
- 51 AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
- 101 LFEVSAERAG DDFAHA*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m566/g566 93.1% identity in 116 aa overlap

10 20 30 40 50 60

m566.pep MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL

a565	MDSTLSK			ASNTSLRFASP 0 40	NDTGSPALLAT 50	CTRAMSKSS 60
m565.pep a565	1111111	WARTRPTVCPP	LPKPTISTWSD LPKPTISTWSD	111111111111	SSDFMSQLDLT SSDFMSQLDLT	
m565.pep a565	PKRKGAI PKRKGAI	IIDSRTAAVAA IIDSRTAAVAA	1111:11111	PAMASITKPNS PAMASITKPNS	PPCARYKAVLR PPCARYKAVLR	
m565.pep a565	KAMANTT: KAMANTT:	SAFNTSSIANS SAFNTSSIANS		X I X		
The following page 9566.seq.		equence was	s identified i	n <i>N. gonorrh</i>	noeae <seq< td=""><td>ID 1677>:</td></seq<>	ID 1677>:
1	atgccgtctg	aacaatatct	tttcagacgg	cattttgtat	gggggttaac	
51	ggttgttcag	cccgagtacg	tcctgcatat	cgtacaaacc	cgttttgccg	
101					tcatgcggct	
151					gcgaagaggg	
201					aaagccgatg	
251	gtggaaggat	cgcgcggacc	agtgtggcct	tcgcggccgt	aaacggcgca	
301					cccattcgta	
351	a					
This corresponds	s to the amin	o acid seque	nce <seo i<="" td=""><td>D 1678; OR</td><td>F 566.ng>:</td><td></td></seo>	D 1678; OR	F 566.ng>:	
		o dora boque	5241	2 10.0, 010		
g566.pep.		DESMICT TUNIO	DEVUI HTUOT	PENUVENCCA	DGTGGKGHAA	
1	MESEGILERK	NUCCEECCIV	PDAMACADCC	KANGGRIART	SVAFAAVNGA	
51	LFEVAAERAG		ADIVACADGG	KADGGKIAKI	JVALAAVIOA	•
101	LFEVAAERAG	DDFAR5"				
The following pa		equence was	s identified i	n N. mening	itidis <seq< td=""><td>ID 1679>:</td></seq<>	ID 1679>:
1	ATGCCGTCTG	AACAATATCT	TTTCAGACGG	CATTTTGTAT	GGGGGTTAAC	
	GGTTGTTCAG	CCCGAGTACG	TCCTGCATAT	CGTACAAACC	CGTTTTGCCG	
101					TCATGCGGCT	
	GCTGGCCTTG					
201	CGGTGTGGTC	GCCGACGATG	TCGCCTGCGC	GGACGGTGGC	AAAGCCGATG	1
251	GTCGACGGAT	CGCGCGGACC	GGTGTGGCCT	TCGCGGCCGT	AAACGGCGCA	
301	TTGTTTGAGG	TCTCTGCCGA	GCGCGCCGGC	GATGACTTCG	CCCATGCGTA	
351						
This corresponds		o acid seque	ence <seq i<="" td=""><td>D 1680; OR</td><td>F 566>:</td><td></td></seq>	D 1680; OR	F 566>:	
	MPSEQYLFRR	HFVWGLTVVO	PEYVLHIVOT	RFAVDPNCGA	DGTGGKGHAA	
- 51	AGLVGDFHAL	AVGGEEGGVV	ADDVACADGG	KADGRRIART	GVAFAAVNGA	
101	LFEVSAERAG	DDFAHA*				
Computer analys	sis of this an	nino acid sed	uence gave	the following	g results:	
Homology with					-	
monology with	a predicted (אווטוו זעני אוני	gonornioed			
m566/g566	93.1% ide	ntity in 11	6 aa overla	р		

```
MPSEOYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
     g566
                                  20
                                            30
                         10
                         70
                                  80
                                            90
                                                    100
                                                              110
                 AVGGEEGGVVADDVACADGGKADGRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
    m566.pep
                 AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
     g566
                                  80
                                            90
                                                    100
                         70
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1681>:
     a566.seq
              ATGCCGTCTG AACAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
              GGTTGTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTACCG
          51
              TTTACCCAAA CTGCGGCGCG GACGGCGCCG GCGGCAAAGG TCATGCGGCT
         101
              GCTTGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
         151
              CGGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
              GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
              TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
         301
         351
This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:
     a566.pep
              MPSEOYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
           1
              ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
          51
              LFEVSAERAG DDFAHA*
          101
                 94.0% identity in 116 aa overlap
     m566/a566
                                            30
                                                      40
                                                               50
                                                                         60
                         10
                 MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
     m566.pep
                 MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
     a566
                                                                         60
                                                      40
                         10
                                  20
                                            30
                                            90
                                                    100
                         70
                                  80
                 AVGGEEGGVVADDVACADGGKADGRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
     m566.pep
                 AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
     a566
                         70
                                  80
                                            90
                                                    100
                                                              110
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1683>:
   q567.seq..
              atgcgacgac gggcagcggc atcgacaagg cgggtttgca gtccggcgtt
              tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtacgcag
          51
              caaagagggc ggatacggcg tgttgggtgc gaacgcgcgc gcttgccggc
              gcggaaatcg agctggtgca ggaaatcgcc cgggaagtgc gtttgaaaaa
              cgcgctcaag gcagtggcgg aagattacga ctttatcctg atcgactgtc
              cgccttcgct gacgctgttg acgcttaacg gcttggtggc ggcgggcggc
              qtqattqtqc cgatqttqtq cgaatattac gcgctggaag ggatttccga
          301
              tttgattgcg accgtgcgca aaatccgtca ggcggtcaat cccgatttgg
          351
              acatcacggg catcgtgcgt acgatgtacg acagccgcag caggctggtt
              gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgctttttga
              aaccqccatc ccqcqcaata tccqccttqc qqaaqcqccq agccacqqta
              tgccggtgat ggcttacgac gcgcaggcaa agggtgccaa ggcgtatctt
              gccttggcgg acgaactggc ggcgagggtg tcggggaaat ag
This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:
     q567.pep
              MRRRAAASTR RVCSPAFIRS YWAMRTCSRR RYAAKRADTA CWVRTRALAG
            1
              AEIELVQEIA REVRLKNALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
           51
              VIVPMLCEYY ALEGISDLIA TVRKIRQAVN PDLDITGIVR TMYDSRSRLV
          101
              AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
```

ALADELAARV SGK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1685>:

```
m567.seq..
       1 ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
      51 AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
     101 GCGTGCTGGT GGTCGATTTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
     151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
     201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
     251 CTGTGTTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
         CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGA
          AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
     351
          TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
     401
          TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTTGATTG CGACCGTGCG
          CAAAATCCGT CAGGCGGTCA ATCCCGATTT GGACATCACG GGCATCGTGC
     501
     551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
          TTGCGCAGCC ATTTCGGGGA TTTGCTTTTT GAAACCGTCA TCCCGCGCAA
     601
     651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
     701 ACGCGCAGGC AAAGGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
     751 GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

m567.pep..

1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51 GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVEEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLDIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251 AARVSGK*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

m567/g567	98.2% identity	in 168 aa over	lap		
	60 70	80	90 100		
m567.pep	GVYQVLLGDADVQS				
g567	AFIRSYWAMRTCSR				
-	20 30	0 40	50	60	70
	120 130	140	150 160	170	179
m567.pep	YDFILIDCPPSLTL	LTLNGLVAAGGVIV	PMLCEYYALEGI:	SDLIATVRKIR	QAVNPDLDI
	111111111111111				
g567	YDFILIDCPPSLTL				QAVNPDLDI 130
	80 9	0 100	110	120	130
	180 190	200	210 220	0 230	239
m567.pep	TGIVRTMYDSRSRL	VAEVSEQLRSHFGD	LLFETVIPRNIR	LAEAPSHGMPV	
	[] [] [] [] [] [] [] []				
g567	TGIVRTMYDSRSRL				MAYDAQAKG 190
	140 15	0 160	170	180	190
	240 250				
m567.pep	TKAYLALADELAAR	VSGKX			
	:				
g567	AKAYLALADELAAR	VSGKX			
-	200 210				

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1687>:

a567.seq					
	ATGAGTGCGA				
51	AACGACGACG	ACGGTAAATT	TGGCGGCTTC	GCTGGCATCG	CGCGGCAAAC
101	GCGTGCTGGT	GGTCGATTTG	GATCCGCAGG	GCAATGCGAC	GACGGGCAGC
	GGCATCGACA				
201	CGATGCGGAC				
201	CGVICCOCUC	010.111000			

871

```
GCGTGTTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
             CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
         301
             GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
             TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
         401
             TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTTGATTG CGACCGTGCG
         451
         501
             CAAAATCCGT CAGGCGGTCA ATCCCGATTT GGATATCACG GGCATCGTGC
             GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
         551
             TTGCGCAGCC ATTTCGGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
             TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
         701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
             ATGGCGAGGG TGTCGGGGAA ATAG
This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:
    a567.pep
             MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
           1
             GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYGVLGANR ALAGAEIELV
          51
             QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
             CEYYALEGIS DLIATVRKIR QAVNPDLDIT GIVRTMYDSR SRLVAEVSEQ
         201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
         251 MARVSGK*
    m567/a567
                97.7% identity in 257 aa overlap
                                                  40
                                                           50
                                20
                                         30
                MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKAGLQSG
    m567.pep
                MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
    a567
                                                           50
                                         30
                                                  40
                       10
                                20
                                80
                                         90
                                                 100
                                                          110
                                                                   120
                VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
    m567.pep
                VYQVLLGDADVKSAAVRSKEGGYGVLGANRALAGAEIELVQEIAREVRLKNALKAVAEDY
    a567
                                         90
                                                 100
                                                          110
                                                                   120
                       70
                                80
                                                                    180
                                        150
                                                 160
                                                          170
                                140
                       130
                DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDIT
    m567.pep
                DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDIT
    a567
                                                          170
                               140
                                        150
                                                 160
                                                                   180
                       130
                                                                    240
                                                  220
                                                          230
                       190
                                200
                                        210
                GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
    m567.pep
                GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
    a567
                                        210
                                                 220
                                                          230
                       190
                                200
                       250
                KAYLALADELAARVSGKX
    m567.pep
                13111111 11111
                KAYLALADELMARVSGKX
     a567
                       250
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1689>:

```
q568.seq
         atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
      1
         gataccttgc agaatctgcc gattaaagcg ttcgcggctg cccaatattt
     51
         tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
    101
        tgtaaaaaca gccccatcag gaacgaaact tcgtcttcgg ggcgacgcca
    151
    201 gttttcggtt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
    251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcg tttgtgtccc
    301 attatacgcg ggagaaaacg tttttcgcc caacggccgt tgccgtccat
    351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg
```

```
tgctgctctt catatctgcc tttcgcggtt cggcgttcaa atgccgtctg
          401
              aacgccgcgc cgtga
This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:
     g568.pep
              MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCKA
              CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFTIF SNASKPRLCP
          51
              IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
          101
              NAAP*
          151
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1691>:
     m568.seq
              ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
           1
              GATGCCTTGC AGAATCTGCC GGTTGAAGCG TTCGCGGCTG CCCAATATCT
          51
              TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
          101
              TGTAAAAACA GCCCCATCAG GAACGAAACT TCGTCTTCGG GGCGGCGCCA
          151
          201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
              CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
          251
              ATTATGCGCG GGAGGAAACG TTTTTTCGCC CAACGGCCGT TGCCGTCCAT
          301
              AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
          351
              TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CGGCATTCAA ATGCCGTCTG
          401
              AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
          451
              TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTTGAACC
          501
              GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
          551
              GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
          601
              CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
          651
              CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
          701
              TGCCGGGTTC AGTCCCAAGT TTGA
This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:
     m568.pep..
              MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCKA
           1
              CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFTIF SNASKPRLCP
           51
               IMRGRKRFFA QRPLPSIITA <u>ICLGMAVCSK TACVLLFMSA</u> FRGSAFKCRL
          101
              NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
              EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
          201
              CRVQSQV*
          251
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
                 94.8% identity in 154 aa overlap
     m568/q568
                                   20
                                             30
                         10
                 MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCKACKNSPIRNET
     m568.pep
                  MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCKACKNSPIRNET
     g568
                                                      40
                                                                50
                                                                          60
                          10
                                   20
                                             30
                                             90
                                                     100
                                   80
                  SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA
     m568.pep
                  SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIIRGRKRFFAQRPLPSIITA
     q568
                                                                         120
                                             90
                                                     100
                                                               110
                          70
                                                                         180
                                  140
                                            150
                                                     160
                                                               170
                         130
                  ICLGMAVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ
     m568.pep
                  MCLGMAVCSKMVCVLLFISAFRGSAFKCRLNAAPX
     q568
                                  140
                                            150
                         130
```

200

190

m568.pep

210

FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1693>: a568.seq
```

700.0cq					
1	ATGCTCAGGG	TCAGGCCGGT	ATTGTTTGCC	GTCAAGGCTT	CCGCCTCTTC
51	GATGCCCTTC	AGGATTTGAC	GGTTGAAGCG	TTCGCGGCTG	CCCAGTATTT
101	TCAGGCGCAT	ATTGTTTTCG	TGCAGGCGGC	GTACCTGTTT	
151	TGTAAAAACA	GCCCCATCAG	GAACGAAACT	TCGTCTTCGG	GGCGGCGCCA
201	GTTTTCGGTT	GAAAAGGCAA	ACACGGTCAG	ATATTGCACA	CCCAGTTTGG
251	CGCAATGCTT	CACCATATTT	TCCAATGCGT	CCAAACCGCG	TTTGTGTCCC
301	ATTATGCGCG	GGAGGAAACG	TTTTTTCGCC	CAACGGCCGT	TGCCGTCCAT
351	AATCACGGCG	ATATGCTTGG	GAATGGCGGT	GTGTTCCAAA	ACGGCCTGCG
401	TGCTGCTTTT	CATGTCTGCC	TTTCGCGGTT	CGGCATTCAA	ATGCCGTCTG
451	AACGCCGAAC	CGTGCAGGTT	AAATTGCCAT	CAAATCTTCT	TCTTTGGCAG
501	TCAGGAGTTT	GTCGGCTTCG	GTAATGTATT	TGTCGGTCAG	TTTTTGAACC
551	GCTTCTTCGC	CGCGACGTGC	CTCGTCTTCG	GAAATTTCTT	TGTCTTTGAG
601	GAGTTTTTTG	ATGTGGTCGT	TGGCATCGCG	GCGCACGTTG	CGGATGGAGA
651	CGCGGCCTTC	TTCCGCTTCG	CCGCGTACGA	CTTTAATCAG	GTCTTTGCGG
701	CGTTCCTCGG	TCAGCATGGG	CATCGGCACG	CGGATCAGGT	CGCCGACAGC
751		AGTCCCAAGT			

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

to the animo dota sequence 52 2 12 17 , 12 1 1 1 1	
MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCKA	
CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFTIF SNASKPRLCP	
IMRGRKRFFA ORPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL	
NAFECRINCH OIFFFGSOEF VGFGNVFVGO FLNRFFAATC LVFGNFFVFE	
EFFDYWGIA AHVADGDAAF FRFAAYDFNO VFAAFLGOHG HRHADOVADS	
CK/Q5Q/	
00 19 identity in 257 as overlan	
98.1% Identity in 237 ad Overlap	
10 20 30 40 50 6	3
10 20 44	
	n I
10 20 30 40 50 6	J
	_
, ,	-
	1
SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIIT	Α
130 140 150 160 170 18	C
TCLGMAVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVG	Ç
130 140 130 100 110	•
100 200 210 220 230 24	n
100 110 110 110	
ELNRE MAICLUSE ONE OF EEEE DVV VOI AMIVADORAL IN MAIL DE MOVINGE DOOR	1
	ı
190 200 210 220 230 24	J
···	
HRHADQVADSCRVQSQVX	
	130 140 150 160 170 186 ICLGMAVCSKTACVLLFMSAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVG

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1695>: g569.seq..

atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct

- 51 gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
- 101 tgattgccct gaccgccttg tgggagtatg cccgtatggc cggtttgtgc

```
151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
251 tggcattttg gctcgccgtt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgtat ccctggcgcc cgcatcccga tga
```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>: g569.pep

- 1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
- 51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
- 101 LNGGWQVYAV GWLLLMPFWF ALVSLAPASR *

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1697>: m569.seq.

```
1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
    GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
 51
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGGTTT TCGGCGTGGT
TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGCTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GGCGGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>: m569.pep..

- 1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
- 51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR 101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
- 151 FSGKAFGKHK IAPAISPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
- 201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRTDSL
- 251 IAVISVYAAM MSVLN*

m569/g569 95.3% identity in 127 aa overlap

	_					
	1.0	20	30	40	50	60
m569.pep	MLKQRVITAMWLLP	LMLGMLFYAF	QWLWAAFCGL	TALIALWEY?		AALYHW.
		11111111111			: :	
q569	MLKQRVITAMWLLP	LMLGMLFYA	QWLWAAFCGL:	[ALTALWEY <i>]</i>	RMAGLCKTET	NHYLAA
-	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWM	LPNLVWYVVI	AFWLAVMPLW	LRFKWRLNGO	WQVYAVGWLI	VMPFWF
		111111111111			1111111111	:
g569	TLVFGVVAYAGGWM	LPNLVWYVVI	AFWLAVMPLW	LRFKWRLNGO	WQVYAVGWLI	LMPFWF
3302	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHPDDALP	LLAVMGLVWV	/ADICAYFSGK	AFGKHKIAP <i>I</i>	AISPGKSWEGA	AIGGAVC
moos.pop	11111					
g569	ALVSLAPASRX					
9505	130					
	130					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1699>:

```
a569.seq
```

- ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT 1
- GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
- 101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

151	AAAATTAAAA	CCAACCATTA	CCTCGCCGCA	ACCTTGGTTT	TCGGCGTGGT
201	TGCCTATGCG	GGCGGCTGGA	TGCTGCCTAA	TTTGGTTTGG	TATGTTGTTT
251	TGGCATTTTG	GCTCGCCGTT	ATGCCTTTAT	GGTTGAGATT	CAAATGGAGG
301	CTCAACGGCG	GTTGGCAGGT	TTATGCCGTC	GGCTGGCTTC	TGGTCATGCC
351	GTTTTGGTTC	GCGCTCGTAT	CCCTGCGCCC	GCATCCCGAT	GATGCCCTGC
401	CGCTGCTCGC	CGTGATGGGT	TTGGTGTGGG	TTGCCGATAT	TTGCGCGTAT
451	TTCAGCGGCA	AGGCGTTCGG	CAAACACAAA	ATCGCACCGG	CAATCAGCCC
501	CGGCAAAAGC	TGGGAAGGTG	CAATCGGCGG	CGCGGTTTGC	GTGGCCGTGT
551	ACATGACCGC	CGTACGAAGT	GCCGGCTGGC	TGGCATTCGA	TACAGGCTGG
601				ACCGTTGTCA	
651				GGCAGGCATC	
701	GCAACCTGCT	GCCCGGACAC	GGCGGCGTGT	TCGACCGCAC	CGACAGCCTG
751	ATTGCCGTTA	TCAGCGTCTA	TGCAGCGATG	ATGTCGGTTT	TAAATTGA

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```
a569.pep
        MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
      1
        KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
     51
        LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
    101
        FSGKAFGKHK IAPAISPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
    151
        FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRTDSL
        IAVISVYAAM MSVLN*
    251
           99.6% identity in 265 aa overlap
m569/a569
                                            40
                                                     50
                           20
                                   30
           MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA
m569.pep
           MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA
a569
                                                             60
                           20
                  10
                                                             120
                                   90
                                           100
                                                    110
                  70
           TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
m569.pep
           TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
a569
                                           100
                                                    110
                                                             120
                                   90
                  70
                           80
                          140
                                   150
                                           160
                                                    170
                                                             180
                 130
           ALVSLRPHPDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAISPGKSWEGAIGGAVC
m569.pep
           ALVSLRPHPDDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAISPGKSWEGAIGGAVC
a569
                                                    170
                                                             180
                 130
                          140
                                   150
                                           160
                                           220
                                                    230
                                                             240
                          200
                                   210
                 190
           VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSKLLPGH
m569.pep
           VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSNLLPGH
a569
                                           220
                                                    230
                                                             240
                 190
                          200
                 250
                          260
           GGVFDRTDSLIAVISVYAAMMSVLNX
m569.pep
           11111111111111111111111111111111
           GGVFDRTDSLIAVISVYAAMMSVLNX
a569
                 250
                          260
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1701>: g570.seq..

```
1 atgatecgtt tgaceegeege gtttgeegee geettgateeg gtttatgetg
51 caceacaagge gegeaegeeg acacetteea aaaaateegee tttateaaca
101 cegagegeat etacetegaa tecaageagg egegeaacat ecaaaaaacg
151 ctggaeggeg aatttteege eegteaggae gaattgeaaa aactgeaacg
201 cgaaagaettg gatttggaaa ggeagetege eggegeaaaa ettaaggaeg
251 caaaaaagge geaageegaa gaaaaatgge gegggetggt egaagegtte
301 egeaaaaac aggegeagtt tgaagaagae tacaacetee geegeaaega
351 agagtttgee teeeteeage aaaaegeeaa eegegteate gteaaaateg
```

```
401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
    acccaatacg acgttaccga cagcgtcatt aaagaaatga acgcccgctg
```

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>: g570.pep..

- MIRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
- 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
- 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
- 151 TQYDVTDSVI KEMNAR*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1703>: m570.seg.

```
1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
    CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
-51
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
501 A
```

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>: m570.pep

- MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
- 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
- RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIYVN 101
- TQYDVTDSVI KEMNAR*

m570/g570 94.6% identity in 166 aa overlap

```
20
                                30
          {\tt MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD}
m570.pep
          MIRLTRAFAAALIGLCCTTGAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD
g570
                                30
                                       40
                                               50
                                                       60
                        20
                1.0
                                90
                                      100
                        80
          \verb"ELQKLQREGLDLERQLAEGKLRNAKKAQAEEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA"
m570.pep
          ELQKLQREGLDLERQLAGGKLKDAKKAQAEEKWRGLVEAFRKKQAQFEEDYNLRRNEEFA
g570
                        80
                                90
                                      100
                                              110
                                                      120
                70
                       140
                               150
                                      160
               130
          SLOONANRVIVKIAKQEGYDVILQNVIYVNTQYDVTDSVIKEMNARX
m570.pep
          SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
g570
                       140
                               150
                                      160
               130
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1705>:

```
a570.seq
         ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
      1
     51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
         CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
    101
    151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
    201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
    251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
    301 CGCAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
    351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
    401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
    451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
```

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```
a570.pep
        MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
        LDSEFSAROD ELOKLOREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
     51
       RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
       TOYDVTDSVI KEMNAR*
           97.6% identity in 166 aa overlap
m570/a570
                                          40
                                                   50
          MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD
m570.pep
           {\tt MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD}
a570
                                  30
                         20
                 10
                                                          120
                 70
                         80
                                  90
                                         100
                                                  110
           ELQKLQREGLDLERQLAEGKLRNAKKAQAEEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA
m570.pep
           ELQKLQREGLDLERQLAEGKLKDAKKAQAEEKWCGLVAAFRKKQAQFEEDYNLRRNEEFA
a570
                                         100
                                                  110
                                  90
                         80
                 70
                         140
                                 150
                                         160
                130
           SLQQNANRVIVKIAKQEGYDVILQNVIYVNTQYDVTDSVIKEMNARX
m570.pep
           SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX
a570
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1707>: g571.seq

150

160

140

```
atgcgcgttt tccgagtaaa ccgatttgtt gttaccgttt tcggcggcgg
```

- 51 tataggttet geegteecae aegetgeetg egteggeaaa eaggeteagg
- 101 eggacggtgc gtgcgtcttt egcacegggc ategggaaga geagetegge
- ggagacgttg gcttttttgt tgccgccgta gctgattttt tcgccgtatt
- 201 cgtcatacac tttcgggccg agcgtgccgc tttcgtagcc gcgcaccgaa
- 251 cccaggccgc cgccgtagaa gttttcaaag aaggggattt ctttggttct gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
- 351 ttttgct...

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

g571.pep (partial)

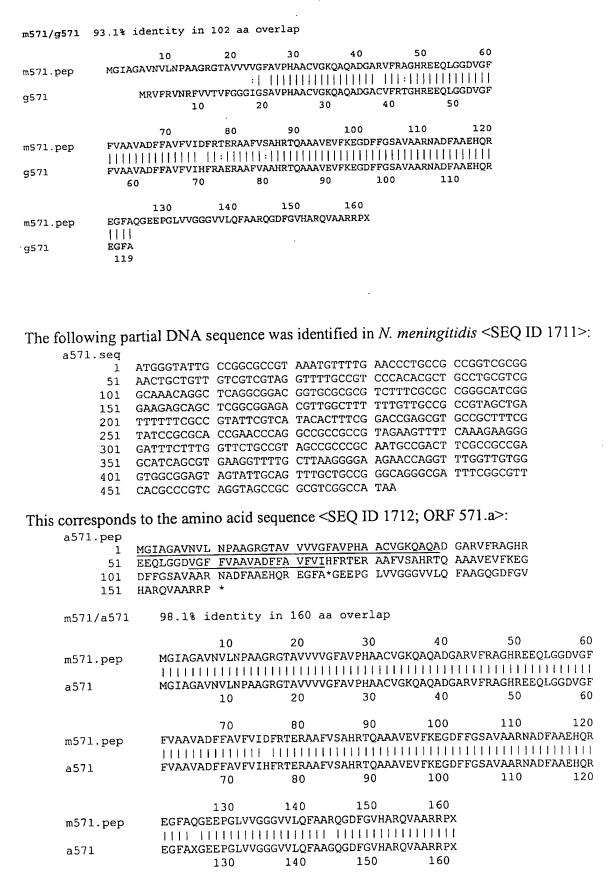
- MRVFRVNRFV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG 1
- GDVGFFVAAV ADFFAVFVIH FRAERAAFVA AHRTQAAAVE VFKEGDFFGS
- 101 AVAARNADFA AEHQREGFA...

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1709>: m571.seg

- ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCCTGCCG CCGGTCGCGG 1 51 AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG 101 GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
 - 151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
 - 201 TTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
 - TATCCGCGCA CCGAACCCAG GCCGCCGCCG TAGAAGTTTT CAAAGAAGGG 251
 - GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
 - 351 GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCGGCGTT
 - CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>: m571.pep

- MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 - 51 EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
 - 101 DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDFGV
 - 151 HARQVAARRP *



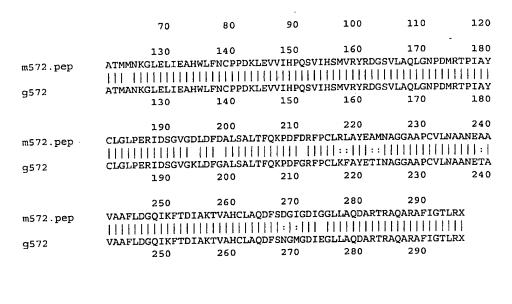
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1713>: g572.seg..

m572.pep

g572

```
atgtgcgcca tcgtcggggc ggcggggctg ccttccgcgc tcgcagcggc
         qcaaaaaggc aaaaccattt atctggcaaa caaagaaacg ctggtggttt
     51
         ccggcgcgtt gtttatggaa accgcccgcg caaacggcgc ggcagtgttg
    101
    151 cccgtcgaca gcgaacacaa cgccattttc caagttttgc cgcgcgatta
    201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
    251 ccggcggccc gtttttaaca accgatttaa gcacgttcga cagcattacg
    301 cccgagcagg cggtcaaaca ccccaattgg cgtatggggc gcaaaatctc
         cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
    401 attggctgtt caactgtccg cccgacaaac tcgaagtcgt catccatccc
    451 caatcogtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
    501 gcaactgggc aatcccgata tgcgaacgcc catcgcctat tgtttgggct
    551 tgcccgagcg catcgattcg ggtgtcggca aactcgattt cggcgcattg
         tecgegetga cettecaaaa gecegaette ggeegettee eetgeetgaa
    651 gttcgcctat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
    701 acgccgccaa cgaaaccgcc gtcgccgcct ttttggacgg acagattaag
     751 tttaccgaca ttgccaaaac cgtcgcccac tgtcttgcac aagacttttc
     801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccggacac
         gcgcacaagc gcgggcattt atcggcacac tgcgctga
This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:
g572.pep..
         MCAIVGAAGL PSALAAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
      1
         PVDSEHNAIF QVLPRDYTDR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
     51
    101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
     151 QSVIHSMVRY RDGSVLAQLG NPDMRTPIAY CLGLPERIDS GVGKLDFGAL
     201 SALTFQKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1715>:
m572.seq.
      1 ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
     51 GCAAAAAGGC AAAACCATTT ATCTGGCAAA CAAAGAAACG CTGGTGGTTT
         CCGGCGCGTT GTTTATGGAA ACCGCCCGTG CAAACGGCGC GGCAGTGCTG
     151 CCCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTGC CGCGCGATTA
     201 CGCCGGCCGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
     251 CCGGCGGCCC GTTTCTGACC GCCGATTTAA ACACGTTCGA CCGCATTACG
     301 CCCGCCCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
     351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
         ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
     451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGCTGGC
     501 GCAACTGGGC AATCCCGATA TGCGAACGCC CATCGCTTAT TGTTTGGGTT
     551 TGCCCGAGCG CATCGATTCG GGTGTCGGCG ACCTGGATTT CGACGCATTG
     601 TCCGCGCTGA CCTTCCAAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAG
         GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TGCGTATTGA
     701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCCT TTTTGGACGG ACAGATTAAG
     751 TTTACCGACA TTGCCAAAAC CGTCGCCCAC TGTCTTGCAC AAGACTTTTC
     801 AGACGGCATA GGCGATATAG GGGGGCTCTT GGCGCAAGAT GCCCGGACAC
     851 GCGCACAAGC GCGAGCATTT ATCGGCACAC TGCGCTGA
This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:
m572.pep.
         MCAIVGAVGL PSALAAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
         PVDSEHNAVF QVLPRDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
      51
         PAQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
     151 QSVIHSMVRY RDGSVLAQLG NPDMRTPIAY CLGLPERIDS GVGDLDFDAL
     201 SALTFQKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
     251 FTDIAKTVAH CLAQDFSDGI-GDIGGLLAQD ARTRAQARAF IGTLR*
m572/g572 92.9% identity in 295 aa overlap
                                                           50
                                        30
                                                  40
             MCAIVGAVGLPSALAAAQKGKTIYLANKETLVVSGALFMETARANGAAVLPVDSEHNAVF
m572.pep
             MCAIVGAAGLPSALAAAQKGKTIYLANKETLVVSGALFMETARANGAAVLPVDSEHNAIF
g572
                     10
                              20
                                        30
                                                  40
                                                                    120
                               80
                                        90
                                                 100
                                                          110
```

QVLPRDYAGRLNEHGIASIILTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS



The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1717>:

O 1		-			
a572.seq					
1	ATGTGCGCCA				
51	GCAAAAAGGC		ATCTGGCGAA		
101	CCGGCGCGTT		ACCGCCCGTG		
151	CCCGTCGACA		CGCCGTTTTC		
201	CACAGGTCGC		ACGGCATCGC		
251	CCGGCGGCCC	GTTTCTGACC	GCCGATTTAA	ACACGTTCGA	CAGCATTACG
301	CCCGACCAAG		CCCCAATTGG		
351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGGAGCTG	ATTGAAGCGC
401	ATTGGCTGTT	CAACTGTCCG	CCCGACAAAC	TCGAAGTCGT	CATCCATCCG
451	CAATCTGTGA	TACACAGCAT	GGTGCGCTAC	CGCGACGGCT	CCGTGTTGGC
501	GCAACTGGGC	AATCCCGATA	TGCGAACGCC	TATCGCTTAT	TGTTTGGGTT
551	TGCCCGAGCG	CATCGATTCG	GGTGTCGGCG	ACCTGGATTT	CGACGCATTG
601	TCCGCGCTGA	CCTTCCAAAA	GCCCGACTTT	GACCGCTTCC	CCTGCCTGAA
651	GCTCGCCTAT	GAAGCCATGA	ACGCAGGCGG	AGCCGCGCCC	TGCGTATTGA
701	ACGCCGCCAA	CGAAGCCGCC	GTCGCCGCCT	TTTTGGACGG	ACAGATTAAG
751	TTTACCGACA	TTGCCAAAAC	CGTCGCCCAT	TGTCTTTCAC	AAGACTTTTC
801	AGACGGCATA	GGCGACATAG	GGGGGCTCTT	GGCGCAAGAT	GCCCGGACAC
851	GCGCACAAGC	GCGGGCATTT	ATCGGCACAC	TGCGCTGA	

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

Correspond	, to the unima	0 4014 5044		,		
a572.pep						
1	MCAIVGAVGL	PSALAAAQKG	KTIYLANKET	LVVSGALFME	TARANGAAVL	
51	PVDSEHNAVF	QVLPRDYTGR	LNEHGIASII	LTASGGPFLT	ADLNTFDSIT	
101				IEAHWLFNCP		
151	QSVIHSMVRY	RDGSVLAQLG	NPDMRTPIAY	CLGLPERIDS	GVGDLDFDAL	
201	SALTFQKPDF	DRFPCLKLAY	EAMNAGGAAP	CVLNAANEAA	VAAFLDGQIK	
251	FTDIAKTVAH	CLSQDFSDGI	GDIGGLLAQD	ARTRAQARAF	IGTLR*	
m572/a572	98.3% id	dentity in 3	295 aa over:	lap		
			20 30		50	60
m572.pep	MCAIVGA	/GLPSALAAAQ	KGKTIYLANKE'	rlvvsgalfme:	rarangaavlp	VDSEHNAVF
	111111					
a572	MCAIVGA	JGLPSALAAAQ	KGKTIYLANKE'	TLVVSGALFME'		
		10	20 3	0 40	50	60
			80 9		110	120
m572.pep	QVLPRDY	AGRLNEHGIAS	IILTASGGPFL	TADLNTFDRIT	PAQAVKHPNWR	MGRKISVDS
• •	111111	:	1111111111	11111111111111		
a572	QVLPRDY'	rgrlnehgias	IILTASGGPFL	TADLNTFDSIT	PDQAVKHPNWR	MGRKISVDS
	-		80 9		110	120

```
160
                                             170
               130
                       140
                              150
          ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY
m572.pep
          ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY
a572
                              150
                                      160
                                             170
               130
                       140
                              210
                                      220
               190
                       200
          CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA
m572.pep
          CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLKLAYEAMNAGGAAPCVLNAANEAA
a572
                       200
                                      220
                                              230
               190
                                      280
                              270
               250
                       260
          VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGGLLAQDARTRAQARAFIGTLRX
m572.pep
          VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGGLLAQDARTRAQARAFIGTLRX
a572
                              270
                                      280
                                              290
                       260
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1719>: g573.seq.

```
atgecetgtt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
 51 gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
     aaagcagcgg caaaagtcag accetgetta teattgaegt taacetgatt
     gatgcccggc aggttaatct cggcagggtc ttccgccgtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaacccg tcggaccggt taccagcacc atcccgtaag gacggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaaccg agctggtcga
     tgttcaaaga cgcggcatcg gaattcaaaa tccgcatcac gaccttttcg
     ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tcctaccgtc ctgcggtatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc gggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac cacctcgcgg agctgcccgt ccacacggaa
601 acggatacgc gcattgtgtt cgtaaaactc gaaatggatg tcggatgccc
     cgctacgcaa ggcatccgac aaagttttat ggataaacct cggaacaggg
 701 cegtettetg cetectegte gtegatatae agggtgtgge ttteetette
751 ctcttgcccc tccccaagct cctgaagcag cgatgtcgaa cgcgaaccca
801 cccaatcgag caaacccgcc aactggtcat cctcgacaat gaccaactca
 851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcatctgggt
901 cggatcggaa accgcaaaaa atactttgtc gcccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgctcctccg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgaataac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacaccg tctga
```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

```
g573.pep..
      1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
     51 DARQVNLGRV FRRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVRTVN
    101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
         LLKGQLHPTV LRYPFFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
    201 TDTRIVFVKL EMDVGCPATQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLF
    251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNRNPCGR NRFLNLRHLG
    301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
    351 RNQCRKRLGR NDTV*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1721>: m573.seq..

```
1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
    GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTACCAAC aCaw_TTTTT TCTGAAACGG CTCAAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
    CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT
```

551 601 651 701 751 801 851 901 951 1001	ACCGCAATGG GCGCTGAAC CACCTCGCG AGCTGCCCGT CCACACGGAA ACGGATACGG GCATTGTGTT CGTAAAACTC GAAATGGATG TCCGATGCCC CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA ACCTCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCC TCTGA	
This corr	responds to the amino acid sequence <seq 1722;="" 5<="" id="" orf="" td=""><td>1/3>:</td></seq>	1/3>:
m573.pep.		
1	MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV FRRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN	
51	RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA	
101 151	LLKGQLHPAV LRYPFFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE	
201	TDTGIVFVKL EMDVRCPAAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLF	
251	LLPLPKLLKO RCRTRTHPIE QTRQLVILDN DQLNLNPCGR NGFLNLRHLC	
301	RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP	
351	RNQCRKRLGR NDTV*	
m573/g573	95.9% identity in 364 aa overlap	
2.5, 6, 50	•	
	10 20 30 40 50	60
m573.pep	MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVI	ILGRV
g573	MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQTLLIIDVNLIDARQVI	VLGRV 60
	10 20 30 40 50	60
	70 80 90 100 110	120
-573	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXFFLKRLKTEL	
m573.pep		
g573	FRRCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVRTVNRFQQQFFLERLKTEL	JDVQR
9573	70 80 90 100 110	120
	130 140 150 160 170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFFGNVQTRHYLI	JPXSK
g573	RGIGIONPHHDLFAKORROCADTEIDRLAALLKGQLHPTVLRYPFFGNVQTRHYLJ	180
	130 140 150 160 170	100
	190 200 210 220 230	240
m573.pep	LPPYRNGRINHLAELPVHTETDTGIVFVKLEMDVRCPAAQGIRQSLMDKPRNRAV	FCLLV
		$\Pi\Pi\Pi$
g573	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVGCPATQGIRQSFMDKPRNRAV	
	190 200 210 220 230	240
	250 260 270 280 290	300
	250 260 270 280 290 VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPCGRNGFLN:	
m573.pep	\D[QQVAF DFDDPDFADDAQACKTRTTF1QTAQDV1DDAQQAAAATCCGACGT	1111
g573	VDIQGVAFLFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNRNPCGRNRFLN:	LRHLG
9373	250 260 270 280 290	300
	310. 320 330 340 350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCR	KRLGR
		11111
g573	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCR	360
	310 320 330 340 350	200
m573.pep	NDTVX	
/ Э . рср		
g573	NDTVX	

a573.seq		
1	ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC	
51	GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC	
101	AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT	
151	GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA	
201	CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA	
251	CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT	
301	CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAAACCG AGCTGGTCGA	
351	TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC	
401	CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG	
451 501	AAATGTCCAA ACGCGACATT ACCTTAATCC GGGAAGCAAG CTGCCCCCTT	
551	ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA	
601	ACGGATACGG GCATTGTGTT CGTAAAACTC GAAATGGATG TCCGATGCCC	
651	CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG	
701	CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC	
751	CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA	
801	CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA	
851	ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT	
901	CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA	
951	CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC	
1001	CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT	
1051	CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA	
This correspond	s to the amino acid sequence <seq 1724;="" 573.a="" id="" orf="">:</seq>	
a573.pep		
1	MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI	
51	DAROVNLGRV FRRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN	
101	RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA	
151	LLKGQLHPAV LRYPFFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE	
201	TDTGIVFVKL EMDVRCPAAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLF	
251	LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPCGR NGFLNLRHLC	
301	RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP	
201		
351	RNQCRKRLGR NDTV*	
351	RNQCRKRLGR NDTV*	
	RNQCRKRLGR NDTV*	
351	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap	.0
351 m573/a573	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 66	0
351	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 66 MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGR	V
351 m573/a573 m573.pep	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 60 MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGR	V
351 m573/a573	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 66 MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGR	V
351 m573/a573 m573.pep	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 66 MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGR	.V V
351 m573/a573 m573.pep	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 66 MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGR	V I V
351 m573/a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V I V 0
351 m573/a573 m573.pep	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V V O O R
351 m573/a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V V O O R
351 m573/a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V O O R R
351 m573/a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V V V V V V V V V
351 m573/a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V V V V V V V V V
351 m573/a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V V V V V V V V V
351 m573/a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V O O O O K
351 m573/a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V O O R O K K K K K K K K K
351 m573/a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V O O R O K K K K K K K K K
351 m573/a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 60 60 60 60 60 60 60 60 60 60 60 60 60	V V O O R R O O K K O O K K O O
351 m573/a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V O O R R O O K K O O
351 m573/a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V O O R R O O K K O O V
351 m573/a573 m573.pep a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap	V V O O R R O O K K O O V
351 m573/a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V 0 0 R R 0 0 K K 0 0 V V
351 m573/a573 m573.pep a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap	V V 0 0 R R 0 0 K K 0 0 V V
351 m573/a573 m573.pep a573 m573.pep a573 m573.pep a573	### RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap	V I V 0 0 R I R 0 0 K I K 0 0 V I V 0
351 m573/a573 m573.pep a573 m573.pep a573 m573.pep a573 m573.pep a573	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 66 MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGF	V I V 0 0 R I R 0 0 K I K 0 0 V I V 0 0
351 m573/a573 m573.pep a573 m573.pep a573 m573.pep a573	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 60 60 60 60 60 60 60 60 60 60 60 60 60	V I V 0 0 R I R 0 0 K I K 0 0 V I V 0 0 C
351 m573/a573 m573.pep a573 m573.pep a573 m573.pep a573 m573.pep a573 m573.pep	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10 20 30 40 50 66 MPCLCRLNRNIGSFQITNLTDHNDVRVLTQERLQSSGKSQALLIIDVNLIDARQVNLGF	V I V O O R I R O O K I K O O V I V O O C I
351 m573/a573 m573.pep a573 m573.pep a573 m573.pep a573 m573.pep a573	RNQCRKRLGR NDTV* 98.6% identity in 364 aa overlap 10	V V O O R R O O O O O O

WO 99/57280 PCT/US99/09346

884

```
310
                        320
                               330
                                       340
          RIGNRKKYFVAPTENRHTVELHHLLLROHPHOHPVARIMTOIKNRITEHPRNOCRKRLGR
m573.pep
          RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR
a573
                               330
                310
                        320
                                       340
                                               350
          NDTVX
m573.pep
          11111
a573
          NDTVX
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1725>: g574.seq

```
atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
 51 attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
     tgggctggtt tgccgcccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caacaqcqqq cgcqcqgcaa gggagttggc ggaagtcgtc gacggccggc
251 cqcaatcqta tgatttgaac cttaccctcg gcaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaag cgcgggtttg gtcgatcgtg ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgttt
     caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgccgccgtc
751 qaageetatg cegecatega geageaaaac catgeatact tgageatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttcccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg cttaagggcg agaaagaagc
951 cqcgcaaacc gccgtcgagc ttgtccgccg caagcccgac cttaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttggaaa
1051 gccgatgccg acatgatgcg ttcggttatc ggacggcagc tccagcgcag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtcttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa
```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>: g574.pep..

```
MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
    KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQGK PEEGLNRLTG YMQTFPELDL
    INVVYEKSLL LKGEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDLDPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1727>: m574.seq..

```
1 ATGCGCCCGA ATCTACCAAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51 ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
    CAACAGCGGG CGCGCGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GGCGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTTGGGG
451 CTGCAAGACG GTAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGCGTTT
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651	CAATGTCGGC	AAGGCACTCG	AAGCCAACAA	AAAATGCACC	CGCGCCAACA	
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751	CAACCCTATG	CCGCCATCGA	GCAGCAAAAC	CATGCATACT	TGAGCATGGT	
801	CCCCCAGAAG	CTTTACGAAG	CCTATGCCGC	GCAGGGAAAA	CCTGAAGAAG	
	CGGCGAGAAACCC	TCTGACAGGA	TATATGCAGA	CGTTTCCCGA	ACTTGACCTG	
851	GCTTGAACCG	TGTACGAGAA	ATTCCCTCCTC	CTTAAGTGCG	AGAAAGAAGC	
901	ATCAATGTCG	TGTACGAGAA	MICCCIGCIG	CARCCCCCAC	CTTANCCCCC	
951	CGCGCAAACC	GCCGTCGAGC	TIGICCGCCG	CAAGCCCGAC	CITAACGGCG	
1001	TGTACCGCCT	GCTCGGTTTG	AAACTCAGCG	ATATGAATCC	GGCTTGGAAA	
1051	GCCGATGCCG	ACATGATGCG	TTCGGTTATC	GGACGGCAGC	TACAGCGCAG	
1101	CGTGATGTAC	CGTTGCCGCA	ACTGCCACTT	CAAATCCCAA	GTCTTTTTCT	
1151	GGCACTGCCC	CGCCTGCAAC	AAATGGCAGA	CGTTTACCCC	GAATAAAATC	
1201	GAAGTTTAA					
1201	01212					
mı ·		the emine	ocid cequer	ce <seo i<="" td=""><td>D 1728 OR</td><td>F 574>·</td></seo>	D 1728 OR	F 574>·
This corre	esponas to	me ammo a	acia sequei	ice /SEQ I	D 1728; OR	1 3/42.
m574.pep.	•					
1	MRPNLPNSLK	KADMDNELWI	ILLPIILLPV	<u>FFAMG</u> WFAAR	VDMKTVLKQA	
51	KSIPSGFYKS	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	
101	GENDKAINIH	RTMLDSPDTV	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	
. 151	LODGKMAREA	RQHLLNIYQQ	DRDWEKAVET	ARLLSHDDQT	YQFEIAQFYC	
	EL VOVVIERS	NFDVARFNVG	KALEANKKCT	RANMILGDIE	HROGNFPAAV	
201	TAVA A TEOON	HAYLSMVGEK	TAEDADDOCK	PEEGLNRLTG	YMOTFPELDL	
251	EAYAATEQQN	LKCEKEAAQT	PIENTANGON	I MCUVPILCI.	KI.SUMNIDAMK	
301	INVVYEKSLL	LKCEKEAAQI	PODMISHER	LINGVIRDIGI	KNOWEMBIRE	
351	ADADMMRSVI	GRQLQRSVMY	RCRNCHFKSQ	VFFWHCPACN	KWQIFIPNKI	
401	EV*					
m573/q573	97.8% ide	ntity in 40	2 aa overla	ρ		
			20 3		50	60
-574 man	MD DNIT DNI	STRKADMONELI	WIILLPIILLP	VFFAMGWFAAR'	VDMKTVLKQAKS:	PSGFYKS
m574.pep	1 HIII			111:11111		1111111
				(VDMKTVLKQAKS	TPSGFYKS
g574	MLPNLPN				50	60
		10	20 3	0 40	50	60
		70	^^			120
			80 9		110	
m574.pep	LDALVDRI	NSGRAARELAE'	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRT	MLDSPDTV
m574.pep	LDALVDRI	NSGRAARELAE'	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRT	MLDSPDTV
	1111111	NSGRAARELAE'	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI 	MLDSPDTV
m574.pep	1111111	nsgraarelae nsgraarelae	VVDGRPQSYDL VVDGRPQSYDL	NLTLGKLYRQR NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI	MLDSPDTV
	1111111	nsgraarelae sgraarelae	VVDGRPQSYDL	NLTLGKLYRQR NLTLGKLYRQR	GENDKAINIHRTI 	MLDSPDTV MLDSPDTV
	 LDALVDRI	NSGRAARELAE NSGRAARELAE 70	VVDGRPQSYDL VVDGRPQSYDL 80 9	NLTLGKLYRQR NLTLGKLYRQR 0 100	GENDKAINIHRTI GENDKAINIHRTI 110	MLDSPDTV MLDSPDTV 120
	 LDALVDRI	NSGRAARELAE NSGRAARELAE 70	VVDGRPQSYDL	NLTLGKLYRQR NLTLGKLYRQR 0 100 0 160	GENDKAINIHRTI GENDKAINIHRTI 110	MLDSPDTV MLDSPDTV 120
	GEKRARV	NSGRAARELAE NSGRAARELAE 70 130 1 LIFELAONYOSA	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL	NLTLGKLYRQR NLTLGKLYRQR 0 100 0 160 GLQDGKMAREA	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI	MLDSPDTV MLDSPDTV 120 180 DWEKAVET
g574	 LDALVDRI 	NSGRAARELAE NSGRAARELAE 70 130 1 LFELAQNYQSA	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL	NLTLGKLYRQR NLTLGKLYRQR 0 100 0 160 GLQDGKMAREA	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI	MLDSPDTV LDSPDTV 120 180 DWEKAVET
g574	 LDALVDRI 	NSGRAARELAE NSGRAARELAE 70 130 1 LFELAQNYQSA	VVDGRPQSYDL	NLTLGKLYRQR NLTLGKLYRQR 0 100 0 160 GLQDGKMAREA :	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI	MLDSPDTV MLDSPDTV 120 180 DWEKAVET
g574 m574.pep	 LDALVDRI GEKRARV GEKRARV	NSGRAARELAE	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL	NLTLGKLYRQR NLTLGKLYRQR 0 100 0 160 GLQDGKMAREA :	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI	MLDSPDTV LDSPDTV 120 180 DWEKAVET
g574 m574.pep	 LDALVDRI GEKRARV GEKRARV	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR NLTLGKLYRQR 0 100 0 160 GLQDGKMAREA :	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET
g574 m574.pep	 LDALVDRI GEKRARV: GEKRARV	NSGRAARELAE NSGRAARELAE 70 130 1 LFELAQNYQSA LFELAQNYQSA 130 1	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230	MLDSPDTV
g574 m574.pep g574	 LDALVDRI GEKRARV: GEKRARV:	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI	MLDSPDTV
g574 m574.pep	 LDALVDRI GEKRARV: GEKRARV:	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE
g574 m574.pep g574 m574.pep	 LDALVDRI GEKRARV: GEKRARV:	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE
g574 m574.pep g574	 LDALVDRI GEKRARV GEKRARV ARLLSHD :	NSGRAARELAE NSGRAARELAE 70 130 1 LFELAQNYQSA LFELAQNYQSA 130 1 190 2 DQTYQFEIAQF	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE
g574 m574.pep g574 m574.pep	 LDALVDRI GEKRARV GEKRARV ARLLSHD :	NSGRAARELAE NSGRAARELAE 70 130 1 LFELAQNYQSA LFELAQNYQSA 130 1 190 2 DQTYQFEIAQF :	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI	MLDSPDTV
g574 m574.pep g574 m574.pep	 LDALVDRI GEKRARV GEKRARV ARLLSHD :	NSGRAARELAE	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLINIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240
g574 m574.pep g574 m574.pep	 LDALVDRI GEKRARV GEKRARV ARLLSHD :	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 300
g574 m574.pep g574 m574.pep	GEKRARV GEKRARV GEKRARV ARLLSHD : AQLLSHD	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEGLNRLTGYM	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 300 QTFPELDL
g574 m574.pep g574 m574.pep g574	 LDALVDRI GEKRARV: GEKRARV: ARLLSHD: : AQLLSHD	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEGLNRLTGYM	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 300 QTFPELDL
g574 m574.pep g574 m574.pep g574	 LDALVDRI GEKRARV: GEKRARV: ARLLSHD: : AQLLSHD	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEGLNRLTGYM	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 300 QTFPELDL
g574 m574.pep g574 m574.pep g574	GEKRARV: GEKRARV: ARLLSHD :: AQLLSHD HRQGNFP HRQGNFP	NSGRAARELAE' NSGRAARELAE' 70 130 1 LFELAQNYQSA LFELAQNYQSA 130 1 190 2 DQTYQFEIAQF : 190 2 AAVEAYAAIEQ AAVEAYAAIEQ	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEEGLNRLTGYM	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 300 QTFPELDL
g574 m574.pep g574 m574.pep g574	GEKRARV: GEKRARV: ARLLSHD :: AQLLSHD HRQGNFP HRQGNFP	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEEGLNRLTGYM	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 300 QTFPELDL
g574 m574.pep g574 m574.pep g574	GEKRARV GEKRARV ARLLSHD :: AQLLSHD HRQGNFP HRQGNFP	NSGRAARELAE' NSGRAARELAE' 70 130 1 LFELAQNYQSA LFELAQNYQSA 130 1 190 2 DQTYQFEIAQF : EQTYQFEIAQF 190 2 250 2 AAVEAYAAIEQ AAVEAYAAIEQ 250 2	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEGLNRLTGYM	MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 300 QTFPELDL
g574 m574.pep g574 m574.pep g574 m574.pep	 LDALVDRI GEKRARV GEKRARV ARLLSHD : AQLLSHD HRQGNFP 	NSGRAARELAE' NSGRAARELAE' 70 130	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 60 27 QNHAYLSMVGE QNHAYLSMVGE 60 27	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEGLNRLTGYM PEEGLNRLTGYM 290 350	MLDSPDTV MLDSPDTV 20 180 DWEKAVET DWEKAVET 180 240 NMILGDIE 240 300 QTFPELDL QTFPELDL 300
g574 m574.pep g574 m574.pep g574	 LDALVDRI GEKRARV GEKRARV ARLLSHD : AQLLSHD HRQGNFP HRQGNFP	NSGRAARELAE' NSGRAARELAE' 70 130	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 60 27 QNHAYLSMVGE QNHAYLSMVGE 60 27 20 33 OTAVELVRRKF	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI EPEEGLNRLTGYM 1990 350 KKLSDMNPAWKAD	MLDSPDTV MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 300 QTFPELDL QTFPELDL 300 ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep	GEKRARV GEKRARV ARLLSHD ARLLSHD HRQGNFP HRQGNFP HRQGNFP	NSGRAARELAE' NSGRAARELAE' 70 130	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 60 27 QNHAYLSMVGE QNHAYLSMVGE 60 27 20 33 QTAVELVRKF	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI EPEEGLNRLTGYM 1990 350 KKLSDMNPAWKAD	MLDSPDTV MLDSPDTV 20 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 QTFPELDL QTFPELDL 300 360 ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep	GEKRARV: GEKRARV: GEKRARV: ARLLSHD: : AQLLSHD: HRQGNFP: HRQGNFP	NSGRAARELAE	VVDGRPQSYDL	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI PEEGLNRLTGYM 190 350 KLSDMNPAWKAD	MLDSPDTV MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE 240 300 QTFPELDL QTFPELDL QTFPELDL ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep g574	GEKRARV: GEKRARV: GEKRARV: ARLLSHD: : AQLLSHD: HRQGNFP: HRQGNFP	NSGRAARELAE	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 60 27 QNHAYLSMVGE QNHAYLSMVGE 60 27 20 33 QTAVELVRKF	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI PEEGLNRLTGYM 190 350 KLSDMNPAWKAD	MLDSPDTV MLDSPDTV 20 180 DWEKAVET DWEKAVET 180 240 NMILGDIE NMILGDIE 240 QTFPELDL QTFPELDL 300 360 ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep g574	GEKRARV: GEKRARV: GEKRARV: ARLLSHD: : AQLLSHD: HRQGNFP: HRQGNFP	NSGRAARELAE	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 60 27 QNHAYLSMVGE QNHAYLSMVGE 20 33 QTAVELVRKF	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI EPEEGLNRLTGYM 1990 350 KKLSDMNPAWKAD ::	MLDSPDTV MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE 240 300 QTFPELDL QTFPELDL QTFPELDL ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep g574	GEKRARV: GEKRARV: GEKRARV: ARLLSHD: AQLLSHD: HRQGNFP: HRQGNFP: INVVYEK: INVVYEK:	NSGRAARELAE' NSGRAARELAE' 70 130	VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE 33 40 33	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI 230 290 PEEGLNRLTGYM PEEGLNRLTGYM 290 KLSDMNPAWKAD KLSDMNPAWKAD KLSDLDPAWKAD	MLDSPDTV MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE 240 300 QTFPELDL QTFPELDL QTFPELDL ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep g574 m574.pep	GEKRARV: GEKRARV: GEKRARV: ARLLSHD: ARLLSHD: HRQGNFP: HRQGNFP: INVVYEK: INVVYEK: GROLORS	NSGRAARELAE' NSGRAARELAE' 70 130	VVDGRPQSYDL VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE 33 80 39 ESQVFFWHCPAC	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM 290 KLSDMNPAWKAD :: KLSDLDPAWKAD	MLDSPDTV MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE 240 300 QTFPELDL QTFPELDL QTFPELDL ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep g574	GEKRARV: GEKRARV: GEKRARV: ARLLSHD: ARLLSHD: HRQGNFP: HRQGNFP: INVVYEK: INVVYEK: GROLORS	NSGRAARELAE' NSGRAARELAE' 70 130	VVDGRPQSYDL VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE 33 80 39 ESQVFFWHCPAC	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM 290 KLSDMNPAWKAD :: KLSDLDPAWKAD	MLDSPDTV MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE 240 300 QTFPELDL QTFPELDL QTFPELDL ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep g574 m574.pep	GEKRARV: GEKRARV: GEKRARV: ARLLSHD :: AQLLSHD HRQGNFP HRQGNFP INVVYEK INVVYEK GRQLQRS	NSGRAARELAE' NSGRAARELAE' 70 130	VVDGRPQSYDL VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL YCELAQAALFK YCELAQAALFK 00 21 YCELAQAALFK 00 27 QNHAYLSMVGE QNHAYLSMVGE QTAVELVRKF QTAVELVRKF 20 33 80 39 SQVFFWHCPAC	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI KALEANKKCTRAI 230 290 PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM RUSDLDPAWKAD	MLDSPDTV MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE 240 300 QTFPELDL QTFPELDL QTFPELDL ADMMRSVI
g574 m574.pep g574 m574.pep g574 m574.pep g574 m574.pep	GEKRARV: GEKRARV: GEKRARV: ARLLSHD :: AQLLSHD HRQGNFP HRQGNFP INVVYEK INVVYEK GRQLQRS	NSGRAARELAE' NSGRAARELAE' 70 130	VVDGRPQSYDL VVDGRPQSYDL VVDGRPQSYDL 80 9 40 15 GLVDRAEQIFL GLVDRAEQIFL 40 15 00 21 YCELAQAALFK YCELAQAALFK 00 21 GOUDHAYLSMVGE QNHAYLSMVGE QNHAYLSMVGE QTAVELVRKF QTAVELVRKF 20 33 80 39 SQVFFWHCPAC	NLTLGKLYRQR	GENDKAINIHRTI GENDKAINIHRTI 110 170 RQHLLNIYQQDRI RQHLLNIYQQDRI 170 230 KALEANKKCTRAI 230 290 PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM PEEGLNRLTGYM 290 KLSDMNPAWKAD :: KLSDLDPAWKAD 350 EEVX	MLDSPDTV MLDSPDTV MLDSPDTV 120 180 DWEKAVET DWEKAVET 180 240 NMILGDIE 240 300 QTFPELDL QTFPELDL QTFPELDL ADMMRSVI

a574

886

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1729>:

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a574.seq
              ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
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              ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
          51
              TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
             AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
             CAACAGCGGG CGCGCGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
              CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
              GGCGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
              CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
              ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTTTGGGG
              CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
             CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGGCTGC
         501
             TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
         551
             GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG CCGCGCGTTT
             CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
         651
             TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
             GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
             CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
         801
             GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
         851
             ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
         901
             CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGGCG
         951
        1001
              TGTACCGCCT GCTTGGTTTG AAACTCAGCG ATTTGGATCC GGCTTGGAAA
              GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
        1051
              CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTTCT
        1101
              GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
        1151
        1201
              GAAGTTTAA
This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:
              MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
              KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
          51
              GENDKAINMH OTLLDSPDTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
         101
              LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
              ELAQAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
              EAYAAIEQQN HAYLSMVGEK LYEAYAAQGK PEEGLNRLTG YMQTFPELDL
              INVVYEKSLL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDLDPAWK
              ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
         351
              EV*
         401
                97.5% identity in 402 aa overlap
    m574/a574
                                                    40
                                                             50
                                                                       60
                                 20
                                           30
                MRPNLPNSLKKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
    m574.pep
                 MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
     a574
                                                    40
                                                             50
                                 20
                                           30
                                                                       60
                                 80
                                           90
                                                   100
                                                            110
                                                                      120
                 LDALVDRNSGRAARELAEVVDGRPQSYDLNLTLGKLYRQRGENDKAINIHRTMLDSPDTV
    m574.pep
                 LDALVDRNSGRAARELAEVVDGRPQSYDLNLTLGKLYRQRGENDKAINMHQTLLDSPDTT
     a574
                                                   100
                        70
                                 80
                                           90
                                                            110
                                                   160
                                                            170
                                          150
                       130
                                 140
                 GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET
    m574.pep
                 GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET
     a574
                                          150
                                                   160
                                                            170
                                                                      180
                       130
                                 140
                                                                      240
                        190
                                 200
                                          210
                                                   220
                                                             230
                 ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE
    m574.pep
```

ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE

	190	200	210	220	230	240
	250	. 260	270	280	290	300
m574.pep	HRQGNFPAAVEAYA	AIEQQNHAYI	LSMVGEKLYE	AYAAQGKPEEG	SLNRLTGYMQ'	FFPELDL
		1111111111				
a574	HRQGNFPAAVEAYA	AIEQQNHAYI	LSMVGEKLYE	AYAAQGKPEEG	LNRLTGYMQ'	rfpeldl
	250	260	270	280	290	300
			-			
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCE	KEAAQTAVEI	LVRRKPDLNG	/YRLLGLKLSI	MNPAWKADA	DMMRSVI
1 1		111111111	11111111	11111111111	::	
a574	INVVYEKSLLLKCE	KEAAQTAVEI	LVRRKPDLNG	/YRLLGLKLSI	LDPAWKADA	DMMRSVI
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GROLORSVMYRCRN	CHFKSOVFFW	HCPACNKWQ	FTPNKIEVX		
mo / 1. pop	111111111111111	mminn				
a574	GROLORSVMYRCRN	CHEKSOVEFW	HCPACNKWQ	TTPNKIEVX		
40.1	370	380	390	400		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1731>: (partial) g575.seq

```
..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
      ccgtcaaaca gtccgctttc ggtttcttct tcggcagaaa cctgttcgac
      aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
101
       gttcggaaac ggtgttaccg gtttcgtcgg tcggcgtgtc gatggcagaa
151
      geggeggett ettggggggg eggattegge ageggtttee gatgeggeag
       tatttgcagc gggtacaggt ccgggttggc gttctgtcgc cgaagccgga
251
       gtttcggaca ctgcgggttt gggttcgggt cgaacggccg gtttttccgc
301
      ttttgcttcg ggcgcggcaa cttttgcttc aggtttttca accggttttt
351
       cgacaggttt ctctatcggt ttctccacag ttgcctgttt ggacggttca
401
       gacggcatgg atgcagtttc ggctttgggt ttcgccgttt gcggtttggg
451
       ttgttccgct ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
501
551
       tcggaatgtg a*
```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

(partial) g575.pep

- ..MPCLRRQAAR CTNRRTDRQT VRFRFLLRQK PVRQVRQRVR RQLHWLFPQQ 1
- VRKRCYRFRR SACRWQKRRL LGGADSAAVS DAAVFAAGTG PGWRSVAEAG 51
- VSDTAGLGSG RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDGS 101
- DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1733>:

1	ATGGTTTCGG	GCGAGGAAGC	CTTCAGGAAG	CCTGCCAGTC	CGGAGGGTGA
51	GGCAGGTTTT	GCGGAAGCTG	TTTCTTCTGT	GCCGATATGG	TTGTTTGAGG
101	GCAGGTTGTC	GGAGAAATCG	GTATCGACGG	TTTCCGGTTT	GTTTTCGGCA
151	GTTTGGGCGA	CAGATTCCGG	TTCGGGCGTG	TCGATGACGA	TTTCGACAGG
201	GTTGTACGGG	TTGAAGGTCT	${\tt CGGGCTCGTA}$	CACGCTGTCT	GTGGATTCGA
251	TGGCGTTCCA	ATCGGCATCC	GCGCGTTTTT	GGGTTTCTTC	ATCCTGCGTA
301	AGTGCGCCGG			GCTGCCAGGC	
351	CAAGTCGATG	CGGTTGGAAG	GCGTATCGGT	TTCGACATCG	AACGTTTGTT
401	TTGCCGATAA	CTCTTCTTCA	GATTCCCCAT	CTAAGGCAAG	TGTGTCGTTT
451	ACATCGTTTT	TCGGAGCGGG	TTCGGGCGTT	GCCGGAGTTT	CGACTTCGGC
501	AAAGGTGATT	TCTATGCCGT	CGTCTGCCGC	GTCGTCAAGG	TCAGGCTCTT
551	CCTCAGGGAC	GGATTCTTCG	GTACGGCGCG	CGCGTTTGGA	TTGGGCAAGG
601	CGCAAAAGCA	••		GCGCCTCCGC	
651	CAAGGTGTAC	GAACCGCCGA	ACAGACCGTC	AAACAGTCCG	CTTTCGGTTT
701	CTTCTTCGGC	AGAAACCTGT	TCGACAGGTT	CGGAAACGGC	GTTACCGGTT
751	TCGTCGGTCG	GCGTGTCGAT	GGCAGAAGCG	GCGGCTTCTT	GGGGGGCGGA
801	TTCGGCAGCG	GTTTCCGATG	CGGCAGTATT	TGCAGCGGGT	ACAGGTTCGG
851	GTCGAACGGC	CGGTTTTTCC	GCTTTTGCTT	CGGGCGCGGC	AACTTTTGCT
901	TCAGGTTTTT	CAACCGGTTT	CTCTACCGTT	GCCTGTTTGG	ACGGTTCGGA
951	CGGCATGGAT	GCGGTTTCGG	CTTTGGGTTT	CGCCGTTTGC	GGTTTGGGTT
1001	GTTCCGCTTT	GATCCTGTTC	AGATTCGGAA	TGTGA	

```
This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:
m575.pep
        MVSGEEAFRK PASPEGEAGF AEAVSSVPIW LFEGRLSEKS VSTVSGLFSA
     51 VWATDSGSGV SMTISTGLYG LKVSGSYTLS VDSMAFQSAS ARFWVSSSCV
    101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
    151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
    201 RKSSSRAINA APPPASSKVY EPPNRPSNSP LSVSSSAETC STGSETALPV
    251 SSVGVSMAEA AASWGADSAA VSDAAVFAAG TGSGRTAGFS AFASGAATFA
    301 SGFSTGFSTV ACLDGSDGMD AVSALGFAVC GLGCSALILF RFGM*
          70.2% identity in 114 aa overlap
m575/g575
                                        270
                       250
                                260
              240
           SSAETCSTGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTG------
m575.pep
                                      LHWLFPQQVRKRCYRFRRSACRWQKRRLLGGADSAAVSDAAVFAAGTGPGWRSVAEAGVS
g575
                                          80
                         60
                                  70 .
                                                      320
                                      309
                                             310
                     290
                              300
            -----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA
m575.pep
                 DTAGLGSGRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA
g575
                    120 130 . 140
                110
                          340
           VCGLGCSALI-----LFRFGMX
m575.pep
           |||||||
           VCGLGCSALIFLGAAALILFRFGMX
a575
                170
                       180
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1735>:

```
a575.seq
         ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
      51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
     101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
     151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
     201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCGA
     251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
     301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTCGAAATC
     351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
         TTGCCGACAA CTCTTCTTCA GATTCCCCAT CTAAGGCAAG TGTGTCGTTT
         ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
         AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
         CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGGA TTGGGCAAGG
     551
     601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG
     651 CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
     701 AAACCTGTTC GACAGGTTCG GAAACGGCGT TACCGGTTTC GTCGGTCGGC
     751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
     801 TTCCGATGCG GCAGTATTTG CAGCGGGTAC AGGTTCGGGT CGAACGGCCG
     851 GTTTTCCGC TTTTGCTTCG GGCGCGGCAA CTTTTGCTTC AGGTTTTTCA
     901 ACCGGTTCT CTACCGTTGC CTGTTTGGAC GGTTCGGACG GCATGGATGC
         GGTTTCGGCT TTGGGTTTCG CCGTTTGCGG TTTGGGTTGT TCCGCTTTGA
     951
         TCCTGTTCAG ATTCGGAATG TGA
    1001
```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

```
a575.pep
         MVSGEEAFRK PASPEGEAGF AEAVSSVPIW LFEGRLSEKS VSTVSGLFSA
      51 VWATDSGSGV SMTISTGLYG LKVSGSYTLS VDSMAFQSAS ARFWVSSSCV
     101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
    151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
     201 RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
     251 VSMAEAAASW GADSAAVSDA AVFAAGTGSG RTAGFSAFAS GAATFASGFS
     301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *
```

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889

```
98.8% identity in 344 aa overlap
    m575/a575
                                 20
                                         30
                                                  40
                                                           50
                                                                     60
                MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV
    m575.pep
                MVSGEEAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV
    a575
                       10
                                 20
                                         30
                                                  40
                                                           50
                                 80
                                         90
                                                 100
                                                          110
                                                                   120
                SMTISTGLYGLKVSGSYTLSVDSMAFQSASARFWVSSSCVSAPDKMPFCAAARLSKSKSM
    m575.pep
                SMTISTGLYGLKVSGSYTLSVDSMAFQSASARFWVSSSCVSAPDKMPFCAAARLSKSKSM
    a575
                                80
                                140
                                        150
                                                 160
                RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR
    m575.pep
                RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSSAASSR
    a575
                      130
                                140
                                        150
                                                 160
                                                          170
                                                                   180
                      190
                                200
                                        210
                                                 220
                                                          230
                                                                   240
                SGSSSGTDSSVRRARLDWARRKSSSRAINAAPPPASSKVYEPPNRPSNSPLSVSSSAETC
    m575.pep
                SGSSSGTDSSVRRARLDWARRKSSSRAINAAPPPASSKVYEPPN----SPLSVSSSAETC
    a575
                                200
                                        210
                                                 220
                                                              230
                      190
                      250
                                260
                                        270
                                                 280
                STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA
    m575.pep
                STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA
    a575
                          250
                                   260
                                            270
                                                     280
                                                              290
                                320
                                        330
                                                 340
                      310
                SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX
    m575.pep
                SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX
    a575
                          310
                                   320
                                            330
                 300
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1737>:
    g576.seq..(partial)
             ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
          1
               ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
          51
               qcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
         101
               ttcctgcagg agcagcaggc taaagccgta gaaaaacaca aggcqqatqc
         151
               gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
         201
               aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
         251
         301
               cagggtgaag gcaaacagcc gacaaaagac gacatcgtta ccgtggaata
               cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
         351
               gcggcccggc caccttccct ttgagccaag tgattccggg ttggaccgaa
         401
               ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
         451
         501
               caaccttgcc taccgcgaac agggtgcggg cgaaaaaatc ggtccgaacg
               ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaac
         551
               gcgcccgcca agcagccgga tcaagtcgac atcaaaaaag taaattaa
This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:
    g576.pep..(partial)
             ..MGVDIGRSLK QMKEQGAEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
          1
               FLOEOOAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
          51
               QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
         101
               GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
         151
               APAKQPDQVD IKKVN*
         201
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1739>:

m576.seq.. (partial)

..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

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890

```
GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
51
      CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
101
151
      GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
      AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
201
      TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
251
      CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
301
      CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
351
      TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
401
      GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
451
      AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
501
      GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
551
      AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
601
      CATCAAAAAA GTAAATTAA
651
```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

```
m576.pep.. (partial)
         ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
       1
            AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVKTTASG
            LOYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
            VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
```

KIGAPENAPA KQPAQVDIKK VN*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

```
m576/q576 97.2% identity in 215 aa overlap
```

m576.pep	10 MQQASYAMGVDIC MGVDIC	11111111111	111111111111111111111111111111111111	40 EAMQAVYDGKE : DAMQAVYDGKE 30		
	70	80	90	100	110	120
m576.pep	EQQAKAVEKHKAI	DAKANKEKGEA	FLKENAAKD	GVKTTASGLQY	KITKQGEGK	QPTKDDIV
-576	EQQAKAVEKHKAI	 	{	CVKTTA SCI.OV	/	
g576	60	70	80	90	100	110
5 D C	130	140	150	160	170	180
m576.pep	TVEYEGRLIDGTV	LILILILIII	·	PGW1EGVQLL1	LILLILLI	IIIIIIII
g576	TVEYEGRLIDGTV	FDSSKANGGE	PATFPLSQVI	PGWTEGVRLL	KEGGEATFYI	PSNLAYRE
3 -	120	130	140	150	160	170
	190	200	210	220		
m576.pep	OGAGDKIGPNATI				ζ	
mo.orpop		111111111	11111111	e îmana	1	
g576	QGAGEKIGPNATI				ζ	
	180	190	200	210		

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1741>:

```
a576.seg
         ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
       1
         ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
      51
         CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
     101
         ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
     151
     201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
     251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
     301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
     351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
     401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
     451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
     501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
     551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
```

```
GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
         601
             AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
         651
             GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
         701
             AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
         751
             CATCAAAAAA GTAAATTAA
This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:
    a576.pep
             MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
           1
             MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEO
          51
             AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVKTTASG
         101
             LOYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
         151
             VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
             KIGAPENAPA KQPAQVDIKK VN*
         251
                99.5% identity in 222 aa overlap
    m576/a576
                                                           20
                                                  10
                                                                    30
                                          MQQASYAMGVDIGRSLKQMKEQGAEIDLKV
    m576.pep
                                           CGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGVDIGRSLKQMKEQGAEIDLKV
    a576
                                40
                                         50
                       40
                                50
                                         60
                                                  70
                                                           80
                FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
    m576.pep
                FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
    a576
                               100
                                        110
                                                 120
                                                          130
                       90
                               110
                                        120
                                                 130
                                                          140
                                                                  150
                      100
                KDGVKTTASGLQYKITKQGEGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ
    m576.pep
                KDGVKTTASGLQYKITKQGEGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ
     a576
                                        170
                                                 180
                                                          190
                                                                   200
                      150
                               160
                                                 190
                                                          200
                                        180
                                                                   210
                               170
                      160
                VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
    m576.pep
                VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
     a576
                                        230
                                                 240
                                                          250
                                                                   260
                      210
                               220
                      220
                KQPAQVDIKKVNX
    m576.pep
                KQPAQVDIKKVNX
     a576
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1743>: g576-

-1.sec					
1	ATGAACACCA	TTTTCAAAAT			
51	ACTTTCCGCC		AAGAAGCCGC		
101	CTGCCGCCGC	TTCTGCCGCG	CAGGGCGACA	CCTCTTCAAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC		GACATCGGAC	
201	ACAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGATG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	000011001110	TGATGATGAA			
351	AGAAAAACAC	AAGGCGGATG	CGAAGGCCAA	CAAAGAAAAA	GGCGAAGCCT
401		AAATGCCGCC			
451		AAATCACCAA			
501	CGACATCGTT	ACCGTGGAAT			
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	CCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACGG	CTTCTGAAAG	AAGGCGGCGA
651	AGCCACGTTC	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG
701	GCGAAAAAAT	CGGTCCGAAC		TATTTGACGT	
751	AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	ATCAAGTCGA
801	CATCAAAAAA	GTAAATTAA			

```
This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:
q576-1.pep
         MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASAA QGDTSSIGST
      1
         MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
     51
         AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVKTTASG
    101
         LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
    151
         VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
    251 KIGAPENAPA KQPDQVDIKK VN*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1745>:
m576-1.seg
        ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
      1
        ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
     51
        CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
    101
         ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
    201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
    251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
         GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
    301
    351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
    401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
         CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
    451
         CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
    551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
    601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
         AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
    651
         GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
    701
         AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
         CATCAAAAAA GTAAATTAA
This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:
m576-1.pep
         MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
      1
         MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
     51
         AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVKTTASG
        LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
         VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
    251 KIGAPENAPA KQPAQVDIKK VN*
                97.8% identity in 272 aa overlap
q576-1/m576-1
                                              40
                                                        50
                   10
                            20
                                     30
            MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASAAQGDTSSIGSTMQQASYAMGV
g576-1.pep
            MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV
m576-1
                                      30
                            20
                   10
                                                                120
                             ឧ០
                                      90
                                             100
            DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH
q576-1.pep
            DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH
m576-1
                                              100
                                                       110
                                                                120
                            80
                                     90
                   70
                  130
                                     150
                                              160
                                                       170
            KADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQGEGKQPTKDDIVTVEYEGRLID
g576-1.pep
            KADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQGEGKQPTKDDIVTVEYEGRLID
m576-1
                                                       170
                                                                180
                  130
                           140
                                     150
                                              160
                           200
                                     210
                                              220
                                                       230
                   190
            GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN
a576-1.pep
            GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN
m576-1
                                              220
                           200
                                     210
                  190
                            260
                  250
            ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVNX
a576-1.pep
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1747>: a576-1.seq

270

ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVNX

250

260

m576-1

			~~ ~~ ~~ ~~ ~		
1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTTCCGCG	CAGGGCGACA	CCTCTTCGAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	GATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	GCAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCTCAGGAAG	TCATGATGAA	ATTCCTTCAG	GAACAACAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA	TAAAGAAAAA	GGCGAAGCCT
401	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGC
451	CTGCAATACA	AAATCACCAA	ACAGGGCGAA	GGCAAACAGC	CGACCAAAGA
501	CGACATCGTT	ACCGTGGAAT	ACGAAGGCCG	CCTGATTGAC	GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	TCACCTTCCC	TTTGAGCCAA
601	GTGATTCTGG	GTTGGACCGA	AGGCGTACAG	CTTCTGAAAG	AAGGCGGCGA
651	AGCCACGTTC	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG
701	GCGACAAAAT	CGGCCCGAAC	GCCACTTTGG	TATTTGATGT	GAAACTGGTC
751	AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
801	CATCAAAAAA	GTAAATTAA			

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>: a576-1.pep

- 1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVKTTASG
 151 LOYKITKOGE GKOPTKDDIV TVEYEGRIID GTVFDSSKAN GGPVTFPLSO
- 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
- 251 KIGAPENAPA KQPAQVDIKK VN*

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLS	AALALSACGK	KEAAPASASEI	PAAASSAQGD	TSSIGSTMQQ	ASYAMGV
			11111111111		111111111	1111111
m576-1	MNTIFKISALTLS	AALALSACGKI	KEAAPASASEE	PAAASSAQGD	TSSIGSTMQQ	ASYAMGV
•	. 10.	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQG	AEIDLKVFTE	AMQAVYDGKE I	KMTEEQAQE	VMMKFLOEOO	AKAVEKH
	1111111111111111					ППП
m576-1	DIGRSLKQMKEQG	AEIDLKVFTE	AMQAVYDGKEI	KMTEEOAOE	VMMKFLOEOO	AKAVEKH
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEA	FLKENAAKDGV	KTTASGLQYK	ITKOGEGKO	TKDDIVTVE	YEGRLID
•	1111111111111					
m576-1	KADAKANKEKGEA	FLKENAAKDGV	KTTASGLQYK	ITKOGEGKO	TKDDIVTVE	
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGP	TFPLSQVILG	WTEGVQLLKE	GGEATFYIPS	NLAYREOGA	SDKIGPN
			111111111			
m576-1	GTVFDSSKANGGP	TFPLSQVIPG	WTEGVQLLKE	GGEATFYIPS	NLAYREOGA	DKIGPN
	190	200	210	220	230	240
	250	260	270 .			
a576-1.pep	ATLVFDVKLVKIGA	APENAPAKQPA	QVDIKKVNX			
			111111111			
m576-1	ATLVFDVKLVKIGA	PENAPAKOPA	QVDIKKVNX			
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTTCCGCG	CAGGGCGACA	CCTCTTCGAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	GATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	GCAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCTCAGGAAG		ATTCCTTCAG		CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA		
401	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG		TGCTTCCGGC
451	CTGCAATACA	AAATCACCAA	ACAGGGCGAA		CGACCAAAGA
501	CGACATCGTT	ACCGTGGAAT	ACGAAGGCCG		GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	• • • • • • • • • • • • • • • • • • • •	TTTGAGCCAA
601	GTGATTCTGG	GTTGGACCGA			AAGGCGGCGA
651	AGCCACGTTC	TACATCCCGT	CCAACCTTGC		CAGGGTGCGG
701	GCGACAAAAT	CGGCCCGAAC	GCCACTTTGG		GAAACTGGTC
751	AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
801	CATCAAAAAA	GTAAATTAA			
	esponds to	tha amina i	noid comen	ce <seo i<="" td=""><td>D 1748: OR</td></seo>	D 1748: OR
s corr	esponds to	me ammo a	acia sequen		ν 1770, ON

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>: a576-1.pep

```
1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
```

201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV

251 KIGAPENAPA KQPAQVDIKK VN*

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSA	ALALSACGK	(EAAPASASEP)	AAASSAQGD1	rssigstmqq <i>p</i>	ASYAMGV
20.0 2.7-2	111111111111111111111111111111111111111	1111111111				111111
m576-1	MNTIFKISALTLSA	ALALSACGK				ASYAMGV
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGA	EIDLKVFTE <i>F</i>	MQAVYDGKEI	KMTEEQAQE	VMMKFLQEQQ <i>I</i>	KAVEKH
m576-1	DIGRSLKOMKEOGA			KMTEEQAQE	VMMKFLQEQQ#	KAVEKH
	70	80	90	100	110	120
			150	1.60	170	180
	130	140	150	160		
a576-1.pep	KADAKANKEKGEAF	LKENAAKDG	KTTASGLQYK	T.T.K.ÖGE.G.K.Ö.	TITITITITITI	
		1				
m576-1		LKENAAKDG 140	7KIIASGLQIK 150	160	170	180
	130	140	150	100	1,0	100
	190	200	210	220	230	240
-F76 1 man	GTVFDSSKANGGPV				SNLAYREOGA	SDKIGPN
a576-1.pep	111111111111111	11111111			шшшіш	
m576-1	GTVFDSSKANGGPV'	TFPLSOVIP	WTEGVOLLKE	GGEATFYIP	SNLAYREQGA	GDKIGPN
1113 / 0-1	190	200	210	220	230	240
	250	260	270 .			
a576-1.pep	ATLVFDVKLVKIGA	PENAPAKQP	AQVDIKKVNX			
		11111111	111111111			
m576-1	ATLVFDVKLVKIGA	PENAPAKQP	AQVDIKKVNX			•
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

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hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, J. Immunol 143:3007; Roberts et al. 1996, AIDS Res Human Retroviruses 12:593; Quakyi et al. 1992, Scand J Immunol Suppl 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1749>:

```
g577.seq..
      atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
         tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
         ttaaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcgtt
    151 tttatttacg gagcaaacat gaaacttatc tataccgtca tcaaaatcat
     201 tatcctgctg ctcttcctgc tgcttgccgt cattaatatg gatgccgtta
     251 ccttttccta tcttccgggg cagagtgtca atctgccgct gattgtcgta
     301 ttgttcggcg cgtttgtcgt cggcatcgtg ttcggaatgt ttgccctgtt
     351 cgggcggctg ctgtccttgc gcggcgaaaa cagccgcctg cgtgcggaag
     401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
     451 caaaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
         MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRSCPCGV
      1
         FIYGANMKLI YTVIKIIILL LFLLLAVINM DAVTFSYLPG QSVNLPLIVV
     51
         LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
         ONAAESAKQP *
     151
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1751>:

```
m577.seq.
      1 ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
     51 TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
    101 TTAAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
    151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
    201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAATACG GATGCCGTTA
    251 CCTTTTCCTA CCTGCCGGGG CAAAAATTCG ATTTGCCGCT GATTGTCGTA
    301 TTGTTCGGCG CATTTGTAGT CGGTATTATT TTTGGAATGT TTGCCTTGTT
    351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
     401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
     451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
      1 MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGGV
      51 FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPG QKFDLPLIVV
     101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
     151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

```
88.1% identity in 160 aa overlap
m577/g577
                                   30
                                            40
                                                     50
                                                              60
                           20
           MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
m577.pep
           MERSGVFGKIVGNRILRMPSEHAAAFYPKPCKSFKLTQSWFRVRSCPCGVFIYGANMKLI
q577
                                    30
                                            40
                                                     50
                                                              60
                           20
                  10
                                           100
                                                             120
                                    90
                                                    110
                           80
           YTVIKIIILLLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
m577.pep
```

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```
YTVIKIIILLFLLLAVINMDAVTFSYLPGQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
    a577
                        70
                                  80
                                           90
                                                   100
                       130
                                 140
                                          150
                 LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
    m577.pep
                 LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAAESAKQPX
    q577
                                 140
                                          150
                       130
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1753>:
    a577.seq
              ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
           1
              TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
          51
              TTAAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
              TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
              TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAATACG GATGCCGTTA
              CCTTTTCCTA CCTGCCGGGG CAAAAATTCG ATTTGCCGCT GATTGTCGTA
         251
              TTGTTCGGCG CGTTTGTCGT CGGCATCGTG TTCGGAATGT TTGCCTTGTT
              CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
              TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
         451
              CAAAATGCGC CCGAATCTGC CAAACAGCCT TGA
This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:
    a577.pep
              MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCPGGV
           1
              FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPG QKFDLPLIVV
          51
              LFGAFVVGIV FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
         101
              ONAPESAKOP
         151
                 98.1% identity in 160 aa overlap
    m577/a577
                        10
                                 20
                                           30
                                                    40
                 MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
    m577.pep
                 MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCPGGVFIYGANMKLI
    a577
                                 20
                                           30
                                                    40
                                                             50
                                                                       60
                        10
                                 80
                                           90
                                                   100
                                                            110
                 YTVIKIIILLLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
    m577.pep
                 YTVIKIIILLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
    a577
                        70
                                 80
                                           90
                                                   100
                                                                     120
                                          150
                       130
                                140
                 LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
    m577.pep
                 a577
                 LSLRGENGRLRAEVKKNARLTGKELTAPPAQNAPESAKQPX
                                                   160
                       1.30
                                140
                                          150
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1755>:
g578.seq..
     1 atgggaaage tegacategg gatattgttt geegatttet teaaagattt
     51 cqcqccacag ttcggtggtt tccaaaacgt tggctttgcc tacggagcag
    101 actttttgc tgcgtttttg ggcggattgg aaggccacgt gggcgatgcg
        geggattteg etttegetgt attteatggt gttgtageet tegtgttege
        cgttttccaa aacacggatg ccgcgcggtt cgccgaaata aatatcgccg
        gtaagttege geacaateaa aatateeaaa eeggeaaega ttteaggett
        gagcgtggag gcgttggcta a
```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>: g578.pep

- MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGDA 1
 - 51 ADFAFAVFHG VVAFVFAVFQ NTDAARFAEI NIAGKFAHNQ NIQTGNDFRL

```
101 ERGGVG*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1757>:
m578.seq..
      1 ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTTCT TCAAAGATTT
     51 CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
    101 ACTITITGC TGCGTTTTTG GGCGGATTGG AAGGCAACAT GGGCAATACG
    151 GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
        CGTTTTCCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
    251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT
This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:
m578.pep..
      1 MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
        ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
     51
    101 QRGGVG*
m578/g578 87.7% identity in 106 aa overlap
                  10
                           20
                                   30
           MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG
m578.pep
           MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDAADFAFAVFHG
g578
                  10
                           20
                                   30
                                            40
                                                    50
                                                             60
                  70
                           80
                                   90
                                           100
           VVAFAFAVFQNADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX
m578.pep
           VVAFVFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX
g578
                  70
                           80
                                   90
                                           100
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1759>:
     a578.seq
              ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTTCT TCAAAGATTT
           1
              CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
           51
          101 ACTITITIGG TGCGTTTTTG GGCGGATTGG AAGGCGACGT GGGCAATACG
          151
              GCGGATTTCG CTTTCGCTGT ATTTCATGGT GTTGTAGCCT TCGCGTTCGC
              CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
          201
              GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
              GAGCGTGGAG GCGTTGGCTA G
This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:
     a578.pep
              MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
              ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
           51
         101
              ERGGVG*
     m578/a578
                 91.5% identity in 106 aa overlap
                                   20
                                             30
                                                      40
                 MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG
     m578.pep
                 {\tt MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG}
     a578
                                   20
                                             30
                                                      40
                         10
                                                                50
                                                                          60
                                   80
                                             90
                 VVAFAFAVFONADAARFAEIDVAGEFAHNQNIQTGNDFRLORGGVGX
     m578.pep
                 VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX
     a578
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1761>: q579.seq..

80

70

90

100

¹ ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

PCT/US99/09346

897

51	TTTGTGTAAT	GTTGCCAATA	TCGGCTTATT	GATTTTGGTG	ATTATTGCCG
101	CATTGGGACG	GTTGGGCGTT	TCCACAACAT	CCGTAACCGC	CTTAATCGGC
151	GGCGCGGGTT	TGGCGGTGGC	GTTGTCCTTA	AAAGACCAGC	TGTCCAATTT
201	TGCCGCCGGC	GCGCTGATTA	TCCTGTTCCG	CCCGTTCAAA	GTCGGCGACT
251	TTATCCGTGT	CGGCGGTTTT	GAAGGATATG	TCCGGGAAAT	CAAAATGGTG
301	CAGACTTCTT	TGCGGACGAC	CGACAACGAA	GAAGTCGTGC	TGCCCAACAG
351	CGTGGTGATG	GGCAACAGCA	TCGTCAACCG	TTCCAGCCTG	CCGCTTTGCC
401	GCGCCCAAGT	GATAGTCGGC	GTCGATTACA	ACTGCGATTT	GAAAGTGGCG
451	AAAGAGGCGG	TGTTGAAAGC	CGCCGCCGAA	CACCCCTTGA	GCGTTCAAAA
501	CGAAGAGCGG	CAGCCCGCCG	CCTACATCAC	CGCCTTGGGC	GACAATGCCA
551	TCGAAATCAC	ATTATGGGCT	TGGGCAAACG	AAGCAGACCG	CTGGACGCTG
601	CAATGCGACT	TGAACGAACA	AGTGGTCGAA	AACCTCCGCA	AAGTCAATAT
651	CAACATCCCG	TTCCCGCAAC	GCGACATACA	CATCATCAAT	TCTTAA

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.pep..

- MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG 1 GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV 101 QTSLRTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA 151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL OCDLNEOVVE NLRKVNINIP FPQRDIHIIN S*
- The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1763>:

m579.seq..

- 1 ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG 51 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC GGCGCGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGATT 251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG 301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC 351 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA 651
- This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.pep..

- MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV OTSLRTTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA 151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*
- Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

98.7% identity in 231 aa overlap m579/g579 30 40 50 60 m579.pep MRAAMTRAQVDATLISFLCNVÄNIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL g579 40 50 10 20 30 70 80 90 100 110 120 KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRTTDNEEVVLPNSVVM m579.pep g579 KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRTTDNEEVVLPNSVVM 70 100 110

	\cdot
	130 140 150 160 170 180
m579.pep	GNSIVNRSTLPLCRAQVIVGVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
g579	GNSIVNRSSLPLCRAQVIVGVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG
9	130 140 150 160 170 180
	190 200 210 220 230
m579.pep	190 200 210 220 230 DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
mo / J. pcp	
g579	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
	190 200 210 220 230
The following n	partial DNA sequence was identified in N. meningitidis <seq 1765="" id="">:</seq>
a579.seq	actial D11/1 soquence was identified in 11. meningulais DDQ ID 1/05%.
1	ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51	TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101	CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 201	GGCGCGGGTT TGGCGGTGGC GTTGTCCTTG AAAGACCAGC TGTCCAATTT TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGATT
251	TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301	CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351	CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401	GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451	AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501	CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 601	TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651	CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA
001	0.110.110.10
This correspond	s to the amino acid sequence <seq 1766;="" 579.a="" id="" orf="">:</seq>
a579.pep	
1	MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51	GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 151	QTSLRTTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201	QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*
	<u></u>
m579/a579	100.0% identity in 231 aa overlap
	10 20 30 40 50 60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL
• •	
a579	${\tt MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL}$
	10 20 30 40 50 60
	70 80 90 100 110 120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRTTDNEEVVLPNSVVM
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRTTDNEEVVLPNSVVM
	70 80 90 100 110 120
	130 140 150 160 170 180
m579.pep	GNSIVNRSTLPLCRAQVIVGVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
a579	GNSIVNRSTLPLCRAQVIVGVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
	130 140 150 160 170 180
	190 200 210 220 230
m579.pep	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
a579	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
	190 200 210 220 230

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1767>: g579-1.seq

WO 99/57280

899

```
ATGGACTICA AACAATITGA TITITTACAC CIGATCAGIG TITCCGGITG
 1
    GGGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCC
151 GTAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
    TTTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG ACGGTTGGGC GTTTCCACAA CATCCGTAAC CGCCTTAATC
301 GGCGGCGCG GTTTGGCGGT GGCGTTGTCC TTAAAAGACC AGCTGTCCAA
    TTTTGCCGCC GGCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
351
    ACTITATCCG TGTCGGCGGT TTTGAAGGAT ATGTCCGGGA AATCAAAATG
401
    GTGCAGACTT CTTTGCGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCAGC CTGCCGCTTT
    GCCGCGCCCA AGTGATAGTC GGCGTCGATT ACAACTGCGA TTTGAAAGTG
551
    GCGAAAGAGG CGGTGTTGAA AGCCGCCGCC GAACACCCCT TGAGCGTTCA
    AAACGAAGAG CGGCAGCCCG CCGCCTACAT CACCGCCTTG GGCGACAATG
    CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
    CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
751
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>: g579-1.pep

- 1 MDFKQFDFLH LISVSGWGHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
- 51 VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
- VQTSLRTTDN EEVVLPNSVV MGNSIVNRSS LPLCRAQVIV GVDYNCDLKV
- 201 AKEAVLKAAA EHPLSVQNEE RQPAAYITAL GDNAIEITLW AWANEADRWT
- 251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1769>: m579-1.seq

```
1 ATGGACTTCA AACAATTTGA TTTTTTACAC CTGATCAGTG TTTCCGGTTG
51 GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTTTGGTC GGAAAATGGG CGGCGAAACG CATTGTCGCT
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
    CCGCATTGGG CAGATTGGGC GTTTCCACAA CATCCGTAAC CGCCTTAATC
301 GGCGGCGCG GTTTGGCGGT GGCGTTGTCC CTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GGCGCACTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAAATG
451 GTGCAGACTT CTTTGCGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GGCGTCGATT ACAACTGCGA TTTGAAAGTG
    GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCTG CCGCCTACAT CACCGCCTTG GGCGACAATG
    CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
    CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
751
    TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>: m579-1.pep

- 1 MDFKOFDFLH LISVSGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
- 51 VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
- GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
- VQTSLRTTDN EEVVLPNSVV MGNSIVNRST LPLCRAQVIV GVDYNCDLKV
- 201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
- 251 LQCDLNEQVV ENLRKVNINI PFPQRDIHII NS*

98.6% identity in 282 aa overlap m579-1/g579-1

10 20 30 40 MDFKQFDFLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ m579-1.pep MDFKQFDFLHLISVSGWGHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ g579-1 20 30 40 50 10 80 90 100 110 VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA m579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA q579-1 70 80 90 100 110 170 150 160 130 140 GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRTTDNEEVVLPNSVVMGNSIVNRST m579-1.pep

	!
	190 200 210 220 230 240 LPLCRAQVIVGVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
	250 260 270 280 AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
,	g partial DNA sequence was identified in N. meningitidis <seq 1771="" id="">:</seq>
51 GGA 101 CGC 151 GTG 201 TTT 251 CCG 301 GGC 351 TTT 401 ATT 451 GTG 501 CAG 551 GCC 601 GCG 651 AAA 701 CCA 751 CTG	GACTTCA AACAATTTGA TTTTTTACAC CTGATAAGTG CTTCCGGCTG GCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG TGCTTAT TTTTTGGTC GGAAAATGGG CGGCGAAACG CATTGTCGCC ATGAGGG CGGCGATGAC GCGCGCAACG CGCTGATTAG TTTGTTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG CATTGGG CAGATTGGCC GTTTCCACAA CATCCGTAAC CGCCTTAATC GGCGCGG GTTTGGCGGT GGCGTTGTCC TTGAAAGACC AGCTGTCCAA TGCCGCC GGCGCGTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG TTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAAATG CAGACTT CTTTGCGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA CGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCACA CTGCCGCTGT GAAAGAGG CGGTGTTGAA AGCCGCGTC GAAACACCCCT TGAGCGTTCA CGAAGAG CGGTGTTGAA AGCCGCCTC GAACACCCCT TGAGCGTTCA CGAAGAG CGGCAGGCCG CCGCCTACAT CACCGCCTTG GGCGACAATG CCGAAGAG CGCAGGCCG CCGCCTACAT CACCGCCTTG GGCGACAATG CCGAAGAC CACATTATGG GCTTGGGCAA ACAACTCCC GCAAAGTCAA CACATTACCG ACAGTGGTC GAAAACCTCC GCAAAGTCAA CACATCACC CCGCTTCCCCC AACGCGACAA ACAACTCATC AATTCTTAA ONDS to the amino acid sequence SEQ ID 1772; ORF 579-1.a>:
a579-1.pep	KOFDFLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
101 <u>GGA</u> 0 151 VQT: 201 AKE	AAMTRAQ VDATLISFLC NVANIGLIL VIIAALGRIG VSTTSVTALI GLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM SIRTTDN EEVVLPNSVV MGNSIVNRST LPLCRAQVIV GVDYNCDLKV AVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT DLNEQVV ENLRKVNINI PFPQRDIHII NS*
a579-1/m579-1	99.6% identity in 282 aa overlap
	10 20 30 40 50 60 MDFKQFDFLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ
	70 80 90 100 110 120 VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
	130 140 150 160 170 180 GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSLRTTDNEEVVLPNSVVMGNSIVNRST
	190 200 210 220 230 240 LPLCRAQVIVGVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
a579-1.pep 1	250 260 270 280 AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX

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901

```
AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX
m579-1
                  260
            250
                        270
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1773>: g580.seq

- atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
- 51 cgcgtcgcag cccatttcga tggcaaggca gacttcgccg atcatgtcgc
- 101 caccettegg acceacaate ceecegecga teatgeggee gettteggea
- 151 togaaaatca gottggtaaa googttgtog caacogttgg caatogcacg
- 201 accggaagcc gcccatggga agttggcttt.ggtaattttg cggcctgatg
- ctttggcaga caattcggtt tcaccgaccc atgccacttc gggggaagtg
- 301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>: g580.pep..

- 1 MDSPKVGCGW MVLPMSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
- 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV

101 *

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1775>: m580.seq.

- 1 ATGGATTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTGC CGATGTCTGC
- 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
- 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCGGCA
- 151 TCAAAAATCA GCTTGGTAAA GCCGTTGTCG CAACCGTTGG CAATCGCACG 201 GCCGGAAGCC GCCCACGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
- 251 CTTTGGCGGA CAGTTCGGTT TCGCCCACCC ACGCCACTTC GGGGGAAGTG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>: m580.pep..

- 1 MDSPKVGCGW MVLPMSAASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
- 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
- 101

m580/g580 97.0% identity in 100 aa overlap

20 30 40 10 MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMMRPVSASKISLVKPLS m580.pep MDSPKVGCGWMVLPMSAASQPISMARQTSPIMSPPFGPTMPPPMMRPVSASKISLVKPLS q580 10 20 30 40 50 80 90 QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX m580.pep OPLAIARPEAAHGKLALVILRPDALADNSVSPTHATSGEVX q580 90 100 70 80

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1777>:

a580.seq

- 1 ATGGATTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTGC CGATGTCTGC
- CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCGC 51
- CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCAGCA 101
- TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG
- GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG 201
- CTTTGGCAGA CAATTCGGTT TCGCCCACCC ATGCCACTTC AGGAGAAGTG 251
- 301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep

- MDSPKVGCGW MVLPMSAASO PISMAROTSP IMSPPFGPTM PPPMMRPVSA 1
- SKISLVKPLS OPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

g581

g581

902

101 m580/a580 98.0% identity in 100 aa overlap 10 20 30 40 MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMMRPVSASKISLVKPLS m580.pep MDSPKVGCGWMVLPMSAASQPISMARQTSPIMSPPFGPTMPPPMMRPVSASKISLVKPLS a580 40 70 80 90 m580.pep QPLAIARPEAAHGKLALVILRPEALADSSVSPTHATSGEVX QPLAIARPEAAHGKLALVILRPEALADNSVSPTHATSGEVX a580 70 90 The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1779>: g581.seq.. 1 atgcacttcg cccagcttgt gggtcaaacc ggtatagaac aaaatacgtt 51 ctgtcgtcgt ggttttaccc gcatcgatat gggcggaaat accgatgttg 101 cggtacaggc tgatcggggt cttacgagcc attttattag cctttcaaaa 151 ttagaaacgg aagtgagaga atgetttgtt ggetteagee ataeggtgta 201 ettetteaeg tttttteaae geaeegeeae ggeettegga egeateaate 251 aactegeetg ccaaacgcag atccatggat tteteaceae gtttgeggge 301 cgcgtcgcga acccaacgca ttgccaaagc cagacggcgt ga This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>: q581.pep.. 1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG 101 RVANPTHCQS QTA* The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1781>: m581.seq. 1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA 51 101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA 151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA 201 CTTCTTCACG TTTTTTCAAC GCACCGCCAC GGCCTTCGGA CGCATCAATC 251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC 301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>: m581.pep.. 1 MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTVQADRG LTSHFISLSK LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLTTFAG 51 101 RIANPAHCQS QTA* m581 / g581 93.8% identity in 113 aa overlap 20 30 40 $\verb|MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRGLTSHFISLSKLETEVRECFV|\\$ m581.pep MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAVQADRGLTSHFISLSKLETEVRECFV 10 30 40 50 80 90 100 GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX m581.pep GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRVANPTHCQSQTAX 70 80 90 100

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1783>:

```
903
```

```
a581.seq
              ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
              CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
             CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
         101
             TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
         151
         201 CTTCTTCACG TTTTTTCAAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
         251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
         301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA
This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:
    a581.pep
              MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LTSHFISLSK
              LETEVRECEV GESHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLTTFAG
          51
             RINPAHCQS QTA*
         101
    m581/a581
                 98.2% identity in 113 aa overlap
                         10
                                  20
                 MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRGLTSHFISLSKLETEVRECFV
    m581.pep
                 {\tt MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTVQADRGLTSHFISLSKLETEVRECFV}
    a581
                                  20
                                            30
                                                     40
                                                               50
                                                    100
                                                              110
                         70
                                            90
                                  80
                 GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX
    m581.pep
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1785>: g582.seq..

80

GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRIANPAHCQSQTAX

90

100

110

```
1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51 agagaccgcg ctgcaatgcg ccgctttgac ggacaatgtt acgcgtttgg
     151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
     cagettggat aagggegagg eggteattgt tgttgaaaaa ggeggggatg
    cgcttcctgc cgacagtgcg ggcgaaaccg ccgatatcta tacgcctttg
251
301 agcctgatgt acgacttgga caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatge eccgagtteg ecgaegegeg gtacgaetgt acaggaaaaa
451 ttcqqacagc agaaacgtgc ggaaaccaaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaacccg cgcggatctg tggttcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccqttccgca atacggatta caaacctgaa attttcctga cccagcctgt
651 gaaggeggat ttgccgttcg geggcagget gegtatgete ggtgegggtt
 701 ttgtccacca gtccaacgga cagagecgtc ccgaatcgcg ttcgtggaac
     aggatttatg ccatggcagg catggaatgg ggcaaattga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggtatggcg acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgctaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
     tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga
```

70

a581

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>: g582.pep ..

MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ 51 EGOESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL 101 SLMYDLDKND LRGLLGVREH NPMYLMPFWY NNSPNYAPSS PTRGTTVQEK 151 FGQQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA 201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN 251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIADYM GYGDVKLQYR 301 LNDRONVYSV LRYNPKTGYG AIEAAYTFPI KGKLKGVVRG FHGYGESLID 351 YNHKQNGIGI GLMFNDWDGI *

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1787>:
m582.seg
         ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
      1
         AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
     51
         101
         GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
    151
         CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTTGAAAAA GGCGGGGATG
         CGCTTCCTGC CGACAGTGCG GGCGAAACCG CCGACATCTA TACGCCTTTG
    251
         AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTTGGGCGT
    301
         ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAATTCGC
    351
         CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
    401
         TTCGGACAGC AGAAACGTGC GGAAACCAAA TTGCAGGTTT CGTTCAAAAG
         CAAAATTGCC GAAGATTTGT TTAAAACCCG CGCGGATCTG TGGTTCGGCT
    501
         ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
    551
         CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
    601
         GAAGGCGGAT TTGCCGTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
    651
         TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
         AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
    751
         GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CGGCGATAAA AACGACAATC
    801
         CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
    851
         CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
    901
         GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTTCCGATT AAGGGCAAAC
    951
         TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
   1001
         TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
   1051
         GGACGGCATC TGA
   1101
This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:
m582.pep
         MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
         EGOESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
     51
         SLMYDLDKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
    101
         FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
         PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNG QSRPESRSWN
    201
         RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIADYM GYGDVKLQYR
         LNDRQNVYSV LRYNPKTGYG AIEAAYTFPI KGKLKGVVRG FHGYGESLID
    301
        YNHKONGIGI GLMFNDLDGI *
    351
m582 / g582 98.6% identity in 370 aa overlap
                                     30
                   10
                            20
                                              40
                                                       50
           MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
m582.pep
            \verb|MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN|
q582
                   10
                            20
                                     30
                                              40
                                     90
                                             100
                            80
            LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLDKNDLRGLLGVREH
m582.pep
            LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLDKNDLRGLLGVREH
9582
                   70
                            80
                                     90
                                             100
                                                      110
                                                               120
                                                      170
                  130
                           140
                                    150
                                             160
            NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAETKLQVSFKSK1AEDLFKTRADL
m582.pep
           g582
            npmylmpfwynnspnyapssptrgttvqekfgqqkraetklqvsfkskiaenlfktradl
                                                      170
                  130
                           140
                                    150
                                             160
                                                               180
                           200
                                    210
                                             220
                                                      230
                                                               240
           WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG
m582.pep
           WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG
g582
                           200
                                                      230
                  190
                                    210
                                             220
                                                               240
                           260
                                    270
                                             280
                                                      290
           QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIADYMGYGDVKLOYR
m582.pep
           g582
            OSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDIADYMGYGDVKLQYR
                           260
                                    270
                                             280
                                                      290
                  250
                                                               300
```

310

320

330

340

350

360

```
\verb"LNDRQNVYSVLRYNPKTGYGAIEAAYTFPIKGKLKGVVRGFHGYGESLIDYNHKQNGIGI"
m582.pep
          LNDRQNVYSVLRYNPKTGYGAIEAAYTFPIKGKLKGVVRGFHGYGESLIDYNHKQNGIGI
g582
               310
                      320
                              330
                                     340
                                             350
               370
         GLMFNDLDGIX
m582.pep
         GLMFNDWDGIX
g582
               370
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1789>:

a582.se	q					
	1	ATGCGCTATA	TTCTTTTGAC	AGGACTGTTG	CCGATGGCAT	CCGCTTTTGG
5	1	AGAGACCGCG	CTGCAATGCG	CCGCTTTGAC	GGACAATGTT	ACGCGTTTGG
10	1	CGTGTTACGA	CAGGATTTTT	GCGGCACAGC	TTCCGTCTTC	GGCAGGGCAG
15	1	GAAGGGCAGG	AGTCGAAAGC	CGTACTCAAT	CTGACGGAAA	CCGTCCGCAG
20	1	CAGCCTGGAT	AAGGGCGAGG	CGGTCATTGT	TGTTGAAAAA	GGCGGGGATG
25	1	CGCTTCCTGC	CGACAGTGCG	GGCGAAACCG	CCGACATCTA	TACGCCTTTG
30	1	AGCCTGATGT	ACGACTTGGA	CAAAAACGAT	TTGCGCGGGC	TGTTGGGCGT
35	1	ACGCGAACAC	AATCCGATGT	ACCTTATGCC	GCTCTGGTAC	AACAATTCGC
40	1	CCAACTATGC	CCCGGGTTCG	CCGACGCGCG	GTACGACTGT	ACAGGAAAAA
45	1	TTCGGACAGC	AGAAACGTGC	GGAAACCAAA	TTGCAGGTTT	CGTTCAAAAG
50	1	CAAAATTGCC	GAAGATTTGT	TTAAAACCCG	CGCGGATCTG	TGGTTCGGCT
55	1	ACACCCAAAG	ATCCGATTGG	CAGATTTACA	ACCAAGGCAG	GAAATCCGCG
60	1	CCGTTCCGCA	ATACGGATTA	CAAACCTGAA	ATTTTCCTGA	CCCAGCCTGT
65	1	GAAGGCGGAT	TTGCCGTTCG	GCGGCAGGCT	GCGTATGCTC	GGTGCGGGTT
70	1	TTGTCCACCA	GTCCAACGGA	CAGAGCCGTC	CCGAATCGCG	TTCGTGGAAC
75	1	AGGATTTACG	CCATGGCAGG	CATGGAATGG	GGCAAATTGA	CGGTGATTCC
80	1	GCGCGTGTGG	GTGCGTGCGT	TCGATCAGAG	CGGCGATAAA	AACGACAATC
85	1	CCGATATTGC	CGACTATATG	GGGTATGGCG	ACGTGAAGCT	GCAGTACCGC
90	1	CTGAACGACA	GGCAGAATGT	GTATTCCGTA	TTGCGCTACA	ATCCCAAAAC
95	1	GGGCTACGGC	GCGATTGAAG	CCGCCTACAC	GTTTCCGATT	AAGGGCAAAC
100	1	TCAAAGGCGT	GGTACGCGGA	TTCCACGGTT	ACGGCGAGAG	CCTGATCGAC
105	1	TACAACCACA	AGCAGAACGG	TATCGGTATC	GGGTTGATGT	TCAACGACTT
110	1	GGACGGCATC	TGA			

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>: a582.pep

-	******				-	~ ~	
51	EGQESKAVLN	LTETVRSSLD	KGEAVIVVE	K GGDALPA	DSA GETADI	\mathtt{YTPL}	
101	SLMYDLDKND	LRGLLGVREH	NPMYLMPLW	Y NNSPNYA	PGS PTRGTT	VQEK	
151	FGQQKRAETK	LQVSFKSKIA	EDLFKTRAD	L WFGYTQR	SDW QIYNQG	RKSA	
201	PFRNTDYKPE	IFLTQPVKAD	LPFGGRLRM	L GAGFVHQ	SNG QSRPES	RSWN	
251	RIYAMAGMEW	GKLTVIPRVW	VRAFDQSGD	K NDNPDIA	DYM GYGDVK	LQYR	
301	LNDRONVYSV	LRYNPKTGYG	AIEAAYTFP	I KGKLKGV	VRG FHGYGE	SLID	
351	YNHKONGIGI	GLMFNDLDGI	*				
						š	•
m582/a582	100.0% i	dentity in	370 aa ov	erlap			
		•		•			
		10	20	30	40	50	60
m582.pep	MRYILLTG	LLPMASAFGE'	ralqcaaltd	NVTRLACYDI	RIFAAQLPSS	AGQEGQESKA'	VLN
• •		111111111	1111111111	111111111	1111111111	111111111	Ш
a582	MRYILLTG	LLPMASAFGE'	PALQCAALTD	NVTRLACYDI	RIFAAQLPSS	AGQEGQESKA'	VLN
				30	40	50	60
		70	80	90	100	110	120
m582.pep	LTETVRSS	LDKGEAVIVV	EKGGDALPAD	SAGETADIY'	rplslmydld	KNDLRGLLGV	REH
	1111111	1111111111	11111111	11111111	111111111	111111111	HI
a582	LTETVESS	LDKGEAVIVV	EKGGDALPAD	SAGETADIY	TPT.ST.MYDT.D	KNDLRGLLGV	REH
a302	BIBITANDO	-					120
		, ,					120
	1	.30 1	40 1	50	160	170	180
	J.	.50	10 1		.00	1.0	100

MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ

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906

m582.pep	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAE	TKLQVSFKSKIAEDLFKTRADL
a582	NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQQKRAE	
	130 140 150 1	170 180
	130 100 110	220 230 240
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPV	(ADLPFGGRLRMLGAGFVHQSNG
a582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVF	
	190 200 210 2	220 230 240
	200	290 300
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSG	
	[] [] [] [] [] [] [] [] [] []	
a582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSO	
	250 260 270 2	290 300
		340 350 360
m582.pep	LNDRQNVYSVLRYNPKTGYGAIEAAYTFPIKGKLKGVV	-
a582	LNDRQNVYSVLRYNPKTGYGAIEAAYTFPIKGKLKGVV	
	310 320 330 3	350 360
	370	
m582.pep	GLMFNDLDGIX	
a582	GLMFNDLDGIX	
	370	

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1791>: q583.seq..

```
1 atgataattg accaaagcca aatatttacc catcttgcct tctgtgcctt
 51 ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagtteggaa agagegagae tgtaacegat geecagegtt tttetteeaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaacgca ctcaacgcat cgctcatcgc cgcgcccggt ttgtcggcgg
351 ttacgccggt tactgcgacc aacccgacgg caataatcga cagcgcgccc
401 aacqqcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
    gaaaaataa
```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>: g583.pep..

- 1 MIIDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ 51 QFGKSETVTD AQRFSSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI 101 GERTORIAHR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS 151 OORPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
- 201 EK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1793>: m583.seg..

```
1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCG GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTCGGCGG
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAGGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
```

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907

CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG

551

```
601
        GAAAAATAA
This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:
m583.pep..
        MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSOO
     1
        OFGKSETVTD AORFSSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
     51
        GERTQRIAHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
    101
        QORPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
    151
    201
             98.5% identity in 202 aa overlap
m583 / g583
                           20
                                   30
                                            40
                  10
           MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQQFGKSETVTD
m583.pep
           MIIDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQQFGKSETVTD
g583
                                            40
                  10
                           20
                                   30
                                                    50
                                                             60
                           80
                                   90
                                           100
                                                    110
           {\tt AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG}
m583.pep
           AORFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
g583
                                           100
                                                    110
                           80
                                   90
                                                            120
                  70
                                  150
                                           160
                                                    170
                                                            180
                 130
                          140
           YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
m583.pep
           YCDQPDGNNRQRAQRHNLADNGGNHTDKHSQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
g583
                 130
                          140
                                  150
                                           160
                                                    170
                          200
                 190
           RFETOFHHIDLRKKDRPEKSEKX
m583.pep
           11111111111111111111111
           RFETQFHHIDLRKKDRPEKSEKX
q583
                          200
                 190
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1795>:
     a583.seq
              ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
           1
               TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
           51
               ATAATGCCGC CGCCGCGCG GGTATTGGAA GGGGTAACGG GAGCCAGCAG
          101
               CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
          151
              AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
          201
              AAACCGCGCG AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
          251
              GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCGGCGG
          301
              TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
          351
              AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC
          401
              CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
          451
              AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
          501
              CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
          551
              GAAAAATAA
This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:
     a583.pep
              MIVDQSQIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSOO
           1
              QFGKSETVTD AQRFSSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
           51
              GERTORIAHR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
          101
              OORPSLRLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
          151
          201
              EK*
     m583/a583
                  99.0% identity in 202 aa overlap
                                   20
                                             30
                                                       40
                                                                           60
                         10
                                                                 50
                 MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQOFGKSETVTD
     m583.pep
```

```
MIVDOSOIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQQFGKSETVTD
a583
                         20
                                 30
                 70
                                        100
                                                 110
          AORFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
m583.pep
           AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRTRFVGGYAG
a583
                                        100
                         80
                                 90
                 70
                130
                        140
                                150
                                        160
                                                 170
                                                         180
          YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
m583.pep
           YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
a583
                                        160
                                                170
                130
                        140
                                150
                190
                        200
          RFETQFHHIDLRKKDRPEKSEKX
m583.pep
          111111111111
          RFETQFHHIDLRKKDRPEKSEKX
a583
                190
                        200
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1797>: g584.seq..

```
1 atgctgcgtt ctattttggc ggcttccctg ctggcggtat cttttccggc
    ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
 51
101
    gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
    gaaggacggg acaaaaatgc cgtcaatgcc gagtttgtta aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cqcqcagtgc gatgccqcqc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggagggca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
    gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 qqqcqttctq gqtqcqtccq gttataaaat cqtcaaattq aattttggqc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggta cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701
    tctaa
```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>: g584.pep Length:..

```
1 MLRSILAASL LAVSFPAAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51 EGRDKNAVNA EFVKKFNNFT RKSKNGSFKT ELVSRSAMPR YQYTNGRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTDA SLEDTDFSVS RERRNEVIDQ
```

- 151 VSKDAVLRFK ARAEKLAGVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
- 201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1799>: m584.seq..

```
1 ATGTTGCGTC TTGTTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTTCCGGC
51 AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101
    GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAATTCAA
201 CAAGTTCATC AGAAAATCGA AAAATGGTAG CTTTAAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTTAAG GTCGAAGGTA GAGATTTTGA
    TGAGTTAAAC CGTTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
351
    ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCKATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651
    CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCAGT
    TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

```
m584.pep..
        MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
        EGRDKNAVNA EFVKKFNKFI RKSKNGSFKT ELVSRSAMPR YQYTNGRRIQ
     51
        TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
        VSKDAVLRFK ARAEKLAGVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
    201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*
m584 / g584 89.7% identity in 234 aa overlap
                                   30
                                           40
                                                    50
                                                            60
                          20
                  10
           MLRLVLAASLSAVSFPAAAEALNYNIVEFSESAGVEVAQDTMSARFQVTAEGRDKNAVNA
m584.pep
           MLRSILAASLLAVSFPAAAEALNYNIVEFSESAGIEVAQDTMSARFQVAAEGRDKNAVNA
q584
                                                   50
                                                            60
                          20
                                   30
                                           40
                  10
                                   90
                                          100
                                                   110
                  70
                          80
           EFVKKFNKFIRKSKNGSFKTELVSRSAMPRYQYTNGRRIQTGWEERAEFKVEGRDFDELN
m584.pep
           EFVKKFNNFTRKSKNGSFKTELVSRSAMPRYQYTNGRRIQTGWEERAEFKAEGRDFDALN
a584
                                   90
                                          100
                          80
                  70
                                                   170
                                                           180
                 130
                         140
                                  150
                                          160
           RFIADIQADAALXYTDFHVSRERRNEVIXQVSKDAVLRFKARAEKLAGVLGASGYKIVKL
m584.pep
           RFIADVQTDASLEDTDFSVSRERRNEVIDQVSKDAVLRFKARAEKLAGVLGASGYKIVKL
q584
                         140
                                  150
                                          160
                                                   170
                 130
                                  210
                                          220
                                                   230
                 190
                         200
           NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
m584.pep
           NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKGTDSAAPGVEEISISINGTVQFX
a584
                         200
                                  210
                                          220
                                                   230
                 190
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1801>:
     a584.seg
              ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
           1
              .....ATTGT CGAATTTTCT GAATCGGCGG
          51
              GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
          101
              GAAGGACGGG ACAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
          151
              CAATTTCACC AGAAAATCAA AAAATGGTAG CTTTAAAACC GAATTGGTAT
          201
              CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
          251
              ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
          301
              TGCGTTGAAC CGTTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
          351
              ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
          401
              GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
          451
              GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
          501
              ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
          551
              CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
          601
              CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTCAGT
          651
          701
              TCTGA
This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:
     a584.pep
           1
              MLRSILAASL L...... IVEFS ESAGVEAVQD TMSARFQVTA
              EGRDKNAVNA EFVKKFNNFT RKSKNGSFKT ELVSRSAMPR YQYTNGRRIQ
          51
              TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
          101
              VSKDAVLRFK ARAEKLAGVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
          151
              RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*
          201
                 88.9% identity in 234 aa overlap
     m584/a584
                                   20
                         10
                                            30
                                                      40
                                                               50
                 MLRLVLAASLSAVSFPAAAEALNYNIVEFSESAGVEVAQDTMSARFQVTAEGRDKNAVNA
     m584.pep
                 111:111
                                         MLRSILAASLL+-----IVEFSESAGVEAVQDTMSARFQVTAEGRDKNAVNA
     a584
                         10
                                                20
                                                                   40
                                                          30
```

WO 99/57280

910

```
90
                                      100
                                             110
                                                     120
                70
                       80
          EFVKKFNKFIRKSKNGSFKTELVSRSAMPRYQYTNGRRIQTGWEERAEFKVEGRDFDELN
m584.pep
          EFVKKFNNFTRKSKNGSFKTELVSRSAMPRYQYTNGRRIQTGWEERAEFKVEGRNFDALN
a584
                          70
                                  80
                                                     180
                                      160
                                             170
               130
                       140
                              150
          RFIADIQADAALXYTDFHVSRERRNEVIXQVSKDAVLRFKARAEKLAGVLGASGYKIVKL
m584.pep
          RFIADVQADAALEYTDFHVSRERRNEVIDQVSKDAVLRFKARAEKLAGVLGASGYKIVKL
a584
                  120
                         130
                                 140
                                      220
                                             230
               190
                       200
                              210
         NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
m584.pep
          NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVOFX
a584
                         190
                                 200
                  180
          170
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1803>: g585.seq..

```
1 atgaaactgt tccaacgcat tttcgccaca ttttgcgcgg ttatcgtctg
51 cgcaatcttt gtggcgagtt tttctttttg gctggtgcag aacacccttg
101 ccgaaaacca attcaaccaa cgccgcacca tcgaaaccac attgatgggc
151 agcattattt ccgcattcaa gacacggggc gacaacggcg cgcgcgaaat
201 cctgaccgaa tggaaaaaca gccccgtctc atccgccgtt tacgtcatac
251 agggcgacga gaaaaaagac atcttaaacc gctatatcga caattacacc
301 ataqaacgcg cccggctgtt tgccgccaac aacccccatt ccaaccttgt
351 ccgcatcgaa tacgaccgtt tcggcgaaga atacctgttc ttcattaaag
401 gctgggacaa ccaccaggca caacgcctgc ccagcccgct gtttatcccg
451 ggcctgccgc ttgccccgat ttggcacgaa ttcatcatcc tctccttcat
501 catcattgtc ggactgctga tggcatatat ccttgccggc aacattgcca
551 aacccatcag aatcttaggc aacggcatgg acagggtggc agaacgagaa
601 cttgaagacc gcgtttgcca acaggttcgc gaccgcgacg acgaattggc
651 cgatgttgcc atgcaattcg acacaatggt ggaaaaactg gaataa
```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>: g585.pep..

- 1 MKLFQRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG 51 SIISAFKTRG DNGAREILTE WKNSPVSSAV YVIQGDEKKD ILNRYIDNYT 101 IERARLFAAN NPHSNLVRIE YDRFGEEYLF FIKGWDNHQA QRLPSPLFIP 151 GLPLAPIWHE FIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVAERE 201 LEDRVCQQVR DRDDELADVA MQFDTMVEKL E*
- The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1805>: m585.seq..

```
ATGAAACTGT TCCAACGCAT TTTCGCCACA TTTTGCGCGG TTATCGTCTG
 51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
 201 CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
 251 AGGGCGACGA GAAAAAAGAT ATCCTGAACC GGTATATCGA CAGCTATACC
301 ATCGAACGCG CCCGGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
 401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCCTTCAT
     CATCATCGTC GGACTGCTGA TGGCATATAT CCTCGCCGGC AACATTGCCA
 551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
 601 CTTGAAACCC GTATCTCCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC
 651 CCATCTTGCC ATCCAATTCG ACAAAATGGT GGAAAAACTC GAAAAACTCG
 701 TTGCCAAAGA ACGCCACCTG CTCCATCACG TCTCCCATGA AATGCGTTCT
 751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTCAGG CGCAGCCCCA
     AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
 851 ATACGCTGGC CGGGGAACTG TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAAACA CAACCATCCT TGCCAACGAA
```

```
AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1051
      CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1101
     ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1151
     CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1201
     ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1251
     ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
     CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1351
1401
     GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>: m585.pep..

```
MKLFQRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
  1
    SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKKD ILNRYIDSYT
 51
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
    GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
151
    LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
201
    PLARMQAIVG LIQAQPQKQE QYLKRLEGEL TRMDTLAGEL LTLSRLETSN
    MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
    SYLYRAFDNV IRNAVNYSPE GSTILINIGQ DHKHWIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*
```

m585 / g585 88.3% identity in 231 aa overlap

```
20
                                 30
                                         40
                                                 50
                                                         60
                 10
          MKLFQRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMGSIISAFRARG
m585.pep
          MKLFQRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMGSIISAFKTRG
g585
                                                         60
                                                 50
                 10
                         20
                                 30
                                         40
                         80
                                 90
                                        100
          DAGAREILTEWKDSPVSSGVYVIQGDEKKDILNRYIDSYTIERARLFAAGHPHSNLVHIE
m585.pep
            [[]]]
          DNGAREILTEWKNSPVSSAVYVIQGDEKKDILNRYIDNYTIERARLFAANNPHSNLVRIE
g585
                                 90
                                        100
                         80
                 70
                        140
                                150
                                        160
                                                170
                                                        180
                130
          YDRFGEEYLFFTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
m585.pep
          YDRFGEEYLFFIKGWDNHQAQRLPSPLFIPGLPLAPIWHEFIILSFIIIVGLLMAYILAG
a585
                130
                        140
                                150
                                        160
                                                230
                                                        240
                                        220
                                210
                190
                        200
          NIAKPIRILGNGMDRVANGELETRISQQVDDRDDELSHLAIQFDKMVEKLEKLVAKERHL
m585.pep
          NIAKPIRILGNGMDRVAERELEDRVCQQVRDRDDELADVAMQFDTMVEKLEX
q585
                                                230
                190
                        200
                                210
                                        220
                        260
                                270
                                        280
                                                290
          LHHVSHEMRSPLARMQAIVGLIQAQPQKQEQYLKRLEGELTRMDTLAGELLTLSRLETSN
m585.pep
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1807>:

```
a585.seq
         ATGAAACTGT TCCAACGCAT CTTCGCCACA TTTTGCGCGG TTATCGTCTG
      1
         TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG
      51
         CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
         AGCATCATTT CCGCATTCCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
         CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
         AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
     251
         ATCGAACGCG CCCGGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
          CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
         ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
     401
         GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCCTTCAT
     451
         CATCATCGTC GGACTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
     501
         AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
     551
         CTTGAAACCC GTATCTCCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC
```

a585.pep

651	CCATCTTGCC	ATCCAATTCG	ACAAAATGGT	GGAAAAACTC	GAAAAACTCG
701	TTGCCAAAGA	ACGCCACCTG	CTCCATCACG	TCTCCCATGA	AATGCGTTCT
751	CCCCTTGCGC	GCATGCAGGC	AATTGTCGGA	CTGATTCAGG	CGCAGCCCCA
801	AAAACAGGAG	CAATATCTCA	AACGGCTGGA	AGGCGAACTG	ACCCGCATGG
851	ATACGCTGGC	CGGGGAACTG	TTAACCCTGT	CCCGTCTCGA	AACTTCCAAT
901	ATGGCTTTGG	AAAAAGAAAG	CCTGAAACTC	CTGCCCTTCC	TGGGCAACCT
951	GGTAGAAGAC	AATCAAAGCA	TTGCCCAGAA	AAACGGACAA	ACGGTTACCC
1001	TGTCTGCCGA	CGGAAAAATC	CCCGAAAACA	CAACCATCCT	TGCCAACGAA
1051	AGCTACCTGT	ACCGCGCCTT	CGACAACGTC	ATCCGCAACG	CCGTCAACTA
1101	CAGTCCCGAA	GGCAGCACCA	TCCTGATCAA	CATCGGACAA	GACCACAAAC
1151	ACTGGATAAT	CGACGTTACC	GACAACGGCC	CCGGCGTGGA	CGAAATGCAG
1201	CTCCCGCACA	TCTTCACCGC	TTTCTACCGT	GCAGACTCCA	GTGCCAACAA
1251	ACCCGGAACA	GGACTGGGGC	TTGCATTGAC	CCAACATATT	ATTGAACAGC
1301	ACTGCGGCAA	AATCATCGCC	GAAAACATCA	AACCGAACGG	TCTGCGGATG
1351	CGCTTTATCC	TGCCCAAGAA	AAAAACCGGT	TCCAAAACAG	AAAAAAGTGC
1401	GAACTGA				
			•		

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep	
1	MKLFQRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51	SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEKKD ILHRYIDSYT
101	IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
151	GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201	LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251	PLARMQAIVG LIQAQPQKQE QYLKRLEGEL TRMDTLAGEL LTLSRLETSN
301	MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351	SYLYRAFDNV IRNAVNYSPE GSTILINIGQ DHKHWIIDVT DNGPGVDEMQ
401	LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451	RFILPKKKTG SKTEKSAN*
m585/a585	99.8% identity in 468 aa overlap
	10 20 30 40 50 60
m585.pep	MKLFORIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMGSIISAFRARC
mooo.pep	
a585	MKLFQRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRTIETTLMGSIISAFRARG
a303	10 20 30 40 50 60
	70 80 90 100 110 120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEKKDILNRYIDSYTIERARLFAAGHPHSNLVHIE
mooo.pcp	
a585	DAGAREILTEWKDSPVSSGVYVIQGDEKKDILHRYIDSYTIERARLFAAGHPHSNLVHIE
a303	70 80 90 100 110 120
	70 00 30 100 110 120
	130 ' 140 150 160 170 180
m585.pep	YDRFGEEYLFFTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAC
mooo.pep	
a585	YDRFGEEYLFFTKDWDKLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAC
asas	130 140 150 160 170 180
	130 140 130 100 170 100
	190 200 210 220 230 240
505	NIAKPIRILGNGMDRVANGELETRISQQVDDRDDELSHLAIQFDKMVEKLEKLVAKERHI
m585.pep	
- 505	NIAKPIRILGNGMDRVANGELETRISQQVDDRDDELSHLAIQFDKMVEKLEKLVAKERHI
a585	190 200 210 220 230 240
	190 200 210 220 230 240
	250 260 270 280 290 300
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPQKQEQYLKRLEGELTRMDTLAGELLTLSRLETS
a585	LHHVSHEMRSPLARMQAIVGLIQAQPQKQEQYLKRLEGELTRMDTLAGELLTLSRLETSN
	250 260 270 280 290 300
	310 320 330 340 350 360
m585.pep	MALEKESLKLLPFLGNLVEDNQSIAQKNGQTVTLSADGKIPENTTILANESYLYRAFDN\
a585	MALEKESLKLLPFLGNLVEDNQSIAQKNGQTVTLSADGKIPENTTILANESYLYRAFDN\

	310	320	330	340	350	360
m585.pep	370 IRNAVNYSPEGSTI IRNAVNYSPEGSTI	111111111	11111111111			
a585	370	380	390	400	410	420
	430	440	450	460	469	
m585.pep	GLGLALTQHIIEQH	CGKIIAENII	KPNGLRMRFII	PKKKTGSKT	EKSANX	
505				.PKKKTGSKT	 EKSANX	
a585	430	440	450	460		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1809>: g586.seq..

```
1 atggcagece atetegaaga acaacaagag ttagacaact ttaaatattt
51 ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 toggotactt gggatacacg gtttaccaaa accgtgcggc ttcccaaaat
caggaagcgg cggcggtgct ggcaaacatc gtggaaaagg cgcaaaacaa
201 agccccgcaa agcgaaatca atgccgaact gtccaaactc caacaaagct
251 acceccatte cattteegee geccaageea egetgatgge ggeggeaace
301 gaatttgacg cgcagcgtta cgatgttgcc gaaggtcatt tgaaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttggcg gcgcagcgtc
401 tgggcgttgt gttgttgcaa caaaaaaaat acgatgccgc gcttgccgca
451 ctcgacacgc cggttgaggc ggacttcgcc cccctgctga tggaaactaa
501 aggcgatgtt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaaact
551 acggacaggc tttggaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa
```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>: g586.pep..

- 1 MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRAASQN
- 51 QEAAAVLANI VEKAQNKAPQ SEINAELSKL QQSYPHSISA AQATLMAAAT
- 101 EFDAQRYDVA EGHLKWVLSN QKDSLIQALA AQRLGVVLLQ QKKYDAALAA
- 151 LDTPVEADFA PLLMETKGDV YAAQEKSQEA LKNYGQALEK MPQDSVGREL
- 201 LQMKLDSLK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1811>: m586.seg

```
ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAACT TTAAATATTT
    TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CTTGCTGATT TTGGCGGCAC
 51
101 TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTAAAGT TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTAGAAAAGG CGCAAAGCAA
    AGCCCCGCAA AGCGAAATCA ATGCCGAATT GACCAAACTC CAACAAAGCT
251 ACCCGCATTC CATTTCCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 GTTGTCCAAC CAAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCG
    CTCGATACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
451
    AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAAAAAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>: m586.pep

- MAAHLEEQQE LDNFKYFWKT TGKWLFALLI LAALGYLGYT VYQNRKVSQN 1
- 51 QEAAAVLANI VEKAQSKAPQ SEINAELTKL QQSYPHSISA AQATLMAAAT
- 101 EFDAQRYDVA EGHLKWVLSN QKDSLIQALA AQRLGVVLLQ QKKYDAALAA
- 151 LDTPVEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL
- VQMKLDSLK*

m586 / g586 97.1% identity in 209 aa overlap

30 40 10 MAAHLEEQQELDNFKYFWKTTGKWLFALLILAALGYLGYTVYQNRKVSQNQEAAAVLANI m586.pep

g586 MAA	HLEEQQELDNFKYFWKTTGKWLFALLILAALGYLGYTVYQNRAASQNQEAAAVLANI 10 20 30 40 50 60
	70 80 90 100 110 120 CAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAATEFDAQRYDVAEGHLKWVLSN :
111	130 140 150 160 170 180 SLIQALAAQRLGVVLLQQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA
111	190 200 210 TYGQALEKMPQDSVGRELVQMKLDSLKX
The following p	partial DNA sequence was identified in <i>N. meningitidis</i> <seq 1813="" id="">:</seq>
1 51 101 151 201 251 301 351 401 451 501 551	ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAACT TTAAATATTT TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTGCGGC TTCCCAAAAT CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGCTGATGGC GGCAGCAACC GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT ATTGTCCAAC CAAAAAGACA GCCTGATCCA GGCGTTGGCG GCGCAGCGTC TGGGCGTTGT GTTGTTGCAA CAAAAAAAAT ACGATGCCGC GCTTGCCGCA CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA AGGCGATGTC TATGCCGCAC AGGGAAAAAA CCAGGAAGCC TTAAAAAAACT ACGGACAGGC TTTAGAAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG GTTCAAATGA AACTTGATTC GCTGAAATAA
This correspond	Is to the amino acid sequence <seq 1814;="" 586.a="" id="" orf="">:</seq>
1 51 101 151 201	MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN QEAAAVLANI VEKAQNKAPQ SEINAELAKL QQSYPHSISA AQATLMAAAT EFDAQRYDVA EGHLKWVLSN QKDSLIQALA AQRLGVVLLQ QKKYDAALAA LDTPVEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGREL VQMKLDSLK*
m586/a586	97.6% identity in 209 aa overlap
m586.pep a586	10 20 30 40 50 60 MAAHLEEQQELDNFKYFWKTTGKWLFALLILAALGYLGYTVYQNRKVSQNQEAAAVLANI
m586.pep a586	70 80 90 100 110 120 VEKAQSKAPQSEINAELTKLQQSYPHSISAAQATLMAAATEFDAQRYDVAEGHLKWVLSN : :
m586.pep a586	130 140 150 160 170 180 QKDSLIQALAAQRLGVVLLQQKKYDAALAALDTPVEADFAPLLMETKGDVYAAQGKSQEA

```
190
                       200
          LKNYGQALEKMPQDSVGRELVQMKLDSLKX
m586.pep
          LKNYGQALEKMPQDSVGRELVQMKLDSLKX
a586
                       200
               190
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1815>:

```
a587.seq.
         atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
         ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
         aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
     101
         gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
         ccccattccg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
         ccggcacgct cggtttgcgc tacggactga ccggcaatac cgacatttac
         ggcagcggca gctatctgtg gcacgaagaa cgcaaactcg acggcaacgg
     301
     351 caaaacccgc aacaaacgga tgtccgacat atccgccggc atcagccaca
     401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
     451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
     501 gctttgcccc ttttataact taaggataaa ttatgaatat taa
```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```
g587.pep..
      1 MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENSR
      51 AALAAPVYIQ TGATSFIPIP TEIQENGSNT DMLAGTLGLR YGLTGNTDIY
         GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
         TVYEKSRNKA SLIKKRGLCP FYNLRINYEY *
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1817>:

```
m587.seq..
        ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
      1
        TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
     51
         AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
        GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
        CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
         TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
    251
        GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
    301
    351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
    401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
    451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
    501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
    551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
    601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
    651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
    701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
    751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
    801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
    851 GCGTACAGCA TACATTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```
m587.pep..
      1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
      51 AELAAPVYIQ TGATSFIPIP TEIQENGSNT DMLVGTLGLR YGLTGNTDIY
    101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
     151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLSDGIR
     201 YKSGNYLLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
         AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

```
m587 / g587 95.0% identity in 161 aa overlap
                                                      40
                                                                50
                                                                           60
                                           30
                      10
                                 20
```

m587.pep g587	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
9507	10 20 30 40 50 60
m587.pep	70 80 90 100 110 120 TGATSFIPIPTEIQENGSNTDMLVGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNSKTR
g587	TGATSFIPIPTEIQENGSNTDMLAGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTR 70 80 90 100 110 120
*	130 140 150 160 170 180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
g587	NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKKRGLCPFYNLRINYEY 130 140 150 160 170 180
m587.pep	190 200 210 220 230 240 LSLTAAYRINGSKTLSDGIRYKSGNYLLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587	x .
The following p	artial DNA sequence was identified in N. meningitidis <seq 1819="" id="">:</seq>
a587.seq	
1	ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51	TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101	AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151	GCCGAACTTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
201	TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
251	GGCAGCGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
301	CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
351 401	CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451	ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501	CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCGTCGTC CTCTCATTGA
551	CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601	TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651	CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701	CCGACCGTCT GGACGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751	GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801	ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851	GCGTACAGCA TACGTTTTAA
	s to the amino acid sequence <seq 1820;="" 587.a="" id="" orf="">:</seq>
a587.pep	MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
1 51	AELAAPVYIQ TGATSFIPIP TEIQENGSNT DMLVGTLGLR YGLTGNTDIY
101	GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151	TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 251	YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQH $\overline{ ext{TF}}^{\star}$
m587/a587	95.2% identity in 289 aa overlap
•	10 20 30 40 50 60
m597 non	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
m587.pep	
a587	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
4507	10 20 30 40 50 60
	70 80 90 100 110 120
605	70 80 90 100 110 120 TGATSFIPIPTEIQENGSNTDMLVGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNSKTR
m587.pep	
202	TGATSFIPIPTEIQENGSNTDMLVGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTR
a587	70 80 90 100 110 120

PCT/US99/09346 WO 99/57280

917

m587.pep	130 NKRMSDVSLGISHTF NKRMSDVSLGISHTF 130		1111111111	ППППП		11111:1
	200	* * * *	200	200		100
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTL	SDGIRYKSGN			GIQWLGRQ	PDRTDGK
a587	LSLTAAYRINGSKTL				GIQWLGKQI	
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGA	GFGFTKTTAL	NASARFNVSG	QSSSELKFGV	QHTFX	
	:::::::::::::::::::::::::::::::::::::::	111111111			11111	
a587	KESARNTSTYAHFGA			_		
	250	260	270	280	290	

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1821>:

```
g588.seq
         atgcttaaac atctcgcatt cctactgccc gccatgatgt tcgccctccc
      1
         cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
     51
     101 aaggcgggat cggaaaagac gggcttcctt caggcaaagg catatggcgt
     151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
         cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
         cqttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
         ttcaaacaag gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
    351 aaccctcttt tattatgaaa tgcgaacacg gcatgattaa
```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

g588.pep..

1 MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR 51 CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT 101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1823>:

m588.seq..

1 ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC 51 CACTTCGGCC GCCGTCCTGA CTTCCTATCA AGAACCAGGC TGCACCTACG 101 ACGGCAATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC 151 TGCCAAGACG GGCGCAACTA TACCGGTTCG TTTAAAAACG GCAAATTCGA 201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC 251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG 301 TTCAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAAC TGCCCAAAAA CAAATAA

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

m588.pep..

1 MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAGKGTWR CODGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m588 / g588 82.5% identity in 120 aa overlap

20 30 50 60

	·	
m588.pep	MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPAGKGTWRCQDGR	NYTGS
		:
g588	10 20 30 40 50	60
	70 80 90 100 110	120
m588.pep	FKNGKFDGQGVYTVAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQN	GETLF
		11111 GETT.E
g588	70 80 90 100 110	120
	130 139	
m588.pep	IMKCENGMIKEVKLPKNKX	
g588	YYEMRTRHDX	
9588	130	
The following p	partial DNA sequence was identified in N. meningitidis <seq 1<="" id="" td=""><td>825>:</td></seq>	825>:
a588.seq		
1	ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC	
51	CGCCGCGTCC GCCGTTCTGA CTTCCTATCA AGAACCCGGC TGCACCTACG	
101		
151 201		
251		
301	TTCAAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA	
351		
401	TGCCCAAAAA CAAATAA	
ant for a second and	ds to the amino acid sequence <seq 1826;="" 588.a="" id="" orf="">:</seq>	
	as to the amino acid sequence SEQ ID 1820, ORI 388.42.	
a588.pep	MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPAGKGTWR	
1 51	THE PARTY OF THE P	
101	The state of the s	
m588/a588	8 96.4% identity in 138 aa overlap	
	10 20 30 40 50	60
m588.pep	MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPAGKGTWRCQDGR	
msoc.pep		11111
a588	MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPAGKGTWRCQDGR	RNYTGS
	10 20 30 40 50	60
•	70 80 90 100 110	120
m588.pep		
mood.pep		
a588	FKNGKFDGQGVYTVAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQN	IGETLF
	70 80 90 100 110	120
	130 139	
m588.pep		
mooo.pop		
a588	IMKCENGMIKEVKLPKNKX	
	130	
The following t	partial DNA sequence was identified in N. gonorrhoeae <seq id<="" td=""><td>1827>:</td></seq>	1827>:
a589. sea.		

The fol g589

9.seq.	•				
1	atgcaacaaa				
51	tgcttcgcgc	attgaaaaag	tgttgaacaa	aaaagatttt	gtcgaatcgg
101	cgggagtgaa	ctttgccagt	gaggaagcgc	aggttacgtt	tgacggcagc
151	aaaacctcgg	ttgccgacat	tgccaaaatc	attgagaaaa	ccggttacgg
201	cgcgaaggaa	aaaacggaag	atacattgcc	gcaacctgaa	gcagaacacc
251	atatoggeta	acaattataa	cttttactaa	ccatcaatat	cccattcctt

```
atcggtatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
     ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgcaac
     tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaaggc
401
     gggctggcga atatggacgt actcgttacc atcggcacgg tgtcgattta
451
     cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggcgtga tggtgatcgg ttttgtgtcg
601 ctgggtaagt ttttggaaca ccgcaccaaa aaatccagcc tgaacagctt
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
     cgcaccaacc acggcgaacg catcgctgcc gacggcatta tcgaaagcgg
     cagcggttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
     agaaaaaggc gggcggcaaa gtgttggcgg gcgcgctgat gaccgaaggc
851
901 agcgtggtgt accgcgccgc gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggctg attaagggcg attggacggt
1101 cgcactgatg cacgccgttg ccgttttggt gattgcctgc ccgtgcgcgc
1151 teggtetgge gacceetgee gegattatgg teggeatggg caaageggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtattgg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc cgccgtttat tacgttcccg acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgccg cccacccgct
1401 cgcccgcgcc atcgtctccg ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaacc gttgtcggag caggcattac cgccgaagtg
      gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
      cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
     tatctgtaaa cggcaaaccg atcggcgcat tcgcactctc cgacgcgttg
     aaagccgata ccgccgaagc cataggccgt ctgaaaaaac acaatatcga
1651
     tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1701
     aacaactggg catcgcacac gccttcggta atatgagtcc gtgcgacaaa
1751
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccg tggcgatggt
     cggcgacggc atcaacgacg cgcccgcgt tgccgccgcc aacgtcagct
1851
1901 tegecatgaa aggeggtgeg gaegttgeeg aacacacege eteegeeaeg
1951 ctgatgcagc attcggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatattggg catteegete geegegeteg getttttaaa teeegteata
2101 gcaggcgcgg caatggcggc aagctcggtt tcggtattgg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga
```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

```
g589.pep.
      1 MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
     51 KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
    101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPF YKSAWASIKG
    151 GLANMOVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
    201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
         RTNHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
         SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
         ALLTFIVAWL IKGDWTVALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
         KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAVY YVPDSGFDED
     451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
     501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
     551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
     601 AAEVQKLKAA GKTVAMVGDG INDAPALAAA NVSFAMKGGA DVAEHTASAT
     651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
     701 AGAAMAASSV SVLGNALRLK WVKID*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1829>:

```
m589.seq..
      1 ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
         CGCTTCGCGC ATTGAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
         CGGGGGTAAA CTTCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
         AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
         CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
     251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCCTT
```

```
301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
     GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
    CGTTTTACAA AAGCGCGTGG GCGAGCATTA AGGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCACTGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
     GCAAAGTGTT GGCGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCCAGCTC GGCGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TGCGCGCGTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCCT GCCGTCGTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CGCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTTAAACA CGGTATTTGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCACGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCCG
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTTGGACAT TCCCGCCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACCGCCG AAGTGGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TGCGGTCTCA GTCGATAACA
1601 AACCCATCGG CGCATTCGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
      GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACTCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGCATTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTC
      CTCTCGCCGC GCTTGGCTTT TTAAATCCCG TCATCGCTGG CGCGGCAATG
2051
     GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAAACGGGT
2101
     AAAAATCGAT TAG
2151
```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

```
m589.pep.
       1 MQQKIRFQIE GMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDS
      51 KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLFTINVPFL
     101 IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANM
     151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVYFEVGVMV IGFVSLGKFL
          EHRTKKSSLN SLGLLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDLIRANHG
         ERIAADGIIE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
     301 ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTF
          IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
     351
         FKDAAAMEEA AHVDAVVLDK TGTLTEGSPQ VAAVYCVPDS GFDEDALYRI
     451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
          VKAGKAEFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
     501
         EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
     551
          KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
          VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
     651
          AASSVSVLSN ALRLKRVKID *
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

```
m589 / g589 94.2% identity in 725 aa overlap

10 20 30 40 50 60

MQQKIRFQIEGMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIAKI
```

	MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIA	Ί
g589	10 20 30 40 50	50
	70 80 90 100 1 110	νт
m589.pep	10 80 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIGRHDWN	
g589	TOWN CANDED TI. POPEAEHHTGWRLWLLTINIPELIGHVGMMINGERWITH	30 aT
	140 150 160 170	
m589.pep	PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSP	1 1
g589	PPVWQFVLASIVQLWLAIPFYKSAWASIKGGLANMDVLVIIGIVSIILISVIMMITSS	НА 80
·	130 140 150 150	
	180 190 200 210 220 220 220 220 220 220 220 22	LΡ
m589.pep	:	1 1
g589	190 200 210 220 230 2	40
	240 250 260 270 280 290 240 250 250 250 250 250 250 250 250 250 25	EG
m589.pep	240 250 200 200 200 200 200 200 200 200 20	} I
g589	TROUGTODI TRYNHGERTAADGI IESGSGWADESHLTGESN PEEKKAGGK V LAGALET	00
	300 310 320 330 340 350	37.7 T
m589.pep	SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFIVI	
g589	OTHER A DE COOPLICEMENTAL SEAGGSKAPIAKVADKAAAVEVEI VVGIABBILIV	WL 360
	- ·	

m589.pep	360 370 380 390 400 410 IKGDWTVALMHAVAVLVIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA
m589.pep g589	420 430 440 450 460 470 VVLDKTGTLTEGSPQVAAVYCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL
m589.pep g589	480 490 500 510 520 530 DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP :
m589.pep g589	540 550 560 570 580 590 IGAFALADALKADTAEAIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK :
m589.pep g589	600 610 620 630 640 650 AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA
m589.pep	660 670 680 690 700 710 DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK
m589.pep g589	720 RVKIDX

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1831>:

artial DINA Si	equence was	Idollilliou M	1111 ///	`
_		~~» » » m~~ ~ » »	СССАТСАССТ	GCCAGGCATG
				GTCGAATCGG
TGCTTCGCGC				TGACGACAGC
CGGGGGTAAA				
AAAACCTCAG				
CGCGAAGGAA	-		-	CCCGTTCCTT
ATATCGGCTG	GAGGTTGTGG	0		
ATCGGTATGG	TAGGGATGAT	• • • • • • •		CACGGCATGA
TTGGATGTTG	TCGCCCTTGT	TGCAGTTTGC		GTGGTGCAGC
TTTGGCTGGC	GGTGCCATTT	TACAAAAGCG		CATTAAAGGC
GGGCTGGCGA	ATATGGACGT	ACTCGTTACC		TCTCGATTTA
	GTCTATATGC	TGTTTTTCAG	-	GCGTACGGTA
	GTATTTTGAA	GTAGGCATAA		TTTTGTGTCA
	TTTTGGAACA	CCGCACCAAA	AAATCCAGCC	TGAACAGCTT
		CGCCAACCCA	AGTCAACGTG	CAACGCGATG
				CGACCTAATC
				AATCCCGAAG
			AGCCAAACCC	
				CCGATTGCGC
				TGTGGGCATC
				ATTGGACGCT
				CCGTGTGCAC
CGCATIGATG	CACCCCCTCC	0001111001	-	
	ATGCAACAAA TGCTTCGCGC CGGGGGTAAA AAAACCTCAG CGCGAAGGAA ATATCGGCTG ATCGGTATGG TTGGATGTTG TTTGGCTGGCGA CCTGTATTCC TGGCGCATGT CTGGGTAAAT GGGCTTGCTG GCGCAATCC CGCGCCAATC CAGCGGCTGG AGAAAAAGGC AGCGTGGTGT CATGATGAAC GTGTGGCGAA	ATGCAACAAA AAGTCCGTTT TGCTTCGCGC ATTGAAAAAG CGGGGGTAAA CTTCGCCAGC AAAACCTCAG TAGCCGACAT CGCGAAGGAA AAAACGGAAG ATATCGGCTG GAGGTTGTGG ATCGGTATGG TAGGGATGAT TTGGATGTTG TCGCCCTTGT TTTGGCTGGC GTTGTATTCC GGCTGGCGAA ATATGGACGT CTGGGTAAAT TTTTGGAACA CGGCTTGCTG GTATTTTGAA CTGGGTAAAT TTTTGGAACA GCGCTAGTG GCAGCTACCC CAGCGCCAATC ACGCGCAACA AGAAAAAGGC AGGCGGCAAA AGCGTGGTGT ACCGCGCCGC CATGATGAAC GCGCTCCCG GTGTGGCGGA CAAGGCGGCGC GTGTGGCGGA CAAGGCGGCGC GTGTGGCGGA CAAGGCGGCGC GCACTTTTGA CTTTTATCGC	ATGCAACAAA AAGTCCGTTT CCAAATCGAA TGCTTCGCGC ATTGAAAAAG TGTTGAACAA CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AAAACCTCAG TAGCCGACAT TGCCAAAATC CGCGAAGGAA AAAACGGAAG ATACATTGCC ATGCGTATGG TAGGGATGAT GCTAAAAGGG ATGGGTGGC GTGCCATTT TGCAGTTTGC TTTGGCTGGC GGTGCCATTT TACAAAAGCG CCTGTATTCC GTCTATATGC TGTTTTCAG CTGGGTAAAT TTTTGGAACA CCGCACCAAA CGGGCTGGC GCAGCTACC ACGCCACCAA GGGCTTGCTG CTCAAACTCA CGCCACCAAA CGGCCAATC ACGCCAACCCA ACGCGCAAC ACGCCAACCCA ACGCGCCAAC ACGCCACCAAA CGCGCCAATC ACGCCGAAA GCCATCTTAC CAGCGGCTGG GCGACCGAAA GCCATCTTAC AGAAAAAGGC AGCCGCCGC GCAGCTCGCC CATGATGAAC CCGCCCCC GCAGCTCGCC CATGATGAAC CCGCCCCC GCAGCTCGCC CATGATGAAC CCGCCCCC GCAGCTCGCC CATGATGAAC CCGCCCCC GCAGCTCGCC CATGATGAAC CCGCCCCC GCAGCTCGCC CATGATGAAC CCGCCCCC GCAGCTCGCC CATGATGAAC CCGCCCCC GCAGCTACCC CATGATGAAC CCGCCCCC GCAGCTCGCC CATGATGAAC CCGCCCCC GCAGCTCGCC CATGATGAAC CCAAGCCCAAC CATGATGAAC CCGCCCCC CCAGCCCAAC CATGACGCAACCCAACCCAACCCAACCCA	TGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AGGTAGTGT AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA ACGGAAG AAAACGGAAG ATACATTGCC GCAACCCGAA ATATCGGCTG GAGGTTGTG CTTTTGCTGG CCATCAATAT TTGGATGTTG TCGCCCTTGT TGCAGTTTGC ATTGGCAGT TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGCGAG CCTGTATTCC GTCTATATGC TGTTTTCAG CCCGCACGG CCTGTATTCC GTCTATATGC TGTTTTCAG CCCGCACGCG CCTGGCAAAT TTTTGGAACA CCGCACCAA AAATCCAGCC CGGCCAATC CTCAAACTCA CGCCAACCCA AGTCAACGTG CGGCCAATC CCGGAACCC ATCGACCAA AAATCCAGCC CAGCGGCTGG GCGGCAAAA GCCAACCA AGTCAACGTG CAGCGGCTGG GCGGCAAAA GCCATCTTAC CGCCAACCCA AGCAAAAAGGC AGGCGCAAA GCCATCTAC CGCCAACCCA AGAAAAAAGGC AGGCGCAAA GCCATCTTAC CGCCAACCCA AGCGGCTGGT ACCGCCCACAA GCCAAACCCC CAGCGGCTGG CCGCCCAAAA GCCAAACCCC CAGCGCCAAC CAGCGCAACA GCCAAACCCC CAGCGCCAAC CAGCGCAACCA GCCCAAACCCC CAGCGCCAAC CAGCCCAAAACCCC CAGCGCCAAC CAGCCCAAAACCCC CAGCGCCGCC CCAGCCCAACCCA AGCCCAAACCCC CAGCGCCAACCCA AGCCCAAACCCC CAGCGCCAAC CAGCCCAACCCA AGCCCAAACCCC CAGCGCCAACCCA AGCCCAAACCCC CAGCGCCCCC CCCCCCC CACCCAACCCA

190

a589

	\cdot
	TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1151	TO THE TAX THE PROPERTY A MEMORITURE OF THE PROPERTY OF THE PR
1201	THE TOOK CHICKNESS ACADACTIC LACTURE CARCOCING
1251	CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1301	GCTTTGTACC GCATCGCCG CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1351	GCTTTGTACC GCATCGCCGC CGCCGAGGC GCGCGTTTG GAGATTCCCA CGCCCGTGCC ATCGTCTCCG CCGCCCAGGC GCGCGTTTG GAGATTCCCA
1401	CGCCCGTGCC ATCGTCTCCG CCGCCCAGGC CGGGCATTAC CGCCGAAGTA CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCAAGTA
1451	CCGCACAAAA TGCCCCAAACC ATTGTCGGGGG CCGCAATTTG CCGAACTGAC
1501	AAAGGCGCG GTTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551	AAAGGCGCGG GTTTGGTAAA AGCAGGCGAAA AATCGCCAGT GTGGTTGCCG CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGTTGCC GGACGCGTTG
1601	TATCTGTAAA CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651	AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701	TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751	TRANSPORCE CATCECACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801	COCCCCARC TCCAGAACT CAAAGCCGCC GGCAAAACCG IGGCGAIGGI
1851	ACCOUNT COOL AMOND CONTROL COCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOCCOC
1901	MOCGORMONA ACCOCCUTCOA GACGTTGCCG AACACACCGC ATCCGCCACA
	OF THE COLOR NUTCE COLOR
1951	AGGAGGERG AAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2001	ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTTAAA CCCCGTCATC
2051	GCAGGCGCG CAATGCCGCT AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2101	GCAGGCGCG CAATGCCGC AAGCCCCCCT
2151	GCGCCTGAAA CGGGTAAAAA TCGATTGA
	OFO ID 1922, OPE 590 a>:
This correspond	Is to the amino acid sequence <seq 1832;="" 589.a="" id="" orf="">:</seq>
a589.pep	
	MQQKVRFQIE GMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDS
1	KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
51	IGMVGMMLKG LNWTRHDWML SPLLQFALAS VVQLWLAVPF YKSAWASIKG
101	GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMAHVYFE VGIMVIGFVS
151	GLANMOVLVT IGTVSTILIS VIMILETSTILL OPDCEMBOLD IDOVOIGOLI
201	LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251	RANHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301	SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351	PLIMETARMI TECOMPLAIM HAVAVLVIAC PCALGLATPA AIMVGMGRAV
401	VUCTUEVDA AMERAAHVDA VVLDKTGTLT EGKPQVAAVI CVPDSGEDED
451	TARTARAUE ONARHPIARA TVSAAOARGL EIPTAQNAQT IVGAGITAEV
	WORCHWACK AFFAFITIPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
501	WARDERICO I KKHNIDVYI MSGDNOGTVE YVAKQLGIAH ALGNMAPKUK
551	AAEVOKLKAA GKTVAMVGDG INDAPALAAA NVSFAMKGGA DVAEHTASAT
601	
651	LMQHSVNQLA DALSVSKAIL KNIKQNDITA ITIMISETI
701	AGAAMAASSV SVLSNALRLK RVKID*
	TOE on everlan
m589/a58	9 94.9% identity in 725 aa overlap
	10 20 30 40 50 60
m589.pep	MQQKIRFQIEGMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIAKI
a589	MOOKVR FOTEGMTCOACASRIEKVLNKKDFVESAGVN FASEEAQVV FDDSKISVADIAKI
a303	10 20 30 40 50 60
	70 80 90 100 1 110
	THE TAX TO SEE THE PORT OF THE
m589.pep	
	IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLAINIPFLIGMVGMMLKGLNWTRHDWML
a589	
	70 80 90 100 110 120
	120 130 140 150 160 170
	120 130 140 150 160 170 PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
m589.pep	DDI MOEAL A SUVOLWI A TPFYKSAWASIKGGLANMDV LVTIGIV SI ILI SVIMLE E SENA
	bernotanga Agrantiti i marangan ang ang ang ang ang ang ang ang an
a589	SPLLQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
	SPLLQFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA

AYGMAHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP

220

210

200

230

240

m589.pep	240 250 260 270 280 290 IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG
m589.pep	300 310 320 330 340 350 SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFIVTWL
m589.pep	360 370 380 390 400 410 IKGDWTVALMHAVAVLVIACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA :
m589.pep	420 430 440 450 460 470 VVLDKTGTLTEGSPQVAAVYCVPDSGFDEDALYRIAAAVEQNAAHPLARAIVSAAQARGL
m589.pep a589	480 490 500 510 520 530 DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP : : : : EIPTAQNAQTIVGAGITAEVKGAGLVKAGKAEFAELTLPKFSDGVWEIASVVAVSVNGKP 490 500 510 520 530 540
m589.pep a589	540 550 560 570 580 590 IGAFALADALKADTAEAIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK
m589.pep a589	600 610 620 630 640 650 AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA
m589.pep	660 670 680 690 700 710 DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK
m589.pep a589	720 RVKIDX RVKIDX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1833>: g590.seq...

```
1 atgaaaaaac ctttgattc agttgcggca gtattgctcg gcgttgcttt
51 gggtacacct tattatttgg gtgtcaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggcttt tgaccgtcga atcgcaccag
151 tatgatcgag gctggtttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtgttgga acagccggtt acgctggtaa accatatcac gcacggcct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgcctgaa acggaaaaaag ttttggaacg cttttttggg aaacaagttc
401 cggtttccct tgccaatacc gtttatttca acggcagcg taaaatggaa
451 gtcagtgtc ccgctttcga ttatgaagaa ctgtcgggca tcaggctgca
```

```
501 ctgggaaggc ctgacggggg aaacggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttgttca aaatcaagct ggcagacaaa
601 ggcgatgccg cgtttgaaaa agcgcatttc gattcggaaa cttcagacgg
651 catcaatccg cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggt gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcategea cettecaaaa tegaagtegg caagetgget ttttcaacca
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951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgcgg cagtcaaagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag ggaaaaattg
1151 atgtgggcgg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tcctcaaaaa atgttggaag atttggcggt aagtcaggct ggaaatattt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatggtggac agtacggtcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgccctg aagttaaacg ggaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a
```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>: g590.pep..

```
1 MKKPLISVAA VLLGVALGTP YYLGVKAEES LTQQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKPEL LHNAQKYLPD NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSYRNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMKKEDLN
401 QLGLMLKKTE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEARASIAD
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1835>:

```
m590.seq (partial)
         ..TGGTTTACCT CTATGGAAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
            GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAAACA GTGTTGGAAC
      51
           AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
            TTCGGCACGC AGGCGTACAT TGAAACCGAG TTCAAATACG CGCCTGAAAC
     151
            GGAAAAAGTT CTGGAACGCT TTTTTGGAAA ACAAGTCCCG GCTTCCCTTG
            CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCC
     251
            GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG.CTGCACT GGGAAKGCCT
     301
            GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGCTAC CGGAACGGCT
     351
            ATGATGCCCC CTTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
     401
            TTTGAAAAAG TGCATTTCGA TTCGGAAACT TCAGACGGCA TCAATCCGCT
     451
            TGCTTTGGGC AGCAGCAATC TGACCTTGGA AAAATTCTCC CTAGAATGGA
            AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTTGTT
     551
            ACCGATTTGC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
     601
            TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
     651
            CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
     701
            TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
     751
            CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
     801
            CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
     851
            GTCAAAGGAG AGGCTTCCGG ACTGTTCACC AACAATCCCG TATTGGACAT
     901
            TAAAACTTTC CGATTCACGC TGCCATCGGG AAAAATCGAT GTGGGCGGAA
     951
            ARATCATGTT TARAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
     1001
            ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAAT
     1051
            GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
     1101
             CCGAAGATGA GGCGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
     1151
            TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
     1201
             TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTTCT CTGAAAAACA
     1251
             ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
     1301
             TTTGATGAAG GCGGTATGGT TTCAGAGCCG CAGCAGTAA
     1351
```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590.pep(p 1 51 101 151 201 251 301 351	WFTSMETTVI RLKPELLNNA RKYLPDNLKT VLEQPVTLVN HITHGPFAGG FGTQAYIETE FKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSVP AFDYEELSGI XLHWEXLTGE TVYQKGFKSY RNGYDAPLFK IKLADKGDAA FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVDYN VKLNELVNLV TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMTE EQIRNDLIAA VKGEASGLFT NNPVLDIKTF RFTLPSGKID VGGKIMFKDM KKEDLNQLGL MLKKTEADIR MSIPQKMLED LAVSQAGNIF SVNAEDEAEG RASLDDINET LRLMVDSTVQ SMAREKYLTL NGDQIDTAIS LKNNQLKLNG KTLQNEPEPD
401	FDEGGMVSEP QQ*
451	
m590 / g590	93.1% identity in 462 aa overlap 10 20 30
m590.pep	WFTSMETTVIRLKPELLNNARKYLPDNLKT
g590	VKAEESLTQQQKILQKTGFLTVESHQYDRGWFTSTETTVIRLKPELLHNAQKYLPDNLKI 30 40 50 60 70 80
	40 50 60 70 80 90 VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
m590.pep	
g590	VLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN 90 100 110 120 130 140
	100 110 120 130 140 150
m590.pep	GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
	CCCVMEUSUPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNSYDAPLIFKIKUADKODIU
g590	150 160 170 180 190 200
	160 170 180 190 200 210
m590.pep	THE COUNTY OF THE PRESIDENCE O
((S 30 . pcp	
g590	FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN 210 220 230 240 250 260
	250 270
	220 230 240 250 250 250 250 250 250 250 250 250 25
m590.pep	
g590	PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLV IGDERIGFEDITITALISM
	270 280 230
	280 290 300 310 320 330 SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
m590.pep	
g590	SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGDASGIFTIDI 380
_	330 340 350 500
	340 350 360 370 380 390
m590.pep	340 350 360 VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
g590	VGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQRHLEDHAVSQAGATIS
9390	390 400 410 420 430 440
	400 410 420 430 440 450
m590.pep	TINCHOTOTAL SLKNNOLKLNGKTLONEPEPD
	RASLDDINETLRLMVDSIVQSMAREKIHIMGSQLDI:: :
g590	450 460 470 480 490 500
m590.pep	460 FDEGGMVS-EPQQX
	[[1] [1] :[:
g590	FDEGDMVSGQPHX 510

m590.pep

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1837>:

```
a590.seq
              ATGAAAAAAC CTTTGATTTC GGTTGCGGCA GCATTGCTCG GCGTTGCTTT
              GGGCACGCCT TATTATTTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
          51
             AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
         101
             TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
         201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
             CAGTGTTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
              TTTGCCGGCG GATTCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
              CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
              CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
              GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
             CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
         551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
         601 GGCGATGCCG CGTTTGAAAA AGTGCATTTC GATTCGGAAA CTTCAGACGG
         651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
         701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
         751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
         801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
         851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
         901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
         951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
              TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
        1001
        1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
             AGTATTGGAC ATTAAAACTT TCCGATTCAC GCTGCCATCG GGAAAAATCG
        1101
        1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAC
              CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
        1201
              TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
        1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
         1251
        1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
        1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
        1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
              CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
         1501
         1551 A
This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:
     a590.pep
               MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE AGFLTVESHQ
               YERGWFTSTE TTVIRLKPEL LHNAQKYLPD NLKTVLEQPV TLVNHITHGP
              FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
               VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSYRNGYDA PLFKIKLADK
              GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
               VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
              GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
              LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
               QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
               INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNNQL KLNGKTLQNE
               PEPDFDEGGM VSEPQQ*
          501
                  97.8% identity in 462 aa overlap
     m590/a590
                                                                  20
                                                        10
                                                WFTSMETTVIRLKPELLNNARKYLPDNLKT
     m590.pep
                                                1111 111111111111111111111111111111
                  VKAEESLTQQQKILQEAGFLTVESHQYERGWFTSTETTVIRLKPELLHNAQKYLPDNLKT
      a590
                                                              70
                                                    60
                                          50
                                 40
                                                                            90
                                                        70
                                    50
                                              60
                  VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
      m590.pep
                   VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
      a590
                                                                       140
                                                   120
                                                             130
                                100
                                         110
                       90
                                                                           150
                                                                 140
                                                       130
                                    110
                                             120
                  GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
```

a590	GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA 150 160 170 180 190 200
m590.pep	160 170 180 190 200 210 FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
m590.pep	220 230 240 250 260 270 PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGQFRFDTLVYGDEKYGPLDIHIAAEHLDA
m590.pep	280 290 300 310 320 330 SALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
m590.pep a590	340 350 360 370 380 390 VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEG
m590.pep a590	400 410 420 430 440 450 RASLDDINETLRLMVDSTVQSMAREKYLTLNGDQIDTAISLKNNQLKLNGKTLQNEPEPD IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
m590.pep a590	460 FDEGGMVSEPQQX FDEGGMVSEPQQX 510

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1839>: m590-1.seq

90-1.seg	Ī			aar mmaamaa	CCC##CC###
1	ATGAAAAAAC	CTTTGATTTC		GCATTGCTCG	TTGACGCAGC
51	GGGCACGCCT	TATTATTTGG	0101011111	COLUMNIC	
101	AGCAAAAAAT	ATTGCAGGAA	ACGGGCTTCT		ATCGCACCAA
151	TATGAGCGCG	GCTGGTTTAC	CTCTATGGAA	ACGACGGTCA	
201	ACCCGAGTTG	CTGAATAATG	CCCGAAAATA	CCIGCGGG	AACCTGAAAA
251	CAGTGTTGGA	ACAGCCGGTT	ACGCTGGTTA	ACCATATCAC	GCACGGCCCT
301	TTCGCCGGCG	GATTCGGCAC	GCAGGCGTAC	ATTGAAACCG	AGTTCAAATA
351	CGCGCCTGAA		TTCTGGAACG	CTTTTTTGGA	
401	CGGCTTCCCT	TGCCAATACC	GTTTATTTTA	ACGGCAGCGG	TAAAATGGAA
451	GTCAGTGTTC		TTATGAAGAG	CTGTCGGGCA	TCAGGCTGCA
	CTGGGAAGGC		AAACGGTTTA	TCAAAAAGGT	TTCAAAAGCT
501	ACCGGAACGG		CCCTTGTTTA	AAATCAAGCT	GGCAGACAAA
551	GGCGATGCCG			GATTCGGAAA	CTTCAGACGG
601	CATCAATCCG		GCAGCAGCAA	TCTGACCTTG	GAAAAATTCT
651	0111 01 11 1 1 1		GTCGATTACA		AAACGAACTG
701	CCCTAGAATG		GCAGATTGGC		ATCCCAACGG
751	GTCAATCTTG				TTTTCAACCA
801	CAGCATCGCA				GTTCCGTTTC
851	AGACCGGGGA				
901	GATACACTGG				
951	CGCTGCCGAA				
1001	TTGCACAAAT				
1051	TTGATTGCC				
1101	CGTATTGGAC				AGATTTGAAT
1151	ATGTGGGCG				
1201	CAATTGGGTT	TGATGCTGAA	GAAAACCGAA	GCCGACATCA	GAATGAGTAT

```
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
        TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
        ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
        AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
   1351
   1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA
        CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
   1551 A
This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:
      1 MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE TGFLTVESHQ
m590-1.pep
        YERGWFTSME TTVIRLKPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
        FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
     51
        VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSYRNGYDA PLFKIKLADK
    101
        GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
        VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
    251
        DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
        LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
         QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
    351
        INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNNQL KLNGKTLQNE
    451
         PEPDFDEGGM VSEPQQ*
             93.6% identity in 516 aa overlap
m590-1/g590
                                                       50
                                              40
                            20
            MKKPLISVAAALLGVALGTPYYLGVKAEESLTQQQKILQETGFLTVESHQYERGWFTSME
m590-1.pep
            MKKPLISVAAVLLGVALGTPYYLGVKAEESLTQQQKILQKTGFLTVESHQYDRGWFTSTE
q590
                                                       50
                                              40
                                     30
                                                               120
                                                      110
                                             100
                                     90
                            80
                   70
            TTVIRLKPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
m590-1.pep
            ពិយីណ៍មិននេះអណ្តាស មេវិយណាយអេចអញ្ជាន់មួយអាយ
            TTVIRLKPELLHNAQKYLPDNLKIVLEQPVTLVNHITHGPFAGGFGTQAHIETEFKYAPE
q590
                                                      110
                                     90
                   70
                            80
                                                      170
                                             160
                                     150
                           140
            TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
                  130
            m590-1.pep
            TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
g590
                                                      170
                                     150
                                             160
                            140
                  130
                                                                240
                                                       230
                                     210
                                              220
                            200
            FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
            m590-1.pep
            FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
 g590
                                                                240
                                              220
                                     210
                            200
                   190
                                                       290
                                                                300
                                              280
                                     270
                            260
                   250
            VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFSTKTGESGAFINSEGQFRF
             ninningeniumianenminningeniumianen:m:m
 m590-1.pep
            VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRF
 q590
                                              280
                                                       290
                            260
                                     270
                   250
                                     330
                                              340
                                                       350
                            320
             DTLVYGDEKYGPLDIHIAAEHLDASALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGEAS
             m590-1.pep
             DTLVYGDEKYGPLDIHIAAEHLDASALTVLKRKFAQISAKKMTEEQIRNDLIAAVKGDAS
 a590
                                                       350
                                              340
                            320
                                     330
                   310
                                                       410
                                                                420
                                     390
                                              400
                            380
                   370
             GLFTNNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
             инение иниениини ининииниений
 m590-1.pep
             GLFTHDPVLNIKIFRFTLPQGKIDVGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQK
 q590
                                                       410
                                                                420
                                              400
                            380
                                      390
                   370
                                               460
                                      450
                            440
                   430
             MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRLMVDSTVQSMAREKYLTLNGDQID
 m590-1.pep
             инининининины: пинининининин
             MLEDLAVSQAGNIFSVNAEDEAEARASIADINETLRLMVDSTVQSMAREKYLTLDGNQID
 q590
                                                       470
                                                                 480
                                               460
                                      450
                   430
                             440
                             500
                                      510
```

TAISLKNNQLKLNGKTLQNEPEPDFDEGGMVS-EPQQX

m590-1.pep

g590	: TVISLKNNALKLNGKT 490	: LQNEPDPDF: 500	III : : DEGDMVSGQPH 510	x		
a590/m590-1	98.3% identity	in 516 a	a overlap			
a590.pep m590-1	10 MKKPLISVAAALLGVA MKKPLISVAAALLGVA		1 1 1 1 1 1 1			VETSME 60
a590.pep m590-1	70 TTVIRLKPELLHNAQF TTVIRLKPELLNNARF 70		1 1 1 1 1 1 1 1 1 1 1			FKYAPE 120
a590.pep m590-1	130 TEKVLERFFGKQVPVS TEKVLERFFGKQVPAS		1111111	FDYEELSGI	RLHWEGLTGE	TVYQKG 180
a590.pep	190 FKSYRNGYDAPLFKI FKSYRNGYDAPLFKI 190			1 1 1 3 1 1 1 1 1	SSNLTLEKFS 230	LEWKEG 240
a590.pep m590-1	250 VDYNVKLNELVNLVT VDYNVKLNELVNLVT 250			1111111	11111111	11111
a590.pep m590-1	310 GTLVYGDEKYGPLDI DTLVYGDEKYGPLDI 310	111111111	1111111	:		11111
a590.pep m590-1	370 GLFTHNPVLDIKTFF : GLFTNNPVLDIKTFF 370				1	
a590.pep m590-1	430 MLEDLAVSQAGNIFS MLEDLAVSQAGNIFS 430			1 1 1 1 1 1 1 1 1	1 1	11111
a590.pep m590-1	490 TAISLKNNQLKLNG TAISLKNNQLKLNG 490	111111111		111		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1841>:

արար հ	artial Divis	oquonos		Ü	
591.seq				> macanc > mmm	ም ርርምር አርርርጥ
1	TTGCAAACCC	TTCTAGCTTT	TATCTTCGCC	ATCCTGATTI	IGGICAGCCI
51	CCACCAATTC	GGACACTACA	TCGTCGCCAG	GTTGTGCGGC	GTCAAGGTTG
	TGCGTTTTTC	CGTCGGCTTC	GGCAAACCGT	TTTTCACCCG	AAAGCGCGGC
101	GACACCGAAT	COTCOCOTTC	CCCCATTCCC	TTGGGCGGCT	ACGTCAAAAT
151	GACACCGAAT	GGTGCCTCGC	CCCGATICCG	110000001	CCCT TOCOM
201	GGTCGATACG	CGCGAAGGCG	AAGTATCAGA	AGCCGATTTA	CCCTACGCTT
	TTGACAAACA	ACACCCCCCC	AAGCGCATCG	CCATCGTCGC	CGCCGGTCCG
251	TTGACAAACA	ACACCCCCCC	711000011100	macccacacae	actTttcctt
301	CTGACCAACC	TCGCActggc	ggTTTTGCTG	TACGGACTGG	geereeee
351	caacataaCC	GAACTGCGGC	CCtatgtcgg	cacagtcgaA	cccgacaccg
221	cggcgcaco				

WO 99/57280

931

```
ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
     ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
     CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
     AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
     GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
     TGCCGGCGGC GTGGAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
     CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGC ctcaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAACTAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
      CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
      CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G
```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

```
9591.pep..

1 LQTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG
51 DTEWCLAPIP LGGYVKMVDT REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVQDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPAEKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQTHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVLNLL PVPVLDGGHL
401 VFYTVEWIRG KPLGERVQNI GLRFGLALMM LMMAAAFFND VTRLIG*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1843>:

```
m591.seq
          TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
          GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
          TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
          GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
         GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
          TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
     201
         CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
     251
     301
          CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
     351
         TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAAATACA ATCCGTCAAC
     451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
     501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
     551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
     601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
     651 TGCCGGCGC GTGGAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
          CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGC CTCATGGCAA
     701
          GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
      751
          CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
      801
          TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
      851
           CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
          TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
          CAACCCTCAA ATTTTTCGGC AAACTAATCA GCGGCAACGC CTCCGTCAGC
     1001
          CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
     1051
          ACTCGGCTTG CAAAGTTATT TGGAATTTTT AGCACTGGTC AGCATCAGCC
           TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
     1101
           GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
     1151
     1201
           CCAAAACATC GGTTTGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
     1251
           CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G
```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>: m591.pep..

	LHTLLAFIFA	TITIUSTHEE	CHYTVARLCG	VKVVRFSVGF	GKPFFTRKRG
1	DTEWCLAPIP	THILLYSHIPE	PECENCEADI	DAYEDKURDY	KRTAIVAAGP
51	DTEWCLAPIP	LGGYVKMVDT	KEGEAZEMOT	FIREDROMEN	OCCUMENTACION
	D T 7577 T	VCISESEGVT	FIRPYVGTVE	PDTIAARAGE	ÖZGDVIĞZAN
101	GTPVADWGSA	OBSTAINIE A	CKVAVCVOTA	SGAOTVRTID	AAGTPEAGKI
151	GTPVADWGSA	ÖLFIATMTEW	GUANGAGIII	OT UDCDDIMA	ADCKPTASWO
201	AKNOGYIGLM	PFKITTVAGG	VEKGSPAEKA	GLKEGDKLIA	ADGRETADIO
	mp 00 p	CEPTTENVER	ACOTHTADIR	PDTVEQSORT	PIGKAGTUE O
251	PDRAWDAQIR	GWITTHID	DOMONEYERS	UCMTTLKFFG	KLISGNASVS
301	PDRAWDAQIR	RSYRPSVVRA	FOWCMEVIAS	NOWITHKIE O	DUDUI DOCUI
		TACOCATICI.	OSYLEFLALV	SISLGVLNLL	EASATDGGHT
351	HIOGERIAND	KPLGERVQNI	CIRCLALMM	LMMAVAFFND	VTRLLG*
A ∩ 1	VEYTAEWIRG	Khtgrkaður	GUILLOTHIT		

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m591 / g591	97.3% identity in	446 aa ov	erlap			
F.0.1 non	10 LHTLLAFIFAILILVSL	20 HEFGHYIVAR	30 LCGVKVVRFS	40 VGFGKPFFTF	50 KRGDTEWCLA	60 APIP
m591.pep			1 1 1 1 1 1 1			111
g591	LQTLLAFIFAILILVSL	HEFGHYIVAR 20	LCGVKVVRFS 30	40	50	60
	70	80	90	100	110	120 FGVT
m591.pep	LGGYVKMVDTREGEVSE	111111111	1111111111		[] {	
503	LGGYVKMVDTREGEVSE	ADLPYAFDKO	HPAKRIAIVA	AGPLTNLAL	40 PF 1 GF2 t 2 t	GVI
g591	70	80	90	100	110	120
	130	140	150	160	170	180
m591.pep	ELRPYVGTVEPDTIAAF	RAGFQSGDKI	OSVNGTPVADI	ACSAGLEIAP	NLEAGKVAVG	IIII
		:	I I I I I I I I I I I I I I I I I I I	SSAQTEIVL	NLEAGKVAVG	ATQV
g591	130	140	150	160	170	180
	190	200	210	220	230	240
E01 non	CONCENTED A A CTOR	CKI PKNOCA.	IGLMPFKITT	VAGGVEKGSP.	AEKAGLKPGD	RLTA
m591.pep			1 1 1 1 1 5 1 1 1 1	111111111		1111
g591	SGAQTVRTIDAAGTPE	AGKIAKNQGY	IGLMPFKLTT 210	VAGGVERGSP 220	230	240
-	190	200	210	220		
	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLT	RQSPGKKITL	NYERAGOTHT	ADIRPDTVEQ	SDHTLIGRVG	LRPQ
	ADGKPIASWQEWANDI: ADGKPIASWQEWANLT:	111111111	•	111111111	[[] [] [] [] []	1 1 1 1
g591	ADGKPIASWQEWANLT	RQSPGKKITL 260	270	280	290	300
	21.0	320	330	340	350	360
504	310 PDRAWDAQIRRSYRPS	UUDAFCMCWF	KTVSHSWTTI	KFFGKLISGN	IASVSHISGPL	TIAD
m591.pep		1 (1 1 1 1				1 1 1 1
g591	PDRAWDAQIRRSYRPS	VVRAFGMGWE	KTVSHSWTTI	KFFGKLISGN 340	ASVSHISGPI 350	360
,	310	320	330	340	330	500
	370	380	390	400	410	420
m591.pep	OT OGVI ET	TO TO TOUT OF THE	/LNLLPVPVLI	GGHLVFYTAI	EWIRGKPLGE	RVQNI
moor.pep				1		1 1 1 1 1
g591	IAGQSAELGLQSYLEF	FLALVSISLG	390 390	400	410	420
	370	380	330			
	430	440				
m591.pep	GLRFGLALMMLMMAV	AFFNDVTRLL(GX			
		ן	1 1 3X			
g591	420	440				
e following na	tial DNA sequence	was identif	ied in N. m	eningitidis [.]	SEQ ID 1	845>:

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1845>: a591.seq

		መመርመን ርርጥጥጥ	TATCTTCGCC	ATCCTGATTT	TGGTCAGCCT
1	TTGCACACCC	GGACACTACA	TOTTCGCCAG	ATTGTGCGGC	GTCAAGGTTG
51		CGTCGGCTTC	GGCAAACCGT	TTTTCACCCG	AAAGCGCGGC
101	TGCGTTTTTC	GGTGCCTCGC	CCCGATTCCG	TTGGGCGGTT	ACGTCAAAAT
151	GACACCGAAT		_	AGCCGATTTA	CCCTACGCTT
201	GGTCGACACG	ACACCCCGCC	AAGCGCATCG	CCATCGTCGC	CGCCGGCCCG
251	CTGACCAACC	TCGCACTGGC	GGTTTTGCTG	TACGGACTGA	GCTTTTCCTT
301	CGGCGTTACC		CCTATGTCGG	CACAGTCGAA	
351	TTGCCGCCCG	CGCCGGCTTC	CAAAGCGGCG	ACAAAATACA	
401	GGCACACCCG	TTGCAGATTG	GGGCAGCGCG	CAAACCGAAA	
451 501	CCTCGAAGCC		CCGTCGGCGT	TCAGACGGCA	TCGGGCGCGC
551	AAACCGTCCG		GCCGCAGGCA	CGCCGGAAGC	CGGTAAAATC
601		AAGGCTACAT	CGGACTGATG	CCCTTTAAAA	TCACAACCGT
651	TGCCGGCGGC	GTGGAAAAAG		CGAAAAAGCA	GGCCTGAAAC
701	CCCCCCACAG	GCTGACTGCC	GCCGACGGCA	AACCCATCGC	CTCATGGCAA
751	CAATGGGCAA	ACCTGACCCG	CCAAAGCCCC	GGCAAAAAAA	TCACCCTGAC
801	CTACGAACGC	GCCGGACAAA	CCCATACCGC	CGACATCCGC	CCCGATACTG
851	TCGAACAGCC	CGACCACACC	CTGATCGGGC	GCGTCGGCCT	CCGTCCGCAG
901	CCGGACAGGG	CGTGGGACGC	GCAAATCCGC	CGCAGCTACC	GTCCGTCTGT
951	TGTCCGCGCA	TTCGGCATGG	GCTGGGAAAA	AACCGTTTCC	CACTCGTGGA
1001		ATTTTTCGGC		GCGGCAACGC	CTCCGTCAGC
1051	CATATTTCCG				AGTCCGCCGA
1101	ACTCGGCTTG		TGGAATTTTT		AGCATCAGCC
1151	TCGGCGTGCT		CCCGTCCCCG		
1201	GTGTTTTATA		GATACGCGGC	AAACCTTTGG	GCGAACGCGT
1251	CCAAAACATC	GGTTTGCGCT	TCGGGCTTGC	CCTCATGATG	CTGATGATGG
1301	CGGTCGCCTT		GTTACCCGGC	TGCTCGGTTA	G
1001					

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

This correspond	s to the amino acid sequence SEQ ID 1840, ORI 331.22.	
a591.pep 1 51 101 151 201 251 301 351 401	LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRG DTEWCLAPIP LGGYVKMVDT REGEVSEADL PYAFDKQHPA KRIAIVAAGP LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTIAARAGF QSGDKIQSVN GTPVADWGSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI AKNQGYIGLM PFKITTVAGG VEKGSPAEKA GLKPGDRLTA ADGKPIASWQ EWANLTRQSP GKKITLTYER AGQTHTADIR PDTVEQPDHT LIGRVGLRPQ PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVLNLL PVPVLDGGHL VFYTAEWIRG KPLGERVQNI GLRFGLALMM LMMAVAFFND VTRLLG*	
m591/a591	99.6% identity in 446 aa overlap	
m591.pep a591	10 20 30 40 50 60 LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSVGFGKPFFTRKRGDTEWCLAPIF	2 P
m591.pep a591	70 80 90 100 110 120 LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT	T l T
m591.pep a591	130 140 150 160 170 186 ELRPYVGTVEPDTIAARAGFQSGDKIQSVNGTPVADWGSAQTEIVLNLEAGKVAVGVQTX	A I A
m591.pep a591	190 200 210 220 230 24 SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPAEKAGLKPGDRLT	'A 'A

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934

m591.pep	250 ADGKPIASWQEWANL ADGKPIASWQEWANL 250	111111111	1 • 1 1 1 1 1 1 1	111111111	1 111111	, , , , , , ,
m591.pep	310 PDRAWDAQIRRSYRE PDRAWDAQIRRSYRE 310		111111111	1		, , , , , , , ,
m591.pep	370 IAGQSAELGLQSYLE IAGQSAELGLQSYLE 370		1 1 1 1 1 1] [] []] [] [] [1111111
m591.pep a591	430 GLRFGLALMMLMMAV GLRFGLALMMLMMAV 430	[[]]]]]]	[1]			

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1847>: g592.seq..

```
1 atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51 cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgccg ccgccgccgc cgaagtgaaa caccctgttt cgcaaggtat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcgtt tgttcttgca
251 ccgccttcat catcttgatt taccaacage cttatggcga tttgagcggt
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcctc gccgtcatcc tgtttatgtt tgccttttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctggtt ttggcgtggg tctatttcgg
501 cgcggttgcc aatgtgcctt tggtctggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctcgtcgcca tcctgctgct ctcgccattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatcaaat
701 ccgatgtttg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>: g592.pep

- 1 MIPDVFGQIF SGAFKFDAAA GGLLGGLISQ TMMMGIKRGL YSNEAGMGSA
- 51 PNAAAAAEVK HPVSQGMIQM LGVFVDTIIV CSCTAFIILI YQQPYGDLSG 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
- 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
- 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1849>: m592.seq ..

```
1 ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
51 CGCGGCAGCA GGCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCCTG TATTCCAACG AGGCGGGTAT GGGTTCCGCG
151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTTCTTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
451 CTGATTACCG CCGTTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
```

```
601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
        CCCCGAGTTC AAACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
       CCGACGTTTG GTAA
This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:
m592.pep
        MIPDVFGQIF SGAFKFDAAA GGLLGGLISQ TMMMGIKRGL YSNEAGMGSA
      1
        PNAAAAAEVK HPVSQGMIQM LGVFVDTIIV CSCTAFIILI YQQPYGDLSG
    101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
    151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
    201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*
m592 / g592 100.0% identity in 237 aa overlap
                                                              60
                                                     50
                                             40
                                    30
                  10
           {\tt MIPDVFGQIFSGAFKFDAAAGGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK}
m592.pep
           MIPDVFGQIFSGAFKFDAAAGGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK
g592
                                                              60
                                    30
                                             40
                                                     50
                           20
                                            100
                                                    110
                                                             120
                                    90
                           80
                   70
           {\tt HPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL}
m592.pep
            HPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL
q592
                                                    110
                           80
                                    90
                                            100
                  70
                                            160
                                                    170
                                   150
                           140
           AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD
m592.pep
            AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD
g592
                                            160
                           140
                                   150
                  130
                                                     230
                                            220
                           200
                                   210
                  190
            MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMGKDPEFKLSEHPGLKRRIKSDVWX
m592.pep
            MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMGKDPEFKLSEHPGLKRRIKSDVWX
g592
                                                     230
                                   210
                                            220
                           200
                  190
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1851>:
      a592.seq
                ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCCGCT TCAAATTCGA
             1
               CGCGGCAGCA GGCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
            51
               TGGGCATCAA ACGCGGCCTG TATTCCAACG AGGCGGGTAT GGGTTCCGCG
           101
               CCGAACGCCG CCGCCGCC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
           151
               GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTTCTTGCA
           201
               CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
               GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
           351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
           401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
               CTGATTACCG CCGTTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
               CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
               GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
                GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
                CCCCGAGTTC AAACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
               CCGACGTTTG GTAA
 This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:
      a592.pep
                MIPDVFGQIF SGAFKFDAAA GGLLGGLISQ TMMMGIKRGL YSNEAGMGSA
             1
               PNAAAAAEVK HPVSQGMIQM LGVFVDTIIV CSCTAFIILI YQQPYGDLSG
           101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
           151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
                AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*
```

m592/a592 100.0% identity in 237 aa overlap

WO 99/57280

936

50 40 30 20 10 MIPDVFGQIFSGAFKFDAAAGGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK m592.pep MIPDVFGQIFSGAFKFDAAAGGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK a592 40 30 120 110 100 90 70 80 HPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL m592.pep HPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL a592 100 110 90 80 180 170 160 140 150 130 AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD m592.pep AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD a592 160 130 140 150 230 210 220 200 190 MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMGKDPEFKLSEHPGLKRRIKSDVWX m592.pep MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMGKDPEFKLSEHPGLKRRIKSDVWX a592 220 230 200 210 190

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1853>: q593.seq.

atgettgaae tgaaeggaet etgeaaatge tteggeggea aaaeggtege 1 cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcatc gtccggccgg acggcggcga aattcggctg aacggggaaa acattacctg tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg 251 caaaaaatgc cgaaagccga agccgaacgc ctcgccttgt cggcacttgc 301 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccq 351 gaggcgagaa gcaacggttg gcactggcgc gcgctttggt tgtccgccct 401 teectgctgt tgctggatga atcgttttee agtttggaca egeatttgeg 451 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc 501 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac ggcggcggac 551 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga 601 aaccttgatt caaacgcctg ccggcgtgca ggtcgcccgt ctgatggggc 651 tgcccaatac cgacgatgac cgccatattc cgcaaaatgc cgtgtgcttg 701 gacaatcatg gaacggaatg ccgtctgctg tecetegtee geetgeecga 751 801 ctcgctccgg ctttccgccg tccatcccga acacggcgag ctgaccttaa acctgactgt cggacaacat acggacggta tttccggaaa cggtacggtc cgcatccgcg tcgatgaagg gcgtatcgtc cgtttccgat ga

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

a593.pep..

- MLELNGLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI 1 VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
- 101 QKMPKAEAER LALSALAEVG LENEAHRKPE KLSGGEKQRL ALARALVVRP
- 151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
- 201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNGTV 251
- RIRVDEGRIV RFR*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1855>: m593.seq

- ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCAATA AAACCGTCGC
- CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTTGG GGCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
- 101 GTCCGGCCGG ACGGCGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

	magacacacac	GAAAAACGCC	GTATCTCGCT	GATGTTTCAA	GATTACGCGC
201	TATGCCGCCC	TATGAGTGCG	CTGGAAAATG	CGGCATTCGG	TTTGAAAATG
251			ACCCGAACGC		
301	CAAAAAATGC	CTGGAAAACG	ACCCCCACCG	CAAGCCTGAA	AAACTTTCCG
351	CGAAGTCGGA	GCAACGGCTG	AGGCGCACCC	CCCCTTTCGT	TGTCCGCCCT
401	GAGGCGAGAA	GCAACGGCTG	GCG11GGCGC	ACTUTUCCACA	CGCATTTGCG
451	TCCCTGCTGC	TGTTGGACGA	ATCGTTTTCC	TATCCGAAAC	CCCGCCATCC
501	CGGCACGCTG	CGCCGTATGA			GACGGCAGAC
551	CTGCCGTTTT	GGTAACGCAT	TCGCCCGAAG		
601	GAAATCGCCG	TGATGCATAA	AGGGAGGATT	CTACAATACG	GTACGCCCGA
651	AACATTGGTC	AAAACACCAT	CCTGCGTGCA	GGTCGCCCGA	CTGATGGGTT
701	TGCCCAATAC	CGACGATAAC	CGCCATATTC		GGTGCGTTTC
751	GACCAAGACG	GCATGGAGTG	CCGCGTATTA	TCCCGTACCT	GTTTGCCCGA
801	ATCGTTCAGC		TCCATCCGGA	ACACGGCATC	CTGTGGCTGA
851	ACCTCGATAT			CGGGCAAGGA	TACGGTACGC
	AUCCICGATAT	AAGAACGGGA			
901	AICCAIAICG	11101111000011			

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

, 001.00p					
m593.pep				AUT CDCCCCK	COLINITACI
1	MITTNCICKE	FGNKTVADNI	CLTVGRGKIL	AVLGRSGCGR	PILLINITAGE
E 1	UP DOCCETWI.	NGENTTRMPP	EKRRISLMFQ	DYALFPHMSA	LENAAFGLKM
31	OKMPKAEAER	TAMAATAEVC	LENEAHRKPE	KI.SGGEKORL	ALARALVVRP
101	QKMPKAEAER	PWINWPWRAC	DDIVERSON	CCTDAULUTH	CDEEDCTTAD
151	SLLLLDESFS	SLDTHLRGTL	RRMTAERIKN	GGIFAATAIN	SIBLACIAND
201	EIAVMHKGRI	LOYGTPETLV	KTPSCVQVAR	LMGLPNTDDN	RHIPQHAVRE
	DODGMECRVL	CDMCI DECEC	I SVI.HPEHGT	TWINLDMRHA	GAVSGKDTVR
251			DO A DILL DILOT	22	
301	IHIEEREIVR	FR*			•
	111111111111111111		wanaa aarra 1	the following	reculte.

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m593 / g593 83.4% identity in 313 aa overlap

m393 / g333						
	10	20	30	40	50	60
m593.pep	MLELNGLCKRFGNK	TVADNICLTV	GRGKILAVLG	RSGCGKSTLL	111AGIVRPD	GGETMT
m393.pep		11111111111	1111111111	1111111111	:	1111
500	MLELNGLCKCFGGK	TVADNICLTV	GRGKILAVLG	RSGCGKSTLL	MIAGIVRPD	GGEIRL
g593	10	20	30	40	50	60
	10	20				
		80	90	100	110	120
	70	00	DOMEST END			ALAEVG
m593.pep	NGENITRMPPEKRE	RISLMFQDYAL	FPHMSALLINA	MEGUMMATE		
			11111111:			111111
g593	NGENITCMPPEKRI	RISLMFQDYAL	FPHMSALENT	CAFGLKMQKMP	KAEAERLALS	ALALVG
9393	70	80	90	100	110	120
	. •					
	130	140	150	160	170	.180
	LENEAHRKPEKLS	~~EVODININD	LI.IPQQIMITA	JDESESSIDT	HLRGTLRRMI	AERIRN
m593.pep	LENEARKREEKLS	JGENQNUAUAN			111 1111	11111:
	1111111111	{	11111111		ייייי	AFRIRK
g593	LENEAHRKPEKLS	GGEKQRLALAH	KALVVRPSLLI	100 1001 1001	170	180
,	130	140	150	160	170	100
						0.40
	190	200	210	220	230	240
500	GGIPAVLVTHSPE:	EACTTADEIAV	MHKGRILOY	GTPETLVKTPS	CVQVARLMGI	LPNTDDN
m593.pep	GGIFAVEVINOSE	1111.11111	11:1:11	111111::11:	1111111	
	GGIPAVLVTHSPE	•	7MUFCKTI () ()	TPETITOTPA	GVOVARLMG	LPNTDDD
g593		FACI WADE IN	O10	220	230	240
	190	200	210	220	250	2.0

```
299
                                                              290
                                                   280
                                          270
                                 260
                       250
                RHIPQHAVRFDQDGMECRVLSRTCLPESFSLSVLHPEHGILWLNLDM-RHAGAVSGKDTV
                 m593.pep
                 RHIPQNAVCLDNHGTECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISGNGTV
    g593
                                                             290
                                                   280
                                          270
                                 260
                       250
               300
                        310
                 RIHIEEREIVRFRX
    m593.pep
                 11:::1::11111
                 RIRVDEGRIVRFRX
    q593
                       310
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1857>:
     a593.seq
              ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
              CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTTGG
          51
              GGCGGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TGCGGGCATC
         101
              GTCCGGCCGG ACGCCGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
              TATGCCGCCC GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
         201
              TGTTTCCCCA TATGAGTGCA CTGGAAAATG CGGCATTCGG TTTGAAAATG
         251
              CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
         301
              CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAN AAACTTTCCG
         351
              GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
         401
              TCCCTGCTGC TGTTGGACGA ATCGTTTTCC AGTTTGGACA CGCATTTGCG
          451
              CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GGCGGCATCC
              CTGCCGTTTT GGTAACGCAT TCGCCCGAAG AGGCCTGCAC GGCGGCAGAC
          551
              GAAATCGCCG TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCCGA
          601
              AACCTTGGTT CAAACGCCTG CCGGCGTGCA GGTCGCCCAT CTGATGGGGC
          651
              TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
          701
              GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
          751
              ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
              ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAAACGA TACGGTACGC
              ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA
          901
This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:
     a593.pep
              MLELNGLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
              VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAFGLKM
               QKMPKAEAES LAMAALAEVG LENEAHRKPX KLSGGEKQRL ALARALVVRP
              SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
          151
              EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDDD RHIPQHAVRF
          201
               DODGMECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
          251
              IHIEDREIVR FR*
          301
              92.9% identity in 312 aa overlap
m593/a593
                                                               50
                                                                        60
                                                     40
                                            30
                                   20
                  MLELNGLCKRFGNKTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGEIWL
     m593.pep
                  MLELNGLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGEIWL
      a593
                                                     40
                                                               50
                                            30
                                   20
                         10
                                                                       120
                                                              110
                                                    100
                                            90
                         70
                                   80
                  NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEAERLAMAALAEVG
      m593.pep
                  NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMQKMPKAEAESLAMAALAEVG
      a593
                                                                       120
                                                     100
                                                              110
                                            90
                          70
                                   80
                                                                       180
                                                              170
                                           150
                                                     160
                                  140
                         130
                  LENEAHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSSLDTHLRGTLRRMTAERIRN
      m593.pep
                  LENEAHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFSSLDTHLRDRLRRMTAERIRK
      a593
                                                              170
                                                                       180
                                                     160
                         130
                                  140
                                           150
                                                                       240
                                           210
                                                     220
                                  200
                  GGIPAVLVTHSPEEACTTADEIAVMHKGRILQYGTPETLVKTPSCVQVARLMGLPNTDDN
      m593.pep
```

WO 99/57280 PCT/US99/0

939

a593		: CTAADEIA 200	: : VMHEGKILQCG 210	: : PETLVQTP! 220	: : ! AGVQVAHLMGI 230	240
	250 RHIPQHAVRFDQDGM	260	270	280	290 NLDMRHAGAVS	300 SGKDTVR
m593.pep	RHIPQHAVREDQUGM	FULLITIE	CLESISTON			:
502	RHIPQHAVRFDQDGM	ECRVLSRT	CLPESFSLSVL	HPEHGILWL	NLDMPHAGEIS	SGNDTVR
a593	250	260	270	280	290	300
	310					
m593.pep	IHIEEREIVRFRX					
	:					
a593	IHIEDREIVRFRX 310					
	210					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1859>:

```
1 atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51 tctcgtttt agcatactcc ggctgctgtt ccgcatcgga attgggatcg
101 gtaagttcgc cgttcaggcc tttcaggtct ttaagctgct gatctgtacg
151 gttgagcacc caaatcggtt tgccttgca ctcggcggtc agcagctgac
201 ccgcttcgat tttactgaca tccacctcga cggcagcacc ggaggccttg
251 gcttttccg aagggaaaaa actggccaca aacggcgttg ccacacccaa
301 tgctgccact ccgccegcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttgtt gattcttga ttatccatta ttcagtcgtc ctaatatttt
401 gggaatgccg agccattaaa cattgcaatt ttacccagtt tgcagtgata
```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```
g594.pep

1 MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51 VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSVV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1861>:

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```
m594.pep

1 MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51 VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

WO 99/57280

940

m594.pep g594		.	11111111
m594.pep g594	70 80 LGGQQLTRFDFTDIHLDGSTGGLGFFRI !		
m594.pep g594	DFLIIHYSVVLIFWEYRAIKRCNFTQF 		
a594.seq 1 51 101 151 201 251 301 351 401 451	ATGGTTGCAG ATACCGATGG CGACAAGG. TCTCGTTTTT AGCATACTCC GGCTGCTG GTAAGTTCGC CGTTCAGGCC TTTCAGGT GCTTGAGCAC CAAATCGGTT TGCCTTGC CCGCTTCGAT TTTACTGACA TCCACCTC GCTTTTTCCG AAGGGAAAAA ACTGGCCA TGCTGCCACT CCGCCCGCGC CGCAGGTC GGCCGTTGTT GATTTCTTGA TTATCCAT GGGAATACCG AGCCATTAAA CGTTGCAA CTCAAAGCAT TATTTAAAAT AAGGTAA ds to the amino acid sequence <sec mgadtdgdkd="" silrllfr<="" td="" vrlnrtglvf=""><td>AT GTTCGGCTTA TT CCGCATCGA CT TTAAGCTGCT CA CTCGGCGGTC GA CGGCAGCACC CA AACGGCGTTG GC GAGTGTCAGG TA TTCAGTCGTC TT TTACCCAGTT Q ID 1864; ORI IG IGIGKFAVQA</td><td>ATCGAACGGG ATTGGGATCG GATCTGTACG AGCAACTGAC GGCGGCCTTG CCACACCCAA AAACGGCGGC CTAATATTTT TGCAGTGATA F 594.a>: FQVFKLLICT</td></sec>	AT GTTCGGCTTA TT CCGCATCGA CT TTAAGCTGCT CA CTCGGCGGTC GA CGGCAGCACC CA AACGGCGTTG GC GAGTGTCAGG TA TTCAGTCGTC TT TTACCCAGTT Q ID 1864; ORI IG IGIGKFAVQA	ATCGAACGGG ATTGGGATCG GATCTGTACG AGCAACTGAC GGCGGCCTTG CCACACCCAA AAACGGCGGC CTAATATTTT TGCAGTGATA F 594.a>: FQVFKLLICT
51 101 151	VEHPNRFALP LGGQQLTRFD FTDIHLDG CCHSARAAGR ECQETAAAVV DFLIIHYS LKALFKIR*	ST GGLGFFRREK VV LIFWEYRAIK	TGHKRRCHTQ
m594/a594	100.0% identity in 158 aa ov	/errap	
m594.pep a594	10 20 MGADTDGDKDVRLNRTGLVFSILRLLE		
m594.pep a594	70 80 LGGQQLTRFDFTDIHLDGSTGGLGFFF	1111111111	1
m594.pep a594	130 140 DFLIIHYSVVLIFWEYRAIKRCNFTQI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1865>:

```
atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttgggttt
```

⁵¹ gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg 101 gtgagaccca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac

151	gacaatgcct	gcgaaccgat	gaatctgacc	gtgccgagcg	gacaggttgt
201	nttcaatatt	aaaaacaaca	gcggccgcaa	gctcgaatgg	gaaatcctga
251	agggcgtgat		gaacgcgaaa	atatcgcccc	ggggctttcc
301	gagagatga	accgtaacct	actaccagge	gaatacgaaa	tgacctgcgg
351	ccttttgacc	aatccgcgcg	gcaagctggt	ggtagccgac	agcggcttta
401	aadacaccoc	caacgaagcg	gatttggaaa	aactgcccca	
451	gactataaag	cctacgttca	aggcgaggtt	aaagagctgg	cggcgaaaac
501	casascettt	accgaagccg	tcaaagcagg		
551	caaaaccccc	cgccacccgc	atccattacq	aacqcatcqa	accgattgcc
	anacttttca	gcgaactcga	ccccatcatc	gatgcgtgtg	aagacgactt
601	gagettteea	gcgaaagatg	ccaaatttac	concttccac	cgtatcgaac
651	caaagacggc	ggtggaaaaa	gacgtatccg	gcgtgaagga	aaccacaacc
701	acgccctttg	ggtggaaaaa	gacgtacccg	2222322	acceptage
751	aaactgatga	ccgatgtcga	agccctgcaa	aaagaaatcg	
801	gttccctccg	ggcaaagtgg	tcggcggcgc		attgaagaag
851		taaaatcagc	ggcgaagaag	accgttacag	ccacaccgat
901			tgcggacgga	tctaaaaaaa	tcgtcgattt
951		ttgattgagg	ccaaaaacaa	agccttgttg	gaaaaaaccg
1001	ataccaactt	caaacaggtc	aacgaaattc	tggcgaaata	ccgcaccaaa

110

100

90

WO 99/57280

942

```
gacggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
               acaggeteet attaacgege ttgccgaaga cettgcccaa ettegeggea
               tactcggctt gaaataa
         1151
This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:
     q595.pep
               MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIAVN
               DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
           51
               DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
          101
               DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
          201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
          251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
               LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
          301
               DGFETYDKLS EADRKALQAP INALAEDLAQ LRGILGLK*
          351
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1867>:
     m595.seq
               ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
            1
               GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
           51
               GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
          101
               GACAATGCCT GCGAACCGAT GGAACTGACC GTGCCGAGCG GACAGGTTGT
          151
               GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
          201
          251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
               GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
               TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
          401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
          451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
               CAAAACTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
          501
               CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
          551
               GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
               CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTCAC CGTATCGAAT
               ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
          751 AAACTGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
          801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
          851 TGGCGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
          901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
          951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
         1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
               GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
          1051
         1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
          1151 TACTCGGCTT GAAATAA
This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:
      m595.pep
                MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
                DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
                DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
                DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
           201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
           251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
                LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
                DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*
 Computer analysis of this amino acid sequence gave the following results:
 Homology with a predicted ORF from N. gonorrhoeae
      m595 / g595 95.4% identity in 388 aa overlap
                                                         40
                                               30
                                     20
                   MRKFNLTALSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIAVNDNACEPMELT
      m595.pep
                   MRKFNLTALSVMLALGLTACQPPEAEKAAPAASGETQSANEGGSVGIAVNDNACEPMNLT
      g595
                                                                             60
                                                                   50
                                               30
                                     20
                           10
```

70

80

m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGVMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g595	· 70 80 90 100 110 120
	130 140 150 160 170 180
m595.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
g595	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
	130 140 150 100 1.00
	190 200 210 220 230 240 KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
m595.pep	
g595	KAKSLFAATRVHYERIEPIAELFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
	190 200 210 220 233
	250 260 270 280 290 300 DVSGVĶEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD
m595.pep	
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD
	250 260 270 280 290 300
	310 320 330 340 350 360
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDTNFKQVNEILAKYRTKDGFETYDKLG
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDTNFKQVNEILAKYRTKDGFETYDKLS
•	310 320 330 340 350 360
	370 380 389
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX
q595	EADRKALQAPINALAEDLAQLRGILGLKX
_	partial DNA sequence was identified in <i>N. meningitidis</i> <seq 1869="" id="">:</seq>
	partial DNA sequence was identified in 14. meninginals 1994 12 1999
a595.seq	ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51	CACCCCCTCC CACCCCCG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101	CTCACCCCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151	CACAATGCCT GCGAACCGAT GGAACTGACC GTGCCGAGCG GACAGGTTGT
201	CTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251	AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301	GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351	TOTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401	AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451	GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501	CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551	CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601	GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
651	CAAAGACGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701	
751	- $ -$
801	GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851	- $ +$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$ $+$
901	
951	-
1001	- $ -$
1051	THE REPORT OF THE PROCESS OF THE PRO
1101	
1151	TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

a595.pep

1 MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS

101 151 201 251 301 351	DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*	
m595/a595	99.7% identity in 388 aa overlap	
m595.pep a595	10 20 30 40 50 MRKFNLTALSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIAVNDNA	1 1 1 1 1
m595.pep a595	70 80 90 100 110 VPSGQVVFNIKNNSGRKLEWEILKGVMVVDERENIAPGLSDKMTVTLLPGEYF	3 1 1 1 1 1 1 1
m595.pep a595	130 140 150 160 170 NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEX	[]] [] [] []
m595.pep a595	190 200 210 220 230 KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRI	111111
m595.pep a595	250 260 270 280 290 DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGE	1 1 1 1 1 1 1 1
m595.pep a595	310 320 330 340 350 LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDTNFKQVNEILAKYRTKDG	
m595.pep a595	370 380 389 EADRKALQASINALAEDLAQLRGILGLKX	

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1871>: g596.seq.(partial).

(partial).				+
atactactct	tggacgagcc	gaccaaccac	ttggatgcgg	aaccygryga
ataactaaaa	caattcctcq	tgcgcttccc	cggcacagtg	gtcgcggtaa
acggccggag	ctacttcctc	gacaacgccg	ccgaatggat	tttggaactc
Egcacgaceg	magattee	atagaaaaa	aattactcqt	cttggctgga
gaccgcggac	acggcattee	geggaaagge	accept code	accacacaca
gcagaaagaa	aaacgcttgg	aaaacgaggc	gadacccgaa	geegegeg
tgaaggcgat	gaagcaggaa	ttggaatggg	tgcgccaaaa	Egccaaaggc
242234203	arcccaaagc	acatttaaca	cgttttgaag	aaatgagcaa
egccaageca	agecounty	accasactca	ggaaatcttt	atccctqttq
ctacgaatac	Caaaaacyca	acgaaaccaa	++~+~	ttccaaatcc
ccgagcgttt	gggtaacgaa	gtgattgaat	tigigaatgi	ttttaaatty
	atggctggag cgcacgaccg gaccgcggac gcagaaagaa tgaaggcgat cgccaagcca	atgctgctct tggacgagcc atggctggag caattcctcg cgcacgaccg ctacttcctc gaccgcggac acggcattcc gcagaaagaa aaacgcttgg tgaaggcgat gaagcaggaa cgccaagcca agcccaaagc	atgetgetet tggaegagee gaecaaecae atggetgag caatteeteg tgegetteee egeaegaeeg etaetteete gaeaaegeeg gaecgeggae aeggeattee gtggaaagge egeagaaagaa aaaegettgg aaaaegagge tgaaggeat gaagcaagaa ttggaatggg egeaageea ageeaaage gegtttggeg	(partial)atgctgctct tggacgagcc gaccaaccac ttggatgcgg atggctggag caattcctcg tgcgcttccc cggcacagtg cgcacgaccg ctacttcctc gacaacgccg ccgaatggat gaccgcggac acggcattcc gtggaaaggc aattactcgt gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa cgccaagcca agcccaaagc gcgtttggcg cgttttgaag ctacgaatac caaaaacgca acgaaactca gggaaatcttt ccgagcgttt gggtaacgaa gtgattgaat ttgtgaatgt

```
ttcggcgata aagtgctgat tgacggtttg agcttcaaag tgccggcggg
451
       egegattgte ggcatcateg gcccgaacgg egegggtaaa tegacgetgt
       tcaaaatgat tgcgggcaaa gagcagcccg attcgggcga agtgaaaatc
       gggcaaaccg tgaaaatgag cttgattgac caaagccgcg aaggtttgca
       aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
651
       aggtcggaca gtttgaaatc cccgcccgcc aatatttggg acgcttcaac
701
       tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcggcga
751
       acgcggccgt ctgcacttgg caaaaacctt gttgggcggc ggcaatgtgt
801
       tgctgctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcg
851
       ttggaagacg cattgttgga atttgccggc agcgtgatgg tgatttcgca
901
       cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
951
       gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1001
       gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1051
        atacaaaccg gtaacgcgtt aa
1101
```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

```
g596.pep (partial).
          ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
            DRGHGIPWKG NYSSWLEQKE KRLENEAKSE AARVKAMKQE LEWVRQNAKG
            RQAKPKARLA RFEEMSNYEY QKRNETQEIF IPVAERLGNE VIEFVNVSKS
     101
            FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
     151
            GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
            FKGSDQSKIA RQLSGGERGR LHLAKTLLGG GNVLLLDEPS NDLDVETLRA
            LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
            DKKRRLGKEG AKPKRIKYKP VTR*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1873>:

```
m596.seq..
      1 ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
         GCCGCAGAAA ACCATCATTA AAGATATTTC CCTTTCTTTC TTCCCCGGCG
      51
    101 CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
    151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
    201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
    251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
    301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
     351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGAA GCGATTATTG
         CGGCAGGTTC GTCCACGGGC GGCGGTGCGG AACACGAATT GGAAATCGCC
         GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
         CGGCGGTGAA AAACGCCGCG TTGCCTTGTG CAAACTCTTG TTGAGCAAGC
          CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TGCGGAATCG
         GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGCA CAGTCGTTGC
         GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
         AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
     701
         CTGGAGCAGA AAGAAAAACG CTTGGAAAAC GAGGCAAAAT CCGAAGCCGC
         GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
     851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
     901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
     951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
    1001 AATCGTTCGG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
    1051 GCGGGCGCA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
    1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
    1151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
    1201 TTGCAAAACG ACAAAACCGT GTTCGACAAC ATTGCCGAAG GCCGCGACAT
          TTTGCAGGTT GGTCAGTTTG AAATTCCCGC CCGCCAATAT TTGGGGCGTT
    1251
          TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
    1301
          GGCGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGGCGGCAA
    1351
          TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCCTGC
          GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
          TCGCACGACC GTTGGTTCCT CGACCGCATC GCCACGCATA TCTTGGCGTG
          TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
    1551
          AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
    1601
          ATCAAATACA AACCGGTAAC GCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>: m596.pep..

1651

1	MSOOYVYSML	RVSKVVPPQK	TIIKDISLSF	FPGAKIGLLG	LNGAGKSTVL
51	RIMAGVDKEF	EGEAVPMGGI	KIGYLPQEPE	LDPEKTVREE	VESGLGEVAA
101	AOKRLEEVYA	EYANPDADFD	ALAEEQGRLE	AIIAAGSSTG	GGAEHELEIA
151		AKIDNLSGGE			
201	VEWLEOFLVR	FPGTVVAVTH	DRYFLDNAAE	WILELDRGHG	IPWKGNYSSW
251	LEOKEKRLEN	EAKSEAARVK	AMKQELEWVR	QNAKGRQAKS	KARLARFEEM
301	SNYEYQKRNE	TQEIFIPVAE	RLGNEVIEFV	NVSKSFGDKV	LIDDLSFKVP
351	AGAIVGIIGP	NGAGKSTLFK	MISGKEQPDS	GEVKIGQTVK	MSLIDQSREG
401	LONDKTVFDN	IAEGRDILQV	GQFEIPARQY	LGRFNFKGSD	QSKIAGQLSG
451	GERGRLHLAK	TLLSGGNVLL	LDEPSNDLDV	ETLRALEDAL	LEFAGSVMVI
501	SHDRWFLDRI	ATHILACEGD	SKWVFFDGNY	QEYEADKKRR	LGEEGAKPKR
551	IKYKPVTR*				

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m596 g596	98.4% identity in 373 aa overlap
	160 170 · 180 190 200 210 LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTV
m596.pep	
g596	MLLLDEPTNHLDAESVEWLEQFLVRFPGTV
9590	10 20 30
•	220 230 240 250 260 270
m596.pep	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSSWLEQKEKRLENEAKSEAARVKAMKQE
r.o.c	VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSSWLEQKEKRLENEAKSEAARVKAMKQE
g596	40 50 60 70 80 90
	280 290 300 310 320 330
m596.pep	LEWVRQNAKGRQAKSKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
g596	LEWVRQNAKGRQAKPKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS 100 110 120 130 140 150
	100 110 120 130 140 150
	340 350 360 370 380 390
m596.pep	FGDKVLIDDLSFKVPAGAIVGIIGPNGAGKSTLFKMISGKEQPDSGEVKIGQTVKMSLID
g596	FGDKVLIDGLSFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPDSGEVKIGQTVKMSLID
	160 170 180 190 200 210
	400 410 420 430 440 450
m596.pep	OSREGLONDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR
moso.pep	
g596	QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR
-	220 230 240 250 260 270

```
490
                                          500
                           480
           460
                   470
          LHLAKTLLSGGNVLLLDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL
m596.pep
          LHLAKTLLGGGNVLLLDEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL
q596
                                      310
                                             320
                              300
                       290
                                  550
                   530
                           540
          ACEGDSKWVFFDGNYQEYEADKKRRLGEEGAKPKRIKYKPVTRX
m596.pep
          ACEGDSKWVFFDGNYQEYEADKKRRLGKEGAKPKRIKYKPVTRX
q596
                              360
                       350
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1875>:

```
a596.seq
         ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
      1
         GCCGCAGAAA ACCATCATTA AAGATATTTC CCTTTCTTTC TTCCCCGGCG
     51
         CGAAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
         CGGATTATGG CGGGCGTGGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
         GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
    201
         AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
    251
         GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
    301
         GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGGAA GCGATTATTG
    351
    401 CGGCGGGTTC GTCCACGGGC GGCGGTGCGG AACACGAATT GGAAATCGCT
    451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
    501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
    551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGA TGCGGAATCG
     601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCCGGTA CAGTCGTTGC
         CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
         AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
         TTGGAGCAGA AAGAAAAACG TTTGGAAAAC GAGGCGAAAT CCGAAGCCGC
         GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
         AAGGCCGTCA AGCCAAGTCC AAAGCGCGTTT TGGCGCGTTT TGAAGAAATG
         AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
     901
         CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
     951
    1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
         GCGGGCGCGA TTGTCGGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
    1051
         ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
          AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
         TTGCAAAACG ACAAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
    1201
         TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCCAATAT TTGGGACGCT
    1251
         TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCCGGC
    1301
         GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTTGG GCGGTGGCAA
    1351
         TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCCTGC
    1401
          GCGCGTTGGA AGACGCATTG CTGGAATTTG CCGGCAGCGT GATGGTGATT
    1451
          TCGCACGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
          CGAAGGCGAC TCCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
    1551
          AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
         ATCAAATACA AACCGGTAAC GCGTTAA
    1651
```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```
a596.pep

1 MSQQYVYSML RVSKVVPPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51 RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADFD ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSSW
251 LEQKEKRLEN EAKSEAARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSFKVP
351 AGAIVGIIGP NGAGKSTLFK MIAGKEQPDS GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGRLHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNY QEYEADKKRR LGEEGTKPKR
```

			2.0	4.0	50	60							
	10 MSQQYVYSMLRVSKV	20 VPPOKTTIKD	30 tslsffpgakl	40 IGLLGLNGA									
m596.pep		111111111	111111111]								
a596	MSQQYVYSMLRVSKV	VPPQKTIIKD	ISLSFFPGAK:	IGLLGLNGA 40	GKSTVLRIMA 50	GVDKEF 60							
	10	20	30	40	. 50								
	70	80	90	100	110	120							
m596.pep	EGEAVPMGGIKIGYL	PQEPELDPEK	TVREEVESGL	GEVAAAQKR.	LEEVYAEYAN	PDADFD							
<u>-</u> -			 TVPFFVESGI	GEVAAAOKR	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	PDADFD							
a596 ,	EGEAV PMGGIKIGIL 70	80 80	90	100	110	120							
	, •				470	100							
	130 ALAEEQGRLEAIIAA	140	150	160	170 NLSGGEKRRV	180 ALCKLL							
m596.pep		1111111111	1111111111	1111111	1111111	11111							
a596	ALAEEQGRLEAIIAA	.GSSTGGGAEH	ELEIAADALR	LPEWDAKID	NLSGGEKRRV	ALCKLL							
4370	130	140	150	160	170	180							
	190	200	210	220	230	240							
m596.pep	LSKPDMLLLDEPTNE	LDAESVEWLE	OFLVRFPGTV	VAVTHDRYF	LDNAAEWILE	LDRGHG							
moso.pep	14111111111111111	1111111111	1111111111		111111111	11111							
a596	LSKPDMLLLDEPTNF	ILDAESVEWLE 200	QFLVRFPGTV 210	220	230	240							
	190		210										
	250	260	270	280	290	300							
m596.pep	IPWKGNYSSWLEQKE	CKRLENEAKSE	AARVKAMKQE:	TITITITI	GRQANSNARI	HIIIII							
a596	IPWKGNYSSWLEQKE	EKRLENEAKSE	AARVKAMKQE	LEWVRQNAK	GRQAKSKARI	ARFEEM							
a596	250	260	270	280	290	300							
	210	320	330	340	350	360							
FOE non	310 SNYEYOKRNETOEII	TPVAERLGNE	EVIEFVNVSKS	FGDKVLIDE	LSFKVPAGA	CVGIIGP							
m596.pep	SNYEYQKRNETQEI	FIPVAERLGNE	EVIEFVNVSKS	FGDKVLIDE		1 1 1 1 1 1							
m596.pep a596	SNYEYQKRNETQEII SNYEYQKRNETQEII	FIPVAERLGNE FIPVAERLGNE	CVIEFVNVSKS CVIEFVNVSKS	FGDKVLIDE FGDKVLIDE	 LSFKVPAGA	IVGIIGP							
	SNYEYQKRNETQEI	FIPVAERLGNE	EVIEFVNVSKS	FGDKVLIDE		1 1 1 1 1 1							
	SNYEYQKRNETQEII SNYEYQKRNETQEII 310	FIPVAERLGNE 	EVIEFVNVSKS EVIEFVNVSKS 330 390	SFGDKVLIDE SFGDKVLIDE 340 400		1111111 IVGIIGP 360 420							
	SNYEYQKRNETQEII SNYEYQKRNETQEII 310 370 NGAGKSTLFKMISG	FIPVAERLGNE FIPVAERLGNE 320 380 KEOPDSGEVK	EVIEFVNVSKS EVIEFVNVSKS 330 390 IGOTVKMSLII	SFGDKVLIDE SFGDKVLIDE 340 400 QSREGLQNI	DLSFKVPAGA 350 410 OKTVFDNIAE	ITTITION SECTION	a596 m596.pep	SNYEYQKRNETQEII SNYEYQKRNETQEII 310 370 NGAGKSTLFKMISGI	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK	EVIEFVNVSKS	FGDKVLIDE 		111111 IVGIIGP 360 420 GRDILQV
a596	SNYEYQKRNETQEII SNYEYQKRNETQEII 310 370 NGAGKSTLFKMISG	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK	EVIEFVNVSKS	FGDKVLIDE 		111111 IVGIIGP 360 420 GRDILQV							
a596 m596.pep	SNYEYQKRNETQEII SNYEYQKRNETQEII 310 370 NGAGKSTLFKMISGIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	FIPVAERLGNE	EVIEFVNVSKS EVIEFVNVSKS 330 390 IGQTVKMSLII IGQTVKMSLII	FGDKVLIDE FGDKVLIDE 340 400 OQSREGLONE OQSREGLONE 400	J DLSFKVPAGA: 350 410 OKTVFDNIAE(DKTVFDNIAE(410	ITTITITION TO THE PROPERTY OF							
a596 m596.pep a596	SNYEYQKRNETQEII SNYEYQKRNETQEII 310 370 NGAGKSTLFKMISGI NGAGKSTLFKMIAGI 370	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380	EVIEFVNVSKS EVIEFVNVSKS 330 390 IGQTVKMSLII IGQTVKMSLII	FGDKVLIDE FGDKVLIDE 340 400 QQSREGLQNE DQSREGLQNE 400 460	JIIIIIIII DLSFKVPAGA: 350 410 DKTVFDNIAEO IIIIIIIIIII DKTVFDNIAEO 410 470	### PROPERTY OF THE PROPERTY O							
a596 m596.pep	SNYEYQKRNETQEII SNYEYQKRNETQEII 310 370 NGAGKSTLFKMISGI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI	EVIEFVNVSKS	FGDKVLIDE FGDKVLIDE 340 400 QSREGLQNE QSREGLQNE 400 460 RLHLAKTLLS	J DLSFKVPAGA: 350 410 OKTVFDNIAE(I OKTVFDNIAE(410 470 GGGNVLLLDE	### PROPERTY 1							
a596 m596.pep a596	SNYEYQKRNETQEII	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK KEQPDSGEVK 380 440 NFKGSDQSKI	EVIEFVNVSKS	FGDKVLIDE FILL I I I I I I I I I I I I I I I I I I	JIJIIII DLSFKVPAGA: 350 410 DKTVFDNIAE(JIJIIIIIII DKTVFDNIAE(410 470 GGGNVLLLDE:	ITTITITE IVGIIGP 360 420 GRDILQV ITTITE ITTITE ITTITE IVGIIGP 420 480 PSNDLDV ITTITE							
a596 m596.pep a596 m596.pep	SNYEYQKRNETQEII SNYEYQKRNETQEII 310 370 NGAGKSTLFKMISGI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI	EVIEFVNVSKS	FGDKVLIDE FGDKVLIDE 340 400 QSREGLQNE QSREGLQNE 400 460 RLHLAKTLLS	J DLSFKVPAGA: 350 410 OKTVFDNIAE(I OKTVFDNIAE(410 470 GGGNVLLLDE	### PROPERTY 1							
a596 m596.pep a596 m596.pep	SNYEYQKRNETQEII	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500	EVIEFVNVSKS	FGDKVLIDE FGDKVLIDE 340 400 QQSREGLQNE QQSREGLQNE 400 460 RLHLAKTLLS RLHLAKTLLS 460 520	350 410 ATO OKTVFDNIAE OKTVFDNIAE 410 470 GGGNVLLLDE : GGGNVLLLDE 470 530	### PROPERTY 19 19 19 19 19 19 19 1							
a596 m596.pep a596 m596.pep a596	SNYEYQKRNETQEIN SNYEYQKRNETQEIN 310 370 NGAGKSTLFKMISGN NGAGKSTLFKMIAGN 370 430 GQFEIPARQYLGRF NININININININININININININININININININI	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500 GSVMVISHDR	EVIEFVNVSKS	FGDKVLIDE FGDKVLIDE 340 400 QSREGLQNE DQSREGLQNE 400 460 RLHLAKTLLS 460 520 LACEGDSKW	JIIIIIII DLSFKVPAGA: 350 410 OKTVFDNIAE HIIIIIIII DKTVFDNIAE 410 470 GGGNVLLLDE : GGGNVLLLDE 470 530 VFFDGNYQEY	### PROPERTY 19 19 19 19 19 19 19 1							
a596 m596.pep a596 m596.pep a596	SNYEYQKRNETQEIN SNYEYQKRNETQEIN 310 370 NGAGKSTLFKMISGN NGAGKSTLFKMIAGN 370 430 GQFEIPARQYLGRF HILLIHINING 430 GQFEIPARQYLGRF 430 490 ETLRALEDALLEFA	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500 GSVMVISHDR	EVIEFVNVSKS	FGDKVLIDE FGDKVLIDE 340 400 QSREGLQNE DQSREGLQNE 400 460 RLHLAKTLLS 460 520 LACEGDSKW		### PROPERTY 1 1 1 1 1 1 1 1 1							
a596 m596.pep a596 m596.pep a596	SNYEYQKRNETQEIN SNYEYQKRNETQEIN 310 370 NGAGKSTLFKMISGN NGAGKSTLFKMIAGN 370 430 GQFEIPARQYLGRF NININININININININININININININININININI	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500 GSVMVISHDR	EVIEFVNVSKS	FGDKVLIDE FGDKVLIDE 340 400 QSREGLQNE DQSREGLQNE 400 460 RLHLAKTLLS 460 520 LACEGDSKW		### PROPERTY 1 1 1 1 1 1 1 1 1							
a596 m596.pep a596 m596.pep a596	SNYEYQKRNETQEIN	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500 GSVMVISHDR	EVIEFVNVSKS	FGDKVLIDE FILL IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	JIJIJIJI DLSFKVPAGA: 350 410 OKTVFDNIAEC 410 470 GGGNVLLLDE : GGGNVLLLDE 470 530 VFFDGNYQEY 	### Company							
a596 m596.pep a596 m596.pep a596 m596.pep	SNYEYQKRNETQEIN	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500 GSVMVISHDR GSVMVISHDR 500	EVIEFVNVSKS	FGDKVLIDE FILL IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	JIJIJIJI DLSFKVPAGA: 350 410 OKTVFDNIAEC 410 470 GGGNVLLLDE : GGGNVLLLDE 470 530 VFFDGNYQEY 	### Company							
a596 m596.pep a596 m596.pep a596	SNYEYQKRNETQEIN	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500 GSVMVISHDR GSVMVISHDR 500	EVIEFVNVSKS	FGDKVLIDE FILL IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	JIJIJIJI DLSFKVPAGA: 350 410 OKTVFDNIAEC 410 470 GGGNVLLLDE : GGGNVLLLDE 470 530 VFFDGNYQEY 	### Company							
a596 m596.pep a596 m596.pep a596 m596.pep	SNYEYQKRNETQEIN IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500 GSVMVISHDR GSVMVISHDR 500 559	EVIEFVNVSKS	FGDKVLIDE FILL IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	JIJIJIJI DLSFKVPAGA: 350 410 OKTVFDNIAEC 410 470 GGGNVLLLDE : GGGNVLLLDE 470 530 VFFDGNYQEY 	### Company							
a596 m596.pep a596 m596.pep a596 m596.pep	SNYEYQKRNETQEIN	FIPVAERLGNE FIPVAERLGNE 320 380 KEQPDSGEVK: KEQPDSGEVK: 380 440 NFKGSDQSKI: NFKGSDQSKI: 440 500 GSVMVISHDR GSVMVISHDR 500 559	EVIEFVNVSKS	FGDKVLIDE FILL IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	JIJIJIJI DLSFKVPAGA: 350 410 OKTVFDNIAEC 410 470 GGGNVLLLDE : GGGNVLLLDE 470 530 VFFDGNYQEY 	### Company							

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1877>

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAACTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TGCGGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAaagcc
 601 gaacaccgCA TTcaggAtgc ggAagcaaAA agaAAATTGG CTGAagcCaa
651 actGgeggca gecgaaaaag ccagaaaaga ageggegeag cagaaggetg
701 AAGCGCGACG TGCGGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggC GATGTTTGGA AAGGCGTGTT CTATTCCACT
901 GCGCCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
     CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GATCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACGGTCGCGG CAGGAAGCAA AATCGGCACG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCGGGCTG GATACGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597 >:

```
g597.pep
```

```
MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
```

- 51 LNTELNRLKT EVAATKAQIS RFVSGNYKNS RPNAVALFLK NAEPGQKNRF 101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
- 151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
- 201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
- QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST 301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIYAG LSEISAGKGY
- 351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRGQ VLNPSGWIR*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1879>: m597.seq

```
ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
 51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAACTCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTCC
251 TGAAAAACGC CGAACCGGGT CAGAAAAACC GCTTTTTGCG TTATACGCGT
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTTGG AAAAACAGCA
     GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAT TCAGGCAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAAGCCGC AGACAGAATG CCAAAATCGC
     CAAAGATGCC CGAAAACTGC TGGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTTG GAGAAGAAAA AGGCCGAACA CCGCATTCAG
601 GATGCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
    AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCAG AACCGGAGCG
851 GCGGCGATAT TTGGAAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTCG ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
     AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAAATA CGTTATCAAG GTCAGGTATT GAACCCTTCG AGCTGGATAC
```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep 1 MLLHVSNSLK QLQEERIRQE RIRQARGNLA SVNRKQREAW DKFQKLNTEL

- 51 NRLKTEVAAT KAQISRFVSG NYKNSQPNAV ALFLKNAEPG QKNRFLRYTR
- 101 YVNASNREVV KDLEKQQKAL AVQEQKINNE LARLKKIQAN VQSLLKKQGV
- 151 TDAAEQTESR RQNAKIAKDA RKLLEQKGNE QQLNKLLSNL EKKKAEHRIQ
- 201 DAEAKRKLAE ARLAAAEKAR KEAAQQKAEA RRAEMSNLTA EDRNIQAPSV 251 MGIGSADGFS RMQGRLKKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
- 301 ESIAPGTVSY ADELDGYGKV VVVDHGENYI SIYAGLSEIS VGKGYMVAAG
- 351 SKIGSSGSLP DGEEGLYLQI RYQGQVLNPS SWIR*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from N. gonorrhoeae:

```
96.1% identity in 389 aa overlap
m597/q597
                                                  50
                                          40
                         20
                                  30
          MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRLKT
g597.pep
                                  11711111111111111111111111
          MLLHVSNSLKQLQEERIRQERIRQ-
                                  -ARGNLASVNRKQREAWDKFQKLNTELNRLKT
m597
                                      30
                         20
                                         100
                                                 110
                                                         120
                 70
           EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
g597.pep
           EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
m597
                     70
                             80
                                      90
                                             100
             60
                                                 170
                         140
                                 150
                                         160
                130
           QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE
g597.pep
           QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
m597
            120
                             140
                                     150
                                             160
                                                     170
                                         220
                         200
                                 210
                190
           QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQQKAEARRAEM
g597.pep
           QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQQKAEARRAEM
m597
                             200
                                     210
            180
                    190
                250
                         260
                                 270
                                         280
                                                 290
                                                         300
           SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLKKPVDGVPTGLFGQNRSGGDVWKGVFYST
g597.pep
           SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLKKPVDGVPTGLFGQNRSGGDIWKGVFYST
m597
                                                     290
                                             280
            240
                     250
                             260
                                     270
                                         340
                                 330
                 310
                         320
           APATVESIAPGTVSYADELDGYGKVVVIDHGENYISIYAGLSEISAGKGYTVAAGSKIGT
g597.pep
           APATVESIAPGTVSYADELDGYGKVVVVDHGENYISIYAGLSEISVGKGYMVAAGSKIGS
m597
                             320
                                     330
            300
                     310
                370
                         380
                                 390
           SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX
q597.pep
           11111111111111111111111111111111111
           SGSLPDGEEGLYLQIRYQGQVLNPSSWIRX
m597
                     370
                             380
            360
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1881>

```
a597.seq
          ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
          CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
      51
          TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
     101
          CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
     151
          GCAGATTTCC CGTTTCGTAT CGGGGAACTA TAAAAACAGC CAGCCGAATG
     201
          CGGTTGCCCT GTTCCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
     251
          TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
     301
          TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
     351
          ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
     401
          AAAAAACAGG GTGTAACCGA TGCGGCGGAA CAGACGGAAA GCCGCAGACA
     451
          GAATGCCAAA ATCGCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
     501
          ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGGAGAA GAAAAAGGCC
     551
          GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
     601
          ACTGGCGGCA GCCGAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
     651
          AAGCACGACG TGCGGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
     701
          CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
     751
          GCAAGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGACTTTTCG
     801
          GGCAGAACCG GAGCGGCGGC GATGTTTGGA AAGGCGTGTT CTATTCCACT
     851
          GCACCGGCAA CGGTTGAAAG CATTGCGCCG GGAACGGTAA GCTATGCGGA
```

1001 1051 1101	ACATCAGCAT ATGGTCGCGG GGAAGAGGGG	GGCTACGGCA CTATGCCGGT CAGGAAGCAA CTTTACCTGC	TTGAGCGAAA AATCGGCTCG AAATACGTTA	TTTCCGTCGG AGCGGGTCGC	TGCCGGACG
		CTTTACCTGC GATACGTTGA		TCAAGGTCAG	GIATIGAAC

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```
1 MLLHVSNSLK QLQEERIRQE RİRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTELNRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVVDH GENYISIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGQ VLNPSSWIR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from

ORF 597 she	ows 98.5% identity over a 389 as overlap with a predicted Of
N. meningiti	dis
m597/a597	98.5% identity in 389 aa overlap
a597.pep	10 20 30 40 50 60 MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRLKT
m597	10 20 30 40 50
a597.pep m597	70 80 90 100 110 120 EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
a597.pep m597	130 140 150 160 170 180 QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
a597.pep m597	190 200 210 220 230 240 QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQQKAEARRAEM
a597.pep	250 260 270 280 290 300 SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLKKPVDGVPTGLFGQNRSGGDVWKGVFYST IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
a597.pep	310 320 330 340 350 360 APATVESIAPGTVSYADELDGYGKVVVVDHGENYISIYAGLSEISVGKGYMVAAGSKIGS
a597.pep m597	370 380 390 SGSLPDGEEGLYLQIRYQGQVLNPSSWIRX

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1883>:
q601.seq
         ATGTTCCCAA CCGGCAATTT GGTCGACGAA ATTGATGTGC CGAATATAGG
      1
         TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
      51
     101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
     151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
     201 GCTGAAAATG GGTTTGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
     251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
     301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
     351 GAGCATGGGC AAACTGCACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
     401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
     451 ACGCGTAAAG AAGTGCGCTT CGGGCATCCG TCAGGTACGC TGCGTGTCGG
     501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCc aaaqcqqtca
     551 tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGCg cgttcccgat
         gattGTTTTT GA
This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:
g601.pep
         MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
         NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
         SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
         TRKEVRFGHP SGTLRVGAAA ECQDGQWTAA KAVMSRSARV IMESWVRVPD
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1885>:
m601.seq
         ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
       1
      51 CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCTTGA
     101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
     151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
     201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
     251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
     301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTGCTGG TACGCGCCCT
     351 GAGCATGGGC AAACTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
     401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
     451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
     501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
     551 CGGTCATGAG CCGTAGCGCA CGCGTGATGA TGGAAGGTTG GGTCAGGGTG
     601 CCTGAGGATT GTTTTTAA
This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:
m601.pep
       1 MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
      51 NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
     101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
     151 GGTRKEVRFG HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
          PEDCF*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng)
from N. gonorrhoeae:
m601/g601
                                                   40
                                                                      60
                               20
                     10
             MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
m601.pep
             MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
g601
                     10
                               20
                                         30
                                                  40
                                                            50
                                                                      60
                                         90
                                                  100
                                                           110
                                                                     120
             KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
m601.pep
```

g601	 TIRAYGALKMGLI 70	: SDVSEAAARAR 80	 TPKPAFVAPAA 90	 DYTASSGKTVN 100	 AADIDLPVRA 110	 LSMG 120
Woom . E - E	130 KLHHAMMGTASVA KLHHAMMGIASVA 130	1 1111 111		111111111		1111
g601	190 ATKAVMSRSARVM : AAKAVMSRSARVI 80 190	11:11111:11	11			
a601.sec 53 103 153 203 253 303 353 404 455 503 603	ATGTTCCCAA CCGTTTGAAA ATGCCGCCGA AACGATGCCG GCTGAAAATG ACACGCCGAA AGTGGCAAAA GAGCATGGGC TTGCGACCGC GGCGGAACGC CGTCGGTGCA CGGTTATGAG CCGGAAGATT	CCGGCAATTT GCCACGCTCA CTTGGGCTAC CAGCTTTGGA GGTCTGATCA AGTCGCCTTC CCGTGAATGC AAATTGCACC CGCCGCGTG GTAAAGAAGT GCCGCCGAAT CCGCAGCGCA GTTTTTAA	GGTCGATGAA TCAACGCGGG ACGGGCAAAG AAAATTCGAG GCGACGTATC GTCGCGCCCG CGCCGACATC ACGCGATGAT CCCGGTACGC GCGCTTCGGG GTCAGGACGG CGCGTGATGA	ATTGATGTGC CATTCCGACC AGTTGCAAGA AAAATCCGCG CGAAGCTGCC CCGCCGATTA GATTTGCTGG GGGTACCGCC TGGTCAACCT CATCCTTCCG ACAATGGACG TGGAAGGTTG	CGAATATAGG GTTTTCCTGA CGACATCAAC CTTACGGTGC GCCCGCCCCC TACGCGCCCCT TCTGTTGCCA TGCCGCAGGC GCACATTGCCG GCACATTGCCG	
a601.pe	MFPTGNLVDE NDAAALEKFE SGKTVNAADI GGTRKEVRFG	IDVPNIGRLK KIRAYGALKM DLLVRALSMG	ATLINAGIPT GLISDVSEAA KLHHAMMGTA	D 1888; ORI VFLNAADLGY ARAHTPKVAF SVAIATAAAV ATKAVMSRSA	TGKELQDDIN VAPAADYTAS PGTLVNLAAG	3
m601/a601 m601.peg	1111111	10 VDEIDVPNIGR VDEIDVPNIGR	20 3 LKATLINAGIP	TVFLNAADLGY' TVFLNAADLGY'		
m601.pe a601		LKMGLISDVSE LKMGLISDVSE	111111111111	FVAPAADYTAS FVAPAADYTAS	SGKTVNAADII 	111111111
m601.pe	р КLННАММ КLННАММ	GTASVAIATAA GTASVAIATAA	11111111111	.GGGTRKEVRFG .GGGTRKEVRFG	 HPSGTLRVGA	
m601.pe	P ATKAVMS ATKAVMS	RSARVMMEGWV	1111111			

WO 99/57280

954

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1889>:
g602.seq
         ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTTCTGCT
         CGGCGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
     51
         CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
    101
    151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
    201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
         GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
    301 TGCCTGCAAA TgcgagattA TATCACTTGC TTTtggcgGC TGCATTGA
This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:
g602.pep
         MLLHQCDKAR HMRPFLLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
      1
         LIDROVAOIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLSAA
     51
         CLQMRDYITC FWRLH*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1891>:
m602.seq
         ATGTTGCTCC ATCAATGCGA CAAAACGCGA CATATGCGTC CCCTTCTGCT
      1
         CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
     51
    101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
    151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
    201 TAGTGTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
    251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
    301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:
m602.pep
      1 MLLHQCDKTR HMRPLLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
        LIDRQIAQIS AGLHVCNSVH ELFFLNIHVI VEMCAWYGVS AGEYTVNLQM
    101 RDYITRF*QL H*
m602/g602 65.2% identity in 115 aa overlap
                            20
                                      30
            MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS
m602.pep
            MLLHQCDKARHMRPFLLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS
q602
                                               40
                                      30
                   10
                            20
                                      90
                                                 100
                            80
                   70
            AGLHVCNSVHELFFLNIHVIVEMCAWYGVSA-GEYTVN---LQMRDYITRFXQLHX
m602.pep
            AGLHVCNGVHALFVLNIQIIIEMCVLYGRQMPSEKTLSAACLQMRDYITCFWRLHX
g602
                                      90
                                              100
                                                       110
                   70
                            80
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1893>:
     a602.seq
               ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
            51 CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
          101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
          151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
          201 TAGTGTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
           251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
           301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:
     a602.pep
               MLLHQCDKAR HMRTLLLGRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
            51 LIDRQIAQIS AGLHVCNSVH ELFFLNIHVI VEMCAWYGVS TGEYTVNLQM
```

95.5% identity in 111 aa overlap m602/a602

101 RDYITRF*QL H*

```
20
                                30
          MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAOIS
m602.pep
          MLLHQCDKARHMRTLLLGRQVNRHGQTGNCGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS
a602
                                      100
                70
                        8.0
                                90
                                              110
          AGLHVCNSVHELFFLNIHVIVEMCAWYGVSAGEYTVNLQMRDYITRFXQLHX
m602.pep
          AGLHVCNSVHELFFLNIHVIVEMCAWYGVSTGEYTVNLQMRDYITRFXQLHX
a602
                70
                        80
                               90
                                      100
   ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
```

```
The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 1895>:
g603.seq
         TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
      51
         CAGACGGCCC CGCACCAAAA AAACAACCAC AAACTACAAG GAGAAACATC
         ATGTCCGACC AACTCATTCT TGTCCTGAAC TGCGTCAGTT CATCGCTCAA
         AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
         GGGAACGCCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
         AACAAACGCC AAGTTCCCCT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
         GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
         AAGCCATCGG CCGCCGCATC GCCCACGGCG GCGAAAAATA TCACGAGTCC
     451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
    501 CGCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
    551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
     601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
     651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
     701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
     751 CGCATGATTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
     801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
     851 TGGTAATGGG TACACGTTGC GGCGACACCG ATCCGGGCGT ATACAGCTAT
     901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
     951 CGAAAAATCA GGTTTCCCCG GTATTTCcgA actTCCCAAC GACTGCCGCA
    1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTC
    1051 GAAGTCATGA CCTGCCGCCT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
    1101 CTGCGGCAGT GTTGACGCAC TCGTGTTCAC CGGCGGTATC GGCGAAAACT
    1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATTT CTTGGGTCTG
         CACATCGACA CCAAAGCCAA TATGGAAAAA CGCTACGGCA ATTCGGGCAT
          TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
         AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTTGTAG
This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:
g603.pep
         MDSRLRGNDA RKYGIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
         MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
         NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
         VLIDODVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
         QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
         RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
          PTFHAGMDVA QVDEMLNEKS GFPGISELPN DCRTLEIAAD EGREGARLAL
          EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDFLGL
         HIDTKANMEK RYGNSGIISP TDSSPAVLVV PTNEELMIAC DTAELAGIL*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1897>: m603.seq

- CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG 1
 - CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCCTGAT GTCTGC.CTT
 - TTTCAGACGA CCCCACACTA AAAAAACAAC CACAAACTAC AAGGAGAAAC 101
 - 151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
 - 201 CAAAGGCGCC GTTATCGACC GAMAAAGCGG CAGCGTCGTC CTAAGCTGCC
 - 251 TCGGCGAACG CCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

m603.pep

	\cdot
301	GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGAAATTGCC ACGCCGGCGC
351	GGTGGGTATG CTTTTGAACG AACTGGAAAA ACACGGTCTG CACGACCGCA
401	TCAAAGCCAT CGGCCACCGC ATCGCCCACG GCGGCGAAAA ATACAGCGAG
451	TCTGTTTTGA TCGACCAGGC CGTAATGGAC\GAACTCAATG CCTGCATTCC
501	GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTTGCCGCAC
551	AGGAACATTT CCCCGGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTC
601	CACCAAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651	GCGTAAAAA TACGCTTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
701	GTTACGTTGC CCCTGAAGCC GCACGCATCT TGGGCAAACC TCTGGAAGAC
751	ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801	CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851	GTTTGGTAAT GGGTACACGT TGCGGCGACA TCGATCCGGG CGTATACAGC
901	TATCTGACTT CCCACGCCGG GATGGATGTT GCCCAAGTGG ATGAAATGCT
951	GAACAAAAA TCAGGTTTGC TCGGTATTTC CGAACTTTCC AACGACTGCC
1001	GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051	CTCGAAGTCA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101	GGGCTGCGGC GGCGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151	ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201	CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251	CATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301	ATGAAGAACT GATGATTGCC TGCGACACTG CCGAACTTGC CGGCATCTTG
1351	TAG
This corre	sponds to the amino acid sequence <seq 1898;="" 603="" id="" orf="">:</seq>
m603.pep	
1	LSSRRRGRNN DRKCGIRFAQ RGRLKHLAPD VCXFSDDPTL KKQPQTTRRN
51	IMSDQLILVL NCGSSSLKGA VIDRXSGSVV LSCLGERLTT PEAVITFNKD
101	GNKRQVPLSG RNCHAGAVGM LLNELEKHGL HDRIKAIGHR IAHGGEKYSE
151	SVLIDQAVMD ELNACIPLAP LHNPANISGI LAAQEHFPGL PNVGVMDTSF
201	HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ARILGKPLED
251	IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301	YLTSHAGMDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA
351	LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGENSRNIRA KTVSYLDFLG
401	LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELAGIL
451	*
Computer	analysis of this amino acid sequence gave the following results:
Homology	with a predicted ORF from N.gonorrhoeae
Tiomology	1 01 (0) identities are 450 as exerten with a predicted OPE (OPE 603 ng)
ORF 603	shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng)
from N. g	onorrhoeae:
m603/g603	
, 3	
	10 20 30 40 50 60
m603.pep	${ t LSSRR}$ RGRNNDRKCGIRFAQRGRLKHLAPDVCXFSDDPTLKKQPQTTRRNIMSDQLILVL
g603	MDSRLRG-NDARKYGIRFAQRGRLKHTPPNAHPFSDGPAPKKQPQTTRRNIMSDQLILVL
J	10 20 30 40 50
	70 80 90 100 110 120
m603.pep	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNKRQVPLSGRNCHAGAVGM
* *	
g603	NCVSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFNKDGNKRQVPLSGRNCHAGAVGM
_	60 70 80 90 100 110
	130 140 150 160 170 180
m603.pep	LLNELEKHGLHDRIKAIGHRIAHGGEKYSESVLIDQAVMDELNACIPLAPLHNPANISGI
g603	LLNELEKHGLHDRIKAIGRRIAHGGEKYHESVLIDQDVLDELKACIPFAPLHNPANISGI
=	120 130 140 150 160 170

210

LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTSMRYVAPEA

220

```
LAAOEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
q603
                                         220
                                                  230
                                 210
                         200
         180
                 190
                                270
                                        280
                                                 290
                                                         300
                        260
                250
          ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
m603.pep
          ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDTDPGVYS
g603
                                         280
                                 270
                 250
                         260
         240
                                         340
                                                 350
                                                         360
                                 330
                        320
                310
          YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLALEVMTYRLAK
m603.pep
           YPTFHAGMDVAQVDEMLNEKSGFPGISELPNDCRTLE1AADEGREGARLALEVMTCRLAK
q603
                                                  350
                                         340
                         320
                                 330
         300
                 310
                                         400
                                                 410
                                                         420
                                390
                        380
                370
          YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
m603.pep
           YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
q603
                         380
                                 390
                                         400
                 370
         360
                                 450
                430
                         440
          PTDSSPAVLVVPTNEELMIACDTAELAGILX
m603.pep
           PTDSSPAVLVVPTNEELMIACDTAELAGILX
g603
                         440
                                 450
                 430
         420
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1899>:

```
a603.seq
          CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
      1
          CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
      51
          TTTCAGACGA CCCCACACC. AAAAAACAAC CACAAACTAC AAGGAGAAAC
     101
          ATCATGTCCG ACCAACTCAT TCTTGTTCTG AACTGCGGCA GTTCATCGCT
     151
          CAAAGGTGCC GTTATCGACC GCAAAAGCGG CAGCGTCGTC CTAAGCTGCC
     201
          TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
     251
          GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAACTGCC ACGCCGGCGC
     301
          GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
     351
          TTCAAGCCGT CGGCCACCGC ATCGCCCACG GCGGCGAAAA ATACAGCGAG
          TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
          GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
     501
          AGGAACATTT CCCCGGTCTG CCCAATGTCG GCGTGATGGA TACTTCGTTC
     551
          CACCAAACCA TGCCGGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
          GCGTAAAAAA TACGCTTTCC GCCGCTACGG TTTCCACGGC ACCAGTATGC
     651
          GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
     701
          ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
          CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
          GTTTGGTAAT GGGTACGCGC TGCGGCGATA TCGACCCGGG CGTATACAGC
     851
          TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
     901
          GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
     951
          GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
    1001
          CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
    1051
          GGGCTGCGGC GGCGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
    1101
          ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
    1151
          CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
    1201
          TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
    1251
          ATGAAGAACT GATGATTGCC TGCGACACTG CCGAACTTGT CGGCATCTTG
    1301
          TAG
    1351
```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

		-	-		
a603.pep		•			
	LSSRRRGRNN				
51	IMSDOLILVL	NCGSSSLKGA	VIDRKSGSVV	LSCLGERLTT	PEAVITFSKD
101	GNKROVPLSG	RNCHAGAVGM	LLNELEKHEL	HDRIQAVGHR	IAHGGEKYSE
	SVLIDOAVMD				
51 101	IMSDQLILVL GNKRQVPLSG	NCGSSSLKGA RNCHAGAVGM	VIDRKSGSVV LLNELEKHEL	LSCLGERLTT HDRIQAVGHR	PEAVITFSKE IAHGGEKYSE

251 301 351 401	HQTMPERAYT YAVPRELR IRMIIAHLGN GASITAIK YLTSHAGLDV AQVDEMLN LEVMTYRLAK YIASMAVG LHIDTKANME KRYGNSGI	NG KSVDTSM KK SGLLGIS CG GVDALVF	GFT PIEGLV ELS NDCRTI TGG IGENSF	MGTR CGDID EIAA DEGHE NIRA KTVSY	DPGVYS CGARLA YLDFLG	
m603/a603 96.	7% identity in 450 aa	overlap				
	10	20	30	40	50	60
m603.pep	LSSRRRGRNNDRKCGI				TRRNIMSDQLII!!!!!	
a603	LSSRRRGRNNDRKCGI	RFAQRGRLKH	TPPNAHPFSD			
	10	20	30	40	50	60
	70	80	90	100	110 1	120
m603.pep	NCGSSSLKGAVIDRXS					
a603	NCGSSSLKGAVIDRKS	GSVVLSCLGE 80	RLTTPEAVIT	100		/GM L20
	, 0		30			
	130	140	150	160		180
m603.pep	LLNELEKHGLHDRIKA					
a603	LLNELEKHELHDRIQA					
	130	140	150	160	170 1	180
	190	200	210	220	230 2	240
m603.pep	LAAQEHFPGLPNVGVM	DTSFHQTMPE	RAYTYAVPRE			
. 602		ULCEROTWDE.			CEHCTOMPYVAE	
a603	190	200	210	220		240
	• • •		0.50	000	200	
m603.pep	250 ARILGKPLEDIRMIIA	260 HLGNGASTTA	270 TKNGKSVDTS	280 Mgftpteglv		300 7YS
moos.pep	1 1111111111111		111111111	1111111111	111111111111111111111111111111111111111	11
a603	ACILGKPLEDIRMIIA					
	250	260	270	280	290 3	300
	310	320	330	340		860
m603.pep	YLTSHAGMDVAQVDEM					
a603						
4000	310	320	330	340		860
	370	380	390	400	410 4	20
m603.pep	YIASMAVGCGGVDALV					
a603	YIASMAVGCGGVDALV 370	FTGGIGENSR 380	NIRAKTVSYL 390	DFLGLHIDIK 400		120
				•		
	430 PTDSSPAVLVVPTNEE	440 IMIACOTARI	450			
m603.pep						
a603	PTDSSPAVLVVPTNEE	LMIACDTAEL	VGILX			
	430	440	450			

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1901>: g604.seq

- 1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
- 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC

- 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGGCGGCG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GGCGGGTTTC GGCGTGCGC CGCGGGCGGC GGCTTCGGAT

```
251 ACGTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC
         AAATTTTTCC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT
    301
         TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAAAACGGT CGGAATGCCC
    401 GCGTTGATGA GCGTGGCTTT CAGACGACCT ATATTCGGCA CATCAATTTC
     451 GTCGACCAAA TTGCCGGTTG GGAACATACT GCCTTCGCCG TCGGCTGGAT
    501 CTAA
This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:
q604.pep
         MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID
         VGGVYGFAAG GGVIGGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
         KFFORGGIVV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF
         VDQIAGWEHT AFAVGWI*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1903>:
m604.seq
      1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
     51 CCAGCGTACC GGGTACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
    101 CCCATCATCG CGTGGTGCAG TTTGCCCATG CTCAGGGCGC GTACCAGCAA
    151 ATCGATGTCG GCGGCGTTCA CGGTTTTGCC ACTGGAGGCG GTGTAATCGG
    201 CGGCGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG AGCGGCAGCT
         TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
         TTTCTCGAAT TTTTCCAAAG CCGCGGCATC GTTGTTGATG TCGTCTTGCA
         ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
         ATGCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
     401
     451 AATTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
    501 CTGGATC
This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:
m604.pep
         MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
     51 IDVGGVHGFA TGGGVIGGGR DEGDFRRVRA SGSFGYVADQ THFQRTVSAD
    101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
     151 NFIDQIAGWE HTAFAVGWI
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng)
from N. gonorrhoeae:
m604/g604
                                       30
                                                40
                    10
                              20
            MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
m604.pep
            MPEAHFFTRSAACGKVDQRTEHGGG--DGDRGDAHHSVVQFAHAQGAYRQIDVGGVYGFA
g604
                    10
                              20
                                                100
                                       90
                              80
            {\tt TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA}
m604.pep
            AGGGVIGGGRDEGGFRARAGGGFGYVADQTHFQRAICADGFKFFQRGGIVVDVVLQLFA
9604
                                                 100
                                                           110
                      70
                               80
                                         90
                             140
                                      150
                                                160
            CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
m604.pep
             RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX
g604
                                        150
                                                 160
                               140
                     130
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1905>:
     a604.seq
            1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
          51 CCAGCGTACC GGGCACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
          101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
          151 ATCGATGTCG GCGGCATTCA CGGTTTTGCC ACTGGAGGCG GTGTAATCGG
```

201	CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GGCGGCAGCT
251	TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301	TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTTGATG TCGTCTTGCA
351	ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTCAGGAA AACGGTCGGA
401	ATGCCCGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451	AATTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501	CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551	TCGAGCTCAA AATCGCCTGT TTCCAAAACT GCGCCGTTTT GCATCGGTAC
601	ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651	AGATGCCGTC TGA
This correspond	Is to the amino acid sequence <seq 1906;="" 604.a="" id="" orf="">:</seq>
-	in to the aimine acts or from the first of t
a604.pep	MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
1	IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
51	THE PROPERTY OF THE PROPERTY O
101	
151	MGNNGFADVF LPDFDCADAV *
201	MGNNGFADVF LPDFDCADAV "
	7.00/ 11 /// 100 as asserted
m604/a604 97	7.0% identity in 169 aa overlap
	10 20 30 40 50 60
m604.pep	MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
a604	MPEAHFFTRSAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA
	10 20 30 40 50 60
	70 80 90 100 110 120
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFLEFFQSCGIVVDVVLQLFA
	70 80 90 100 110 120
	130 140 150 160 169
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWIKKFDLYFGCRE
	130 140 150 160 170 180
a604	RYAVELKIACFQNCAVLHRYMGNNGFADVFLPDFDCADAVX
	190 200 210 220

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>: 9605.seq

```
ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
 1
 51 AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCta tGCCGGACAG
201 CATCATCACG CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTACCCGT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTTCGGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCcgcCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
    GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
    TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT
```

WO 99/57280

961

```
CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
         CCGATTTTGC CTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
         CGCGCCGCTA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGCGCAGA
         GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
         TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
         CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
    1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
    1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
    1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
    1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
    1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
    1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG
This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:
g605.pep
         MMTEMOORAO LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
      1
         YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
      51
         NEELNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
         KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
    151
         POSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIEEGFF
         GOEINHTTYN LARMNMFLHN VNYNKFHIEL GDTLTNPKLK DSKPFDAVVS
         NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
         RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCIAVNI
     401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
     451 IAONAAQQTV KDNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
     501 LRREIDEVIA EIET*
The following partial DNA sequence was identified in N.meningitidis <SEQ ID 1909>:
m605.seq
         ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
      1
         AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
     51
    101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
         TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
         CATCATCACG CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
    201
         TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
         AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTTACCG CGATTGAAAG
         CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
         ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
         AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTCGGCAA
         TTTTGAAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
         TTTCCAACTA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
         CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
         GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
         TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
         GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
         CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCGACACAC
         TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
         AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
         CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
         CCGATTTTGC CTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
         CGCGCCGCCA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGGCGCAGA
    1101 ACAGAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
         TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
         CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
    1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
    1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
    1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
    1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
         TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
    1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA
This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:
m605.pep
         MMTEMQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
```

51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

101	NEELNTKLKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLAAVLKGV	AELDFGNFEN	HHIDLFGDAY	EYLISNYAAN	AGKSGGEFFT
201	PQSVSKLIAR	LAVHGQEKVN	KIYDPACGSG	SLLLQAKKQF	DEHIIEEGFF
251	GQEINHTTYN	LARMNMFLHN	VNYNQFHIEL	GDTLTNPKLK	DSKPFDAIVS
301	NPPYSINWIG	SDDPTLINDD	RFAPAGVLAP	KSKADFAFIL	HALNYLSGRG
351		FYRGGAEQKI			
401	LVLSKHKDNT	DIQFIDASGF	FKKETNNNVL	IEEHIAEIVK	LFADKADVPH
451	IAQNAAQQTV	KDNGYNLAVS	SYVEAEDTRE	IIDIKQLNAE	IGETVAKIER
501	LRREIDEVIA	EIEA*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from N. gonorrhoeae: m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQQRAQL					
	 MMTEMQQRAQL	HILL HILL		EKOVII GTI E		MOACDESTD
g605	MMTEMQQRAQL	HRQIWKIADE 20	VRGAVDGWDI 30	40	. KF13ENF1D	60
	20					
	70	80	90	100	110	120
m605.pep	YAAMPDSIITP					
~605						
g605	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGL				AELDFGNFENI 	
g605	GYPSEQGIKGL					
9605	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANA					
g605	EYLISNYAANA					
3002	190	200	210	220	230	240
					· ·	
	250	260	270	280	290	300
m605.pep	DEHIIEEGFFG					
g605	DEHILEEGFFG					
3003	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGS					
g605	NPPYSIDWIGS					
9003	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIR	QYLVEGNYVE	TVIALAPNLI	YGTGIAVNII		JIQFIDASGF
g605	FYRGGAEQKIR	OYLVEGNYVE	TVIALAPNLI	FYGTCIAVNII	LVLSKHKDNTI	DIOFIDASGF
5.05	370	380	390	400	410	420
40.0	430	440	450	460	470	480
m605.pep	FKKETNNNVLI					
g605	FKKETNNNVLT					
3-00						

PCT/US99/09346 WO 99/57280

963 470 430 440 450 460 480 500 490 IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX m605.pep VIDIRQLNAEISETVAKIERLRREIDEVIAEIETX 9605 500 490 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1911>: a605.seq

```
ATGATGACCG AAATACAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
   AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTCAAACAAT
51
```

ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTTACCGAC 101 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG 151 CATCATCACG CCCGAAATCA AAGACGATGC CGTCAAAGTC AAAGGCTATT 201 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA 251 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTTACCG CGATTGAAAG 301 CTCCGCCTCC GGCTATCCGT CCGAACAAGA CATTAAAGGC CTGTTTGACG 351 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAGAAC 401 AAACGCCTTG CCGCCGTCCT AAAAGGCGTG GCGGAACTCG ATTTCGGCAG 451 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA 501 TTTCCAACTA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC 551 601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA GAAAGTAAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGCCTGCTCT 651 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC 701 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT 751 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACAC 801 TGACCAATCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTTTCC 851 AATCCGCCCT ATTCCATCAA CTGGATAGGC AGCGGCGACC CCACCTTAAT 901 951 CAACGACGAC CGCTTTGCCC CTGCAGGCGT ACTCGCCCCG AAATCCAAAG CCGATTTTGC CTTCATTCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC

1001 CGCGCCGCCA TCGTCTCATT CCCCGGCATT TTCTATCGCG GCGCGCAGA 1051

GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTCA 1101 TCGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATA 1151 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC 1201

AGGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC ACATTGCCGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT

CGCCGTCAGC AGCTATGTTG AACCCGAAGA CACCCGCGAA ATTATCGACA TCAAACAGCT TAACGCCGAA ATCAGCGAAA CCGTTGCCAA AATCGAACGG

CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA 1501

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

a605.pep MMTEIQQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD 1 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHO 51 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN 101 KRLAAVLKGV AELDFGSFED HHIDLFGDAY EYLISNYAAN AGKSGGEFFT POSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIEEGFF GOEINHTTYN LARMNMFLHN VNYNKFHIEL GDTLTNPKLK DSKPFDAVVS NPPYSINWIG SGDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG 301 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI 401 LVLSKHKDNT DIQFIDAGGF FKKETNNNVL TEEHIAEIVK LFADKADVPH IAQNAAQQTV KDNGYNLAVS SYVEPEDTRE IIDIKQLNAE ISETVAKIER 501 LRREIDEVIA EIEA*

m605/a605 98.1% identity in 514 aa overlap

30 40 50 MMTEMQQRAQLHRQIWKIADEVRGAVDGWDFKQYVLGTLFYRFISENFTDYMQAGDSSID m605.pep a605 MMTEIQQRAQLHRQIWKIADEVRGAVDGWDFKQYVLGTLFYRFISENFTDYMQAGDSSID 30 40 50 70 80 90 100 110 YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS m605.pep

PCT/US99/09346 WO 99/57280

964

a605						
m605.pep	130 GYPSEQDIKGLFDDFE 			1111111111	:11:1111	11111
m605.pep	190 EYLISNYAANAGKSGG EYLISNYAANAGKSGG 190	ППППП			HIHHH	11111
m605.pep	250 DEHIIEEGFFGQEINH !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	111111111		1111111111		11:11
m605.pep	310 NPPYSINWIGSDDPTI !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!				11111111	11111
m605.pep a605	370 FYRGGAEQKIRQYLVE	111111111	1111111111	111111111	нини	11:11
m605.pep a605	430 FKKETNNNVLIEEHIA FKKETNNNVLTEEHIA 430	1111111111		ППППП	1111111	
m605.pep a605	490 IIDIKQLNAEIGETVA IIDIKQLNAEISETVA 490	111111111				

The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 1913>: g606.seq

00.3	-q					
	1	ATGTCCAAAT	TTATCGCCAA	ACAATCGGTC	GGTGCGGAAG	TCATCGACAC
	51	GCCGcgCACC	GAAGAAGAAG	CCTGGCTTCT	${\tt GAACACTGTC}$	GAAGCCCAAg
1	01	cgcGGCAATG	GAATCTGAAA	ACGCCAGAAG	TCGCCATCTA	CCACTCCCCC
1	51	GAACCCAATG	CCTTTGCCAC	GGGCGCATCG	AGAAACAGCT	CCCTGATCGC
2	01	CGTCAGCacc	ggtttgctcg	accaTAtgaC	${\tt GCGCGACgaa}$	gtggaagccg
2	51	tgTTGGCGCA	CGAAATGGCG	CACGTCGGCA	ACGGCGACAT	GGTTACGCTG
3	01	ACGCTGAtTC	AAGGCGTGGT	CAATACCTTT	GTCGTGTTCC	TGTCGCGCAT
3	51	TATTGCCAAC	CTGATTGCCC	GAAACAACGA	CGGCAGCCAG	TCCCAGGGAA
4	01	CTTATTTCCT	AGTCAGCATG	GTATTCCAAA	TCCTGTTCGG	CTTCCTTGCC
4	51	AGCCTGATTG	TCATGTGGTT	CAGCCGCCAA	CGCGAATACC	GCGCCGAcgc
5	01	gggCGcggCA	AAACTGGTCG	GCGCACCGAA	AATGATTTCC	GCCCTGCAAA
5	51	GGCTTAAAGG	CAACCCGGTC	${\tt GATTTGCCCG}$	AAGAAATGAA	CGCAATGGGC
6	01	ATCGCCGGAG	ATACGCGCGA	$\mathtt{CTCCCTGCTC}$	AGCACCCACC	CTTCGCTGGA
6	51	CAACCGAATC	GCCCGCCTCA	AATCGCTTTA	A	

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

965

```
g606.pep
         MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
         EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
     51
         TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
     101
         SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
     151
         IAGDTRDSLL STHPSLDNRI ARLKSL*
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1915>:
m606.seq
         ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
      1
        GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
     51
         CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
    151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
         CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
    251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
    301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
         TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
         CTTATTTCCT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCCTTGCC
     451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
    501 GGGCGCGCA AAACTGGTCG GCGCGCCGAA AATGATTTCC GCCCTGCAAA
     551 GGCTCAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
     601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTCGCTGGA
         CAACCGTATC GCCCGCCTCA AATCGCTTTA A
This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:
m606.pep
         MSKFIAKOSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
         EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
     51
         TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
     101
         SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
         IAGDTRDSLL STHPSLDNRI ARLKSL*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N.gonorrhoeae
ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng)
from N. gonorrhoeae:
m606/g606
                             20
                    10
            MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
m606.pep
            MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
q606
                                               40
                                                         50
                    10
                             20
                                      30
                                               100
                                                        110
                             80
                                      90
            RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN
m606.pep
            RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN
g606
                    70
                             80
                                               100
                                                        110
                                                                 120
                                               160
                   130
                            140
                                     150
            LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
m606.pep
            LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
q606
                                                        170
                   130
                            140
                                     150
                                               160
                                                               . 180
                                               220
                            200
                                     210
            ALORLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX
m606.pep
            ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX
g606
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1917>: a606.seq

210

200

190

220

966

```
1 ATGTCCAAAT TCATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
    GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
 51
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
    GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
151
     CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
201
    TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
251
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
    TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
351
401 CTTATTTCCT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGCA AAACTGGTCG GCGCGCCGAA AATGATTTCC GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTCGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

a606.pep

- MSKFIAKOSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
- EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL 51
- TLIOGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA 101
- SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
- IAGDTRDSLL STHPSLDNRI ARLKSL*

m606/a606 100.0% identity in 226 aa overlap

	10	20	30	40	50	60
m606.pep	MSKFIAKQSVGAEV	IDTPRTEEE	AWLLNTVEAQA	RQWNLKTPE	JAIYHSPEPNA	FATGAS
• •	111111111111111111111111111111111111111	1111111	11111111111		11111111111	
a606	MSKFIAKQSVGAEV	IDTPRTEEE	AWLLNTVEAQA	RQWNLKTPEV	<i>V</i> AIYHSPEPNA	FATGAS
	10	20	30	40	50	60
	/					
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLD	HMTRDEVEA	VLAHEMAHVGN	GDMVTLTLI(QGVVNTFVVFL	SRIIAN
		[] [] [] [] []	111111111111		[]]]]]	
a606	RNSSLIAVSTGLLD	HMTRDEVEA	VLAHEMAHVGN	GDMVTLTLI	QGVVNTFVVFI	SRIIAN
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGT	YFLVSMVFQ	ILFGFLASLIV	MWFSRQREY	RADAGAAKLVG	APKMIS
_		11111111	11111111111			
a 60 6	LIARNNDGSQSQGT	YFLVSMVFQ	ILFGFLASLIV	MWFSRQREYI	RADAGAAKLVO	APKMIS
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPE	EMNAMGIAG	DTRDSLLSTHP	SLDNRIARLI	KSLX	
		111111111	11111111111			
a606	ALQRLKGNPVDLPE:	EMNAMGIAG	DTRDSLLSTHP	SLDNRIARL	KSLX	
	190	200	210	220		

The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 1919>:

q607.seq ATGCTGCTCG accTcgaCCG CTTTTCCTtt tccGTCTTCC TGAAAGAAAT CCGCCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC 51 101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG 151 GAAGATTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA 201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC 251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG 301 ATTTGGTTCG GGCTGATTTT GGGGATTTTC GGCATGATTT TGATGTGGGC 351 GGCGATTACG CCGTTCCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG 401 gcacAAtggc gcAGTATATG CTGTTCACCA GCTTGGCGAT GCCGGCGGCA 451 ATGGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCCGCG 501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA 551 ACTATATTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGTGGCGCA

```
967
```

```
601 GGTTGCGGCG TGGCGACAAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
         GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
         CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
          gGcgcgCCCA TCGGGCTGTC TTATTTTTTG GAAgccaGcg cGTTTTCGTT
          TATCGTGTTT TTGATTGCGC CTttcggCGA GGATTATGTG GCGGCGCAGC
     851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
     901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
          TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCG GGCTGGGTGC
    1001
          TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGCA
          AGCATGTACA ACGATGATCC GGCAGTTTTA AGCATCGCCT CCACCGTCCT
    1051
         GCTGTTCGCC GGCCTGTtcc aACCGGCAGA CTTCACCCAA TGTATCGCGT
    1101
         CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
    1151
         GCCGCCGCCT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
    1201
    1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
    1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGGAAAA ATACAGTATG
    1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA
This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:
q607.pep
       1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTVMAGGAGK
      51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
     101 IWFGLILGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
     151 MVHRALHAYA SSLNRPRLIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
     201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
     251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
     301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFRSPLA
     351 SMYNDDPAVL SIASTVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
     401 AAAFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
     451 ELVKSHKAV*
The following partial DNA sequence was identified in N.meningitidis <SEQ ID 1921>:
m607.seq
         ATGCTGCTCG ACCTCAACCG CTTTTCCTTT CCCGTCTTCC TGAAAGAAGT
      51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
     101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TGCGGGCAAG
     151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
     201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
     251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
     301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
         GGCGATTACG CCGTTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
         GCACGATGGC GCAGTATATG TTGTTCACCA GCTTGGCGAT GCCGGCGGCA
     451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCGCG
     501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
     551 ACTATATTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
     601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
     651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGACTGACGG
     701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
     751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
         TATCGTGTTT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
     851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
     901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
     951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
    1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGTA
    1051 AGTATGTACA ACAATGATCC GGCGGTTTTA AGCATCGCCG CCACCGTCTT
    1101 ACTGTTCGCC GGCTTGTTCC AACCGGCAGA CTTCACCCAA TGTATCGCCT
    1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
   1201 GCCGCCGCT TTTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
   1251 CCGTTCAAT ATGGGCATTT ACGGCTTCTG GACGCCATTG ATTGCCTCGC
         TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAATT GTGCAGTAGG
         GAGATGGTCA GATCGCATAA GGCCGTCTGA
This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:
m607.pep
         MLLDLNRFSF PVFLKEVRLL TTLALPMLLA QVAQVGIGFV DTVMAGGAGK
      51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGROG
```

```
101 IWFGLFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYT SSLNRPRLIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFRSPLV
351 SMYNNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AAAFWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
451 EMVRSHKAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N.gonorrhoeae

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from N. gonorrhoeae:

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1923>:

a607.seq ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC 51 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG 101 151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC 251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG ACGGCAGGGG 301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC GGCGATTACG CCGTTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG GCACAATGGC GCAGTATATG CTGTTCACCA GCTTGGCGAT GCCGGCGGCA 401 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA ACTATATTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT 601 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGACTGACGG 651 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT 751 TATCGTGTTT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC 851 AGGTCGCCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC 901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT 951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTCA GGATGGATGC 1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTC GCCGCTGGTA AGTATGTACA ACAATGATCC GGCGGTTTTA AGCATCGCCG CCACCGTCTT 1051 ACTGTTCGCC GGCTTGTTCC AACCGGCAGA CTTCACCCAA TGTATCGCCT CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC 1151 GCCGCCGCCT TTTGGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAATT GTGCAGTAGG 1301 GAGATGGTCA GATCGCATAA GGCTGTCTGA 1351 This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

a607.pep					
a ou r. pep					
1	MLLDLNRFSF	SVFLKEVRLL	TALALPMLLA	QVAQVGIGFV	DTVMAGGAGK
51	EDLAAVALGS	SAFATVYITF	MGIMAALNPM	IAQLYGAGKT	DEVGETGRQG
101	IWFGLFLGVF	GMVLMWAAIT	PFRNWLTLSD	YVEGTMAQYM	LFTSLAMPAA
151	MVHRALHAYA	SSLNRPRLIM	LVSFAAFVLN	VPLNYIFVYG	KFGMPALGGA
201	GCGLATMAVF	WFSALALWIY	IAKENFFRPF	GLTAKFGKPD	WAVFKQIWKI
251	GAPIGLSYFL	EASAFSFIVF	LIAPFGEDYV	AAQQVGISLS	GILYMIPQSV
301	GSAGTVRIGF	SLGRREFSRA	RYISGVS <u>LVS</u>	GWMLAVITVL	SLVLFRSPLV
351	SMYNNDPAVL	SIAATVLLFA	GLFQPADFTQ	CIASYALRGY	KVTKVPMFIH
401	AAAFWGCGLL	PGYLLAYRFD	MGIYGFWTAL	IASLTIAAIA	LVWCLELCSR
451	EMVRSHKAV*				

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFL	KEVRLLTTL	ALPMLLAQVAÇ	QVGIGFVDTVN	1AGGAGKEDL1	AAVALGS
-		111111111111111111111111111111111111111	[
a607	MLLDLNRFSFSVFL	KEVRLLTAL	ALPMLLAQVAÇ	QVGIGFVDTVN	1AGGAGKEDL <i>i</i>	AAVALGS
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIM	AALNPMIAQ	LYGAGKTDEVG	SETGRQGIWFO		TIAAWML
1 1	111111111111	111111111	1111111111	111111111	11111111	
a607	SAFATVYITFMGIM	AALNPMIAQ1	LYGAGKTDEVO	SETGRQGIWFO	SLFLGVFGMV1	LIAAWML
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEG	TMAQYMLFTS	SLAMPAAMVHF	RALHAYTSSLN	RPRLIMLVSI	FAAFVLN
• •	111111111111111	11111111		11111:111	111111111	
a607	PFRNWLTLSDYVEG	TMAQYMLFT	SLAMPAAMVHF	RALHAYASSLN	RPRLIMLVS	FAAFVLN
	130	140	150	160	170	180
	190	200	210	220	230	240

970

```
VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
m607.pep
          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607
                                       220
                                               230
                       200
                               210
                190
                250
                       260
                               270
                                       280
                                               290
                                                       300
          WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
m607.pep
          WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
a607
                250
                       260
                               270
                                       280
                310
                       320
                               330
                                       340
                                               350
                                                       360
          GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFRSPLVSMYNNDPAVL
m607.pep
          GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMLAVITVLSLVLFRSPLVSMYNNDPAVL
a607
                               330
                                       340
                                               350
                310
                       320
                370
                       380
                               390
                                       400
                                               410
                                                       420
          SIAATVLLFAGLFOPADFTOCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN
m607.pep
          SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD
a607
                               390
                       380
                                       400
                                               410
                                                       420
                370
                       440
                               450
                                       460
                430
          MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
m607.pep
```

The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 1925>:

MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX

450

460

440

430

```
q608.seq
         ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
       1
         CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
     51
         TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
     101
         GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGAT
     151
     201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
     251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
         CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
     301
         catcggcagc CGTGCCACCG ACATCGGACA CGGCaTCaaa cAAATCGGCA
          GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
         aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
         GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
          ACATTTGGAT AGACTAA
```

a607

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>: g608.pep

- MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS 1
- AGNGFADTEI TFRNSAIRKI LQGGEPGAGD IRLEGDLILG IAVLSLLGSL
- RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
- NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

The following partial DNA sequence was identified in N. meningitidis <SEO ID 1927>: m608.seq

- ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA 1
- CAGCCGCTCG GAACTTGCCG CCTTTGCAGG CAAAACACTG ACCCTGAACA 51
- TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG 101
- GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGGT 151
- ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGCCGAC ATCGGGCTCG
- AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
- CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA 301 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA 351
- GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA 401
- AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG

551 ACATTTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>: m608.pep

- MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
- 51 AGNGFADTEI TFRNSAVQKI LQGGEPGAGD IGLEGDLILG IAVLSLLGSL
- 101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
- 151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N.gonorrhoeae

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from N. gonorrhoeae:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQ	SPDSRSELAAF	AGKTLTLNI	AGLKLAGRIT	EDGLLSAGN	GFADTEI
		11111111::1	[11111	
g608	MSALLPIINRLILQ	SPDSRSELTS	AGKTLTLNI	AGLKLAGRI'I	'EDGLLSAGN	GFADTEI
2	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGG	EPGAGDIGLE	BDLILGIAVI	LSLLGSLRSRA	SDELARIFG	TOADIGS
	_	111111				
g608	TFRNSAIRKILQGG	EPGAGDIRLEC	BDLILGIAVI	LSLLGSLRSRA	SDELARIFG'	rqagigs
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGR	NIAEQIGGFSF	RESESANIGN	IEALADCLDEI	SRLRDGVER	LNERLDR
g608	RATDIGHGIKQIGR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
	11111111					
g608	LERDIWIDX					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1929>:

```
a608.seq
         ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
      1
         CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
     51
         TTGCCGGGTT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
         GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCCGCA ACAGCGCGGT
    201
         ACAGAAAATC CTCCAAGGCG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
    251
         AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
    301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
         CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA
    351
    401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
    451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
         GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
    551 ACATTTGGAT AGACTAA
```

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

- MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS AGNGFADTEI TFRNSAVQKI LQGGEPGAGD IGLEGDLILG IAVLSLLGSL RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
- NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

m608.p	ep MSALLPIINRLILQ	SPDSRSELAAFAGKTI	TLNIAGLKLAGRITED	GLLSAGNGFADTEI
•	1111111111111			
a608			LTLNIAGLKLAGRITED	
	10	20 30	0 40	50 60
	70	80 90	100	110 120
m608.p			SIAVLSLLGSLRSRASD	
	•			
a608	TFRNSAVQKILQGG	EPGAGDIGLEGDLILG	SIAVLSLLGSLRSRASD	ELARIFGTQADIGS
	70	80 90	100	110 120
	100	140 150	1.00	170
	130	140 150) 160 ANIGNEALADCLDEISR	170 180
m608.p			WIGNEALADCLDEISK	
a608			MIGNEALADCLDEISR	
4000	130	140 150		170 180
		•		
	189			
m608.p				
a 608	LERDIWIDX			
The followin	g partial DNA sequence	was identified in	N gonorrhoege <	SEO ID 1031>
g609.seq	g partial DIVI sequence	was identified in	111. gonorrhoeue	and in 1991s.
	GTTGTGG ATAGACTCGA AATTC	TCGCT CTCGACGACG	AAACTCTTGA	
51 TGC	GTTTGTC GGCAATCAGC GAAGT	AGCGA CATCGCGCAC	CATATCTTCC	
	SAATTTCG GGTTTTCGTA GGCCT			
	TTTGAGC AGGCCGTAGA GTTGG TAACTTC CTCGATACCG ACTTC			
	TTAACTIC CICGATACCG ACTIC			
	GCAAAGC GAGGTTACGG GAATC			
351 CCC	CGTCTTT CATTTCACCC GTGAG	GCTGA CATCATAATC	CAGtaa	
mu :	1 4 41	- AGEO ID	1022 ODT (00	
	onds to the amino acid s	equence <seq il<="" td=""><td>) 1932; ORF 609.r</td><td>ıg>:</td></seq>) 1932; ORF 609.r	ıg>:
g609.pep	TOTAL TANGET DARK CHORG	CDIAU UIRUREDURU	CI ECNUEET C	
	'DRLEILA LDDETLDAFV GNQRS COAVELAA RLRFHIIDNF LDTDF			
	RGYGNHD LHTVAVCPVF HFTRE	-		
				~~~
The followin	g partial DNA sequence	was identified in	N. meningitidis <	SEQ ID 1933>:
m609.seq				
	GTTGTGG ATAGACTCGA AATTC			
	AATTTCG GGCAATCAGC GAAGI			
	TTTGAGC AGGCCGTAGA GTTGG			
	TGACTTC CTCGATACCG ACTTC			
	TGCGAAC GCTGGTTGTG CGCGC			
	GCAAAGC GAGGTTACGG GAATC CGTCTTT GATTTCGCCC GTGAG			
This correspond	onds to the amino acid so	equence <seq id<="" td=""><td>) 1934; ORF 609&gt;</td><td>:</td></seq>	) 1934; ORF 609>	:
m609.pep			•	
	DRLEILA LDDETLDAFV GNQRS			
	QAVELAA RLRLHIIDDF LDTDF RGYGNHD LHTVAVCPVF DFARE		RAVLGNFFGT	
101 RAK	RGIGNED LHIVAVCEVE DEARE	IDIII Q-		
m609/g609 93.	1% identity in 131 aa ov	erlap		
	-			
	10 20	30 40	50 60	
m609.pep	MVVDRLEILALDDETLDAFVGNQR			
g 609	MVVDRLEILALDDETLDAFVGNQR			
-	10 20	30 40	50 60	
	70 00	00 100	110	
m609.pep	70 80 RLRLHIIDDFLDTDFGIGSQADGN	90 100 VETT.VVEAVI.GNEEGTE	110 120 AKRGYGNHDI.HTVAVCPVE	
wood.beb	:   :			

g609

973

 $\verb|RLRFHIIDNFLDTDFGIGSQadGNVRTLIMRAILGNFFGTRAKRGYGNHDLHTVAVCPVF|$ 

```
90
                                             100
                                                      110
                            80
                  130
            DFARETDIIIQX
m609.pep
            1:11:11111
g609
            HFTREADIIIQX
                  130
The following partial DNA sequence was identified in N. meningitidis <SEO ID 1935>:
     a609.seq
               ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACTCTTGA
            1
               TGCGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
           51
               ACGAATTTCG GGTTTTCGTA GGCTTTTTCG GTAACGTATT TTTCATCGGG
          101
               GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
          151
               CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
               ACGTGCGAAC GCTGGTTGTG CGCGCCATAT TGGGAAATTT CTTTGGAACA
          251
               CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
          301
               CACCGTCTTT CATTTCGCCC GTGAGGCTGA CATCATAATC CAGTAA
This corresponds to the amino acid sequence <SEQ ID 1936; ORF 609.a>:
               MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFV GFFGNVFFIG
            1
               AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
           51
               RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*
          101
     m609/a609
                  96.9% identity in 131 aa overlap
                                     20
                                               30
                                                         40
                  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGFFGNVFFIGAFEQAVELAA
     m609.pep
                  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGFFGNVFFIGAFEOAVELAA
     a609
                          10
                                     20
                                                         40
                                                                   50
                                                        100
                                     80
                                               90
                          70
                                                                  110
                                                                            120
                  RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
     m609.pep
                  RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF
     a609
                                                        100
                                                                  110
                         130
                  DFARETDIIIQX
     m609.pep
                   1111:111111
                  HFAREADIIIQX
     a609
                         130
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1937>:
q610.seq
        ATGATTGGAG GGCTTATGCA ATTTCCTTAC CGCAATGTTC CGGCTTCGCG
      1
        TATGCGCCGT ATGCGCAGGG ATGATTTTTC ACGCCGCCTG ATGCGCGAGC
     51
    101 ATATGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTCGT ATTGGAGGGG
        GCGGCGCGC AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
    201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTGAAG CTCGGTATTC
    251 CGATGTTGGC ACTCTTTCCC GTGGTTACGG CAAACAAAAC CGGGCGTGCG
    301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG tccqaqccTT
        GCGCGAGAGG TttcCcgaac tggggattat gacggatgtc gcgctcgAtc
    401 cttatacggt gcacGGTCAG GACGGACTGA CGGACgaaaa cggttaCGTG
        ATGAAtgATg aaaCCGTAGA AGTCTTGGTG AAACAGGCTT TATGTCATGC
    501 AGAGGCGGGC ACGCAGGTCG TTGCTCCTTC CGATATGATG GACGGGCGTA
    551
        TCGGCGCCAT CCGCGAGGCT TTGGAGGATG CCGGACATAT CCATACGCGG
    601 ATTATGGCAT ATTCCGCCAA ATATGCTTCT GCATTCTACG GCCCTTTCCG
    651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG AAAGGCAGAT AAAAAGACCT
        ATCAGATGGA TCCTGCAAAT ACCGATGAGG CGCTGCATGA AGTGGCGCTC
        GATATTCAGG AAGGTGCGGA TATGGTGATG GTGAAGCCCG GTTTGCCGTA
```

m610.pep

974

```
TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
     801
         CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTTGCCAAC
         GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
     901
         ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
     951
         AGATGCTGAA GCGTTGA
This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:
g610.pep
         MIGGLMOFPY RNVPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
         AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
      51
          OEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
     101
         MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIREA LEDAGHIHTR
     151
         IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
     251
         DIOEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN
         GWLDGGKVVL ESLLAFKRAG ADGILTYYAI EAAKMLKR*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1939>:
 m610.seq
         ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTC CGGCTTCGCG
      1
         TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAAC
      51
         ACACGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTCGT ATTGGAGGGG
     101
         TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
     151
     201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
         CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
     251
         CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
     301
         GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
         CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
     401
         ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
         TGAAGCGGGC GCGCAGGTGG TTGCCCCTTC CGATATGATG GACGGGCGTA
     501
         TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
         ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
     601
         TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
     701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
         GACATTCAGG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTTGCCGTA
     751
     801
         TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
         CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC
     851
         GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
         ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
     951
    1001
         AGATGTTGAA GCGTTGA
This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:
m610.pep
         MIGGLMQFPY RNVPASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
         SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
     51
         QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
     101
         MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
         IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
         DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAIAN
     251
         GWLDGGKVVL ESLLAFKRAG ADGILTYYAI EAAKMLKR*
m610/g610 98.5% identity in 338 aa overlap
                              20
                                       30
                                                 40
            MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
m610.pep
            MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM
g610
                                                                   60
                             20
                                       30
                                                 40
                    10
                             80
                                       90
                                               100
                                                         110
            {\tt PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER}
m610.pep
            {\tt PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER}
q610
                             80
                                       90
                                               100
                                                         110
                   130
                             140
                                      150
                                               160
                                                         170
                                                                   180
            FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQVVAPSDMM
m610.pep
            FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGTQVVAPSDMM
q610
                   130
                            140
                                      150
                                               160
                                                         170
                                                                  180
                                               220
                            200
                                      210
                   190
            DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
```

g610	DGRIGAIREALEDAG	HIHTRIMAYS.	AKYASAFYGP	FRDAVGSSGN:	LGKADKKTYQI	MDPAN
<b>3</b> · · ·	190	200	210	220	230	240
	250	260	270	280	290	300
m610.pep	TDEALHEVALDIQEG	ADMVMVKPGL	PYLDVVRRVKI	DEFGVPTYAY		
g610	TDEALHEVALDIQEG	IIIIIIIII ADMVMVKPGL	[			:   AAVAN
	250	260	270	280	290	300
	310	320	330	339		
m610.pep	GWLDGGKVVLESLLA	FKRAGADGIL'	TYYAIEAAKMI	LKRX		
g610	GWLDGGKVVLESLLA	FKRAGADGIL	TYYAIEAAKMI	LKRX		
,	310	320	330			

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1941>:

a610.seq ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAGC 51 ATACGCTGAC TGCCGATGAT TTGATTTATC CGGTGTTCGT ATTGGAGGGG TCGGCGCGC AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG 301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT 351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC 401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG 451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC 501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA 551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG 601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG 651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT 701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAC GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA 951 1001 AGATGCTGAA GCGTTGA

#### This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

a610.pe	ep					
	1 MIGGLMQFPY RN'	JSASRMRR ME	RRDDFSRRL	MREHTLTADD	LIYPVFVLE	3
5	1 SAREEDVPSM PG	VKRQSLDR LI	LFTAEEAVK	LGIPMLALFP	VVTANKTERA	
10	1 QEAYNPEGLV PS	rvralrer fi	ELGIMTDV .	ALDPYTVHGQ	DGLTDENGY	1
15	1 MNDETVEVLV KQ	ALCHAEAG A	QVVAPSDMM	DGRIGAIREA	LEDAGHIHT	₹
20	1 IMAYSAKYAS AF	YGPFRDAV GS	SSGNLGKAD	KKTYQMDPAN	TDEALHEVA	L
25	1 DIQEGADMVM VK	PGLPYLDV VE	RRVKDEFGV	PTYAYQVSGE	YAMLQAAVAI	1
30	1 GWLDGGKVVL ES	LLAFKRAG AI	GILTYYAI	EAAKMLKR*		
m610/a6	310 99.4% ident	city in 338	aa overl	ap		
	10	20	30	40	50	60
m610.pe	p MIGGLMQFPYI	RNVPASRMRRN	IRRDDFSRRL	MREHTLTADDI	LIYPVFVLEGS	SAREEDVPSM
	11111111					
a610	MIGGLMQFPY	RNVSASRMRRN	IRRDDFSRRL	MREHTLTADDI	LIYPVFVLEGS	SAREEDVPSM
	10	20	30	40	50	60
•	70	80	90	100	110	120
m610.pe	p PGVKRQSLDR1	LLFTAEEAVKI	GIPMLALFP	VVTANKTERA(	QEAYNPEGLVI	STVRALRER
	111111111					
a610	PGVKRQSLDRI	LLFTAEEAVKI	GIPMLALFP	VVTANKTERA(	EAYNPEGLVI	STVRALRER
	70	80	90	100	110	120
	130	140	150	160	170	180

m610.pep	FPELGIMTDVALDP	YTVHGQDGL	rdengyvmndi	ETVEVLVKQA	LCHAEAGAQV	VAPSDMM
	4 1 1 4 1 1 1 1 1 1 1 1 1 1					111111
a610	FPELGIMTDVALDP:	YTVHGQDGLT	r dengyvmndi	ETVEVLVKQAI	LCHAEAGAQV	VAPSDMM
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIREALEDAG	SHIHTRIMA:	YSAKYASAFYO	GPFRDAVGSS	GNLGKADKKT	YQMDPAN
	7111111111111	[[]]]	F11111111111	H H H H H H H H H		111111
a610	DGRIGAIREALEDAG	SHIHTRIMAY	YSAKYASAFYO	SPFRDAVGSS	SNLGKADKKT	YQMDPAN
	190	200	210	220	230	240
	250	260	270	280	290	300
m610.pep	TDEALHEVALDIQE	GADMVMVKPO	GLPYLDVVRRV	/KDEFGVPTY/	AYQVSGEYAMI	LQAAIAN
• •	1111111111111			1111111111		1111:11
a610	TDEALHEVALDIQE	GADMVMVKPO	GLPYLDVVRR\	/KDEFGVPTY/	AYQVSGEYAMI	LQAAVAN
	250	260	270	280	290	300
	•	·				
	310	320	330	339		
m610.pep	GWLDGGKVVLESLL	AFKRAGADG1	ILTYYAIEAAH	KMLKRX		
	11111111111111		11111111111	11111		
a610	GWLDGGKVVLESLL#	AFKRAGADGI	ILTYYAIEAA	KMLKRX		
	310	320	330			

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1943>: g611.seq

1		AAAACGGGAT			
51		TTAAGCCTTG			
101	GCGGTGTCTG	CCGGGGCAGG	TGCTTCGGTT	TTTTCCCGAG	TCGGAGCGTG
151	CGGCGCGTTA	TCTTCCGCCG	CGTCCGCATT	Ctcgcgcagg	ttgtGGCtgt
201	tatcctTGGG	CGGGCTGggt	tgtttgcccg	ccataaTTtc	cagtacctgA
251	TcgcgGTCta	tggtttcCCa	ttCcatcagg	gctttgcaca	TCGTTTCCAT
301	cttgTCGCGG	TTTTcatcga	ggaTTTTGTA	ggcaacCTGA	TACTgctcgt
351	ccaaaAtccg	Gcggatttcc	gcgtcgAtgt	cctgctgggt	tTTCTCGGAA
401	ATGTTTTGCG	AACGGgttac	gctGCGCCCC	AAGAAGACTT	CGCCTTCGTT
451		ACCATCACGC			
501	CCATTTCGCG	TGCCATTTGG	GTTGCGCGTT	CAAAGTCGTT	TGA

#### This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>: g611.pep

- 1 MPSENGMGKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
  - 51 RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAVYGFP FHQGFAHRFH
  - 101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRTGY AAPQEDFAFV
  - 151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1945>: m611.seq

1	ATGCCGTCTG	AAAACGGGAT	GGGAAAACGG	CAGCTTGCGG	GCTGCCGTTT
51	GTTCGGGAAG	TTAAGCCTTG	TTTTCAGGCT	GCTGCTCGGA	CTCTGTCGAA
101	GCGGTGTCTG	CCGGGGCAGG	TGCTTCGGTT	TCTTCCCGAG	TCGGAGCGTG
151	CGGCGCGTTA	TCTTCCGCCG	CGTCCGCATT	CTCGCGCAGG	TTGTGGCTGT
201	AATCTTTGGG	CGGGCTGGGT	TGTTTGCCCG	CCATGATTTC	CAGTACCTGA
251	TCGCGGTCGA	TGGTTTCCCA	TTCCATCAGG	GCTTTGCACA	TCGTTTCCAT
301	CTTGTCGCGG	TTTTCATCGA	GGATTTTGTA	GGCAACCTGA	TATTGCTCGT
351	CCAAAATCCG	GCGGATTTCC	GCGTCGATGT	CCTGCTGGGT	TTTCTCGGAA
401	ATGTTTTGCG	AACGGGTTAC	GCTGCGTCCC	AAGAAGACTT	CGCCTTCGTT
451	TTCCGCATAA	ACCATCACGC	CCATTTTGTC	GCTCATGCCG	TAGCGCGTTA
501	CCATTTCCCC	CCCCATTTCC	GTTGCGCGTT	CAAAGTCGTT	TGA

#### This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>: m611.pep

- 1 MPSENGMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
- 51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGFP FHQGFAHRFH
- LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRTGY AASQEDFAFV FRINHHAHFV AHAVARYHFA RHLGCAFKVV * 101

m611/g611 96.1% identity in 180 aa overlap

20 30 40 50 60

m611.pep	MPSENGMGKRQLAG	CRLFGKLSLVI	FRLLLGLCRS	GVCRGRCFGE	'FPSRSVRRVI	FRRVRI
• •			1111 1111:		1111111111	$\Pi\Pi\Pi\Pi$
q611	MPSENGMGKRQLAG(	CRLFGKLSLVI	FRLLPGLCRG	GVCRGRCFGE	'FPSRSVRRVI	
,	10	20	30	40	50	60
					•••	
	70	80	90	100	110	120
m611.pep	LAQVVAVIFGRAGL	FARHDFQYLIA	AVDGFPFHQG	FAHRFHLVAV	'FIEDFVGNLI	LLVQNP
		,		[	111111111	
g611	LAQVVAVILGRAGLI	FARHNFQYLIA	AVYGFPFHQG	FAHRFHLVAV	FIEDFVGNLI	LLVQNP
•	70	80	90	100	110	120
	130	140	150	160	170	180
m611.pep	ADFRVDVLLGFLGN	/LRTGYAASQI	EDFAFVFRIN	HHAHFVAHAV	'ARYHFARHLG	CAFKVV
• •			111111111	[]][]]	111111 111	
g611	ADFRVDVLLGFLGNV	/LRTGYAAPQE	EDFAFVFRIN	HHAHFVAHAV	ARYHFACHLG	CAFKVV
,	130	140	150	160	170	180
m611.pep	X		•			
• •	1					
g611	X					
7						

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1947>:

a611.seq					
1	ATGCCGTCTG	AAAACAGGAT	GGGAAAACGG	CAGCTTGCGG	GCTĢCCGTTT
. 51	GTTCGGGAAG	TTAAGCCTTG	TTTTCAGGCT	GCTGCTCGGA	CTCTGTCGAA
101	GCGGTGTCTG	CCGGGGCAGG	TGCTTCGGTT	TCTTCCCGAG	TCGGAGCGTG
151	CGGCGCGTTA	TCTTCCGCCG	CGTCCGCATT	CTCGCGCAGG	TTGTGGCTGT
201	AATCTTTGGG	CGGGCTGGGT	TGTTTGCCCG	CCATGATTTC	CAGTACCTGA
251	TCGCGGTCGA	TGGTTTCCCA	TTCCATCAGG	GCTTTGCACA	TCGTTTCCAT
301	CTTGTCGCGG	TTTTCATCGA	GGATTTTGTA	GGCAACCTGA	TACTGCTCGT
351	CCAAAATCCG	GCGGATTTCC	GCATCGATGT	CCTGCTGGGT	TTTCTCGGAA
401	ATGTTTTGCG	AACGGGTTAC	GCTGCGTCCC	AAGAAGACTT	CGCCTTCGTT
451	TTCCGCATAA	ACCATCACGC	CCATTTTGTC	GCTCATGCCG	TAGCGCGTTA
501	CCATTTCGCG	CGCCATTTGG	GTTGCGCGTT	CAAAGTCGTT	TGA

#### This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>: a611.pep

130

51	RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYL	IAVDGFP FHQGFAHRFH	
101	LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLG	NVLRTGY AASQEDFAFV	
151	FRINHHAHFV AHAVARYHFA RHLGCAFKVV *		
m611/a611	98.9% identity in 180 aa overlap		
	•		
	10 20 30	40 50	60
m611.pep	MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCR	SGVCRGRCFGFFPSRSVRRV	IFRRVRI
		[11]	111111
a611	MPSENRMGKRQLAGCRLFGKLSLVFRLLLGLCR	SGVCRGRCFGFFPSRSVRRV	IFRRVRI
	10 20 30	40 50	60
	•		
	70 80 90	100 110	120
m611.pep	LAQVVAVIFGRAGLFARHDFQYLIAVDGFPFHQ	GFAHRFHLVAVFIEDFVGNL	ILLVQNP
• •		11111111111111	1111111
a611	LAOVVAVIFGRAGLFARHDFQYLIAVDGFPFHQ	GFAHRFHLVAVFIEDFVGNL	ILLVQNP
	70 80 90	100 110	120
	130 140 150	160 170	180
m611.pep	ADFRVDVLLGFLGNVLRTGYAASQEDFAFVFRI	NHHAHFVAHAVARYHFARHL	GCAFKVV
		11111111111111111111	1111111
a611	ADFRIDVLLGFLGNVLRTGYAASQEDFAFVFRI	NHHAHEVAHAVARYHEARHL	GCAFKVV

140

150

160

170

180

1 MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV

m611.pep Х

a611 Х

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1949>: g612.seq

- ATGGgcttcg gcggcaatat tgcAAAAAAG CTGGCcggGg taGATGAAAT 1 AGCCTttgac tttgacggcA TCGTCTTTGA TTTCGGGCGT GATGATGCTG 51 101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
- 151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
- 201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC 251 CAAATTTGGC GGTGCAGTTG GGCGCGTTGT TGCATTTCGG TCATCATCGA
- 301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
- 351 ATTTTTTAC GGGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>: g612.pep

- MGFGGNIAKK LAGVDEIAFD FDGIVFDFGR DDAVRHSGVI NAAVAGLHIV 1
- GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR 51
- 101 NPYIKLNKSK SPDIFRRFFY GHSN*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1951>:

- ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT 1
- AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG 51 101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
- 151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
- 201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
- 251 CAAATTTGGC GGTGCAGTTG GGCGCGTTGT TGCATTTCGG TCATCATCGA
- 301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
- 351 ATTTTTTAC GGGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>: m612.pep

- MGFGGNIAKK LAGVDEIAFN FDGIVFDFGR DDAVRHSGVI NTAVACLHIV 1
- GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR 51
- 101 NPYXKLNKSK SPDIFRRFFY GHSN*

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAG	VDEIAFNFDGI	VFDFGRDDAV	/RHSGVINTAV	ACLHIVGEV	ADKAVE
	111111111111111111111111111111111111111	11111111111	11111111111	11111111111111	1 11111111	$\square$
g612	MGFGGNIAKKLAG	VDEIAFDFDGI	VFDFGRDDAV	/RHSGVINAAV	AGLHIVGEV	ADKAVE
9	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVPAI	HRAAYFVGNFP	NLAVQLGALI	LHFGHHRNPYX	KLNKSKSPD	FRRFFY
	1111111111111111	11:111111:11	1111111111	11111111	111111111	нин
g612	KCAENVLFKVPAI	HRAAYFVGDFP	NLAVQLGALI	LHFGHHRNPYI	KLNKSKSPD:	FRRFFY
,	70	80	90	100	110	120

**GHSNX** m612.pep  $\Pi\Pi\Pi$ q612 **GHSNX** 

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1953>:

a612.seq

- ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT 1
- 51 AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
- 101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
- 151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
- 201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
- 251 CAAATTTGGC GGTGCAGTTG GGCGCGTTGT TGTATTTCGG TCATCATCGA 301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
- 351 ATTTTTT.AC GGGCATTCAA ATTAA

```
This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:
     a612.pep
               MGFGGNIAKK LAGVDEIAFD FDGIVFDFGR DDAVRHSGVI NTAVACLHIV
            1.
               GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
           51
          101 NPYXKLNKSK SPDIFRRFFX GHSN*
```

```
96.0% identity in 124 aa overlap
m612/a612
```

		10	20	30	40	50	60
1	m612.pep	MGFGGNIAKKLAG	VDEIAFNFDGI'	VFDFGRDDAV	JRHSGVINTAV	ACLHIVGEV	TADKAVE
			1111:1111			1111111:11	11111
ě	a612	MGFGGNIAKKLAG'	VDEIAFDFDGI	VFDFGRDDAV	/RHSGVINTAV	ACLHIVGKVI	ADKAVE
		10	20	30	40	50	60
		70	80	90	100	110	120
ľ	n612.pep	KCAENVLFKVPAI	HRAAYFVGNFPI	NLAVQLGALI	LHFGHHRNPYXI	KLNKSKSPDI	FRRFFY
		11111111:111			1:1111111		1111
ä	a612	KCAENVLFEVPAI	HRAAYFVGNFPI	NLAVQLGALI	LYFGHHRNPYXI	KLNKSKSPDI	FRRFFX
		70	80	90	100	110	120

m612.pep **GHSNX** HHHGHSNX a612

#### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1955>:

```
q613.seq
         ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
      1
         GCGCAGTCTG CTTATTTCGT CGaggcagtc ggcaagggct tcgttgccgg
     51
         tgtttGcgGA CTCGGGTTCG CGGGAAAATC CGCCGATTTG TTCGGCGATG
    151 TTCCTGCCGA TTTgtttGAt GCCGTGTCCG ATGTCGGTGG CACGgctgcc
    201 gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
    251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
    301 CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCTT GGAGGATTTT
    351 CCGTATCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
    401 CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
    451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
        GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
         ACATATTTTC TGATTGGGGC GGAGAATGCC TGTTGTTGCT GTTGCCGCTT
```

#### This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

- MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS 101 PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP 151 AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
- 201 ILQA*

601 ATTTTACAGG CTTAA

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1957>:

m613.seq ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC 1 GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA 51 101 TGTTTGCGGA CTCGGATTCG CGGGAAAATC CGCCGATTTG TTCGGCGATG 151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC 201 GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG 251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG 301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT 351 CTGTACCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC 401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG 451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG 551 ACATATTTC TGATCGGGGC GGAGAATGCC TGTTGTTGCT GTTGCCGCTT

#### 601 ATTTTACAGG CTTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

m613.pep

- 1 MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
- 51 FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
- 101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFSP
- 151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
- 201 ILQA*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae* 

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRR	STPSRSLLISS	RQSARASLPM	1FADSDSRENP	PICSAMFLP	CLMPCP
					1111111111	
g613	MSRSSLSRRSLRR	STPSRSLLISS	RQSARASLPV	FADSGSRENP	PICSAMFLPI	CLMPCP
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPI	KIRANSSDARE	RRLPSRDSTA	MPRMRSPSSP	MSPAPGSPPV	RIFCTA
			111111111	11111111	111111111	111 1
g613	MSVARLPMPACVPI	KIRANSSDARE	RRLPSRDSTA	MPRMRSPSSL	MSPAPGSPPW	RIFRIA
	70	80	90	100	110	120

	·
m613.pep g613	130 140 150 160 170 180 LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAKAASSERLSGLCRIRRLMMG
m613.pep g613	190 200 RRADIFSDRGGECLLLLPLILQAX
The following p	artial DNA sequence was identified in N. meningitidis <seq 1959="" id="">:</seq>
a613.seq	7
1 51 101 151 201 251 301 351 401 451 501 551	ATGTCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA TGTTTGCGGA CTCGGGTTCG CGGGAAAATC TGCCGATTTG TTCGGCGATG TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCGCCTT GGAGGATTTT CTGTACCGCG CTGTTGCGGA AGGTGATTTC GGTGTCTGCA AAGCCGTTTC CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAACCCG GCAATGTTCA GGGTCAGTGT TTTGCCTGCG AAGGCGGCAA GTTCCGAGCG GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG ACATATTTC TGATCGGGGC GGAGAATGCC TGTTGTTGCT GTTGACGCTT ATTTTACAGG CTTAA  S to the amino acid sequence <seq 1960;="" 613.a="" id="" orf="">:  MSRSSRSRS LRRSTPSRSL LISSRQSARA SLPMFADSGS RENLPICSAM FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS</seq>
101 151 201 m613/a613	PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFPAESKPS SVMRPASFNP AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLTL ILQA*  98.0% identity in 204 aa overlap
m613.pep a613	10 20 30 40 50 60 MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP
m613.pep	70 80 90 100 110 120 MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA
m613.pep a613	130 140 150 160 170 180 LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPAKAASSERLSGLCRIRRLMMG
m613.pep a613	190 200 RRADIFSDRGGECLLLLPLILQAX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1961>:

```
g614.seq
               AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acgggcaaat
            1
               CGAATATTCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
           51
          101
               TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
               ACCGACAAAA GCACCTTCTT CACCAACGCG CCCTTGGATG ACAACCTGAT
               TCAAACCCTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
          201
          251 AACCGAGCGC GCTGACTGCC CTGTTTTACA GCCTGCTGCC CGTCCTGCTG
              CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCG
          301
          351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
          401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
          451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCGCta
               tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCCtgCtg gcgGgcagcc
          501
               CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
          551
               GTGCCGTTCT TCAGCATTTC CGGTTCCGAT TTTGTCGAAA TGTTCGTCGG
               TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
               CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
          701
               GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
          751
               ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
          801
               TTGCGGCAAC CAACCGCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
          851
          901 GGCCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGGACA TCCGGGGGCG
               CGAACAGatn ttGAACGTCC ATTCtaaAAA AGTGCcttTG gacgaATCTg
              tggaTTTATT GTCCCTCGCG CGCGGCACGC ccggtttTTc cggcgcggat
         1051 tTggcgaaac tggtcaacga agccccctg tttgccggcc gccgcaacaa
               agtgaaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT
         1101
               GGGTCCGGAA CGCCGCAGTA TGGTGA
This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:
     g614.pep
               MAAFNALDGK KEDNGOIEYS OFIROVNNGE VSGVNIEGSV VSGYLIKGER
           51
               TDKSTFFTNA PLDDNLIQTL LNKNVRVKVT PEEKPSALTA LFYSLLPVLL
          101
               LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
               KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
          201 VPFFSISGSD FVEMFVGVGA SRVRDMFEQA KKNAPCIIFI DEIDAVGROR
          251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
              GRFDRQVVVP LPDIRGREQX LNVHSKKVPL DESVDLLSLA RGTPGFSGAD
               LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1963>:
     m614.seq
               ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
           51
              CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
              TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
          151 ACCGACAAAA GCACTTTCTT CACCAACGCG CCTTTGGACG ACAACCTAAT
          201 TAAAACACTG CTCGACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
          251 AACCGAGCGC GCTGGCTGCC CTGTTTTACA GCCTGCTGCC CGTCCTGCTG
          301 CTGATTGGCG CATGGTTCTA CTTCATGCGT ATGCAGACGG GCGGCGGCGG
          351
              AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA
              AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
```

```
451
     AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
     TCAAAGCCTG GGCGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
 501
     CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
 551
     GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTCGAAA TGTTCGTCGG
 601
     TGTCGGTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAACG
 651
     CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
701
751
     GGCGCAGGTT TGGGCGGCGG CAATGATGAG CGCGAGCAAA CATTAAACCA
     ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
     TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
     GGCCGTTTCG ACCGCCAAGT GGTTGTCCCC CTGCCGGACA TCCGAGGGCG
     CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
     TGGATTTATT GTCCCTCGCG CGCGCACGC CGGGTTTTTC CGGCGCGGAT
1001
     TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1051
1101
     AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
     GGGTCCGGAA CGCCGCAGTA TGGTGA
```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

m614.pep					
1	MAAFNALDGK	KEDNGQIEYS	QFIQQVNNGE	VSGVNIEGSV	VSGYLIKGER
51	TDKSTFFTNA	PLDDNLIKTL	LDKNVRVKVT	PEEKPSALAA	LFYSLLPVLL
101	LIGAWFYFMR	MQTGGGGKGG	AFSFGKSRAR	LLDKDANKVT	FADVAGCDEA
151	KEEVQEIVDY	LKAPNRYQSL	GGRVPRGILL	AGSPGTGKTL	LAKAIAGEAG
201	VPFFSISGSD	FVEMFVGVGA	SRVRDMFEQA	KKNAPCIIFI	DEIDAVGRQR
251	GAGLGGGNDE	REQTLNQLLV	EMDGFESNQT	VIVIAATNRP	DVLDPALQRP
301	GRFDRQVVVP	LPDIRGREQI	LNVHSKKVPL	DESVDLLSLA	RGTPGFSGAD
351	LANLVNEAAL	FAGRRNKVKV	DOSDLKTPKT	KSIWVRNAAV	W*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae* 

m614/g614 98.0% identity in 391 aa overlap

	4.0	· .				
C1 A a	10	20	30	40	50	60
m614.pep	MAAFNALDGKKEDN					
g614	MAAFNALDGKKEDN					
9014	10	20	30	40	50	60
					30	00
	70	80	90	100	110	120
m614.pep	PLDDNLIKTLLDKN					
			11111:1111	1111111111	11111111:	
g614	PLDDNLIQTLLNKN				WFYFMRMQA	GGGGKGG
	70	80	90	100	110	120
	120	1.40	150	1.60	170	
m614 non	130 AFSFGKSRARLLDK	140	150	160	170	180
m614.pep						
g614	AFSFGKSRARLLDK	በልክጵኒኒሞቴልክኒ	//	TITITITITE	IIIIIIIIIII	I I I I I I I I I I I I I I I I I I I
9014	130	140	150	160	170	180
	200	1.0	130	100	270	100
	190	200	210	220	230	240
m614.pep	AGSPGTGKTLLAKA	IAGEAGVPFI	FSISGSDFVEM	IFVGVGASRVR	DMFEOAKKNA	
• •	1111111111111111					
g614	AGSPGTGKTLLAKA	IAGEAGVPF	FSISGSDFVEM	FVGVGASRVR	DMFEQAKKNA	APCIIFI
	190	200	210	220	230	240
	250	260	270	280	290	300
m614.pep	DEIDAVGRQRGAGL					
~614						
g614	DEIDAVGRQRGAGL	260	270	280	AATNRPDVLL 290	
	250	200	270	280	290	300
	310	320	330	340	350	360
m614.pep	GRFDRQVVVPLPDI					
q614	GRFDRQVVVPLPDI					
-	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSD					
		<b></b>				
g614	FAGRRNKVKVDQSD					
	370	380	390			

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1965>: a614.seq

		-			•	
4.seq		•				
1	ATGGCTGCGT	TCAACGCTTT	AGACGGTAAA	AAAGAAGACA	ACGGGCAAAT	•
51	CGAATATTCT	CAGTTCATCC	AACAGGTCAA	CAACGGCGAA	GTATCCGGCG	•
101	TCAACATCGA	AGGATCCGTC	GTCAGCGGCT	ACCTGATTAA	GGGCGAGCGC	
151	ACCGACAAAA	GCACCTTCTT	CACCAACGCG	CCTTTGGACG	ACAACCTGAT	
201	TAAAACACTG	CTCGACAAAA	ACGTCCGTGT	AAAAGTAACG	CCGGAAGAAA	
251	AACCGAGCGC	GCTGGCTGCC	CTGTTTTACA	GCCTGCTGCC	CGTCCTGCTG	

301 351 401 451 501 551 601 651 701 751 801 851 901 951 1001 1051 1101	CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGGG AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCGC CTACTGGACA AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA TCAAAGCCTG GGCGGCGCG TGCCGCGGG CATCCTGCTG GCGGCAGCC CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTCGAAA TGTTCGTCGG TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAAACCA ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC GGCCGTTTCG ACCGCCAAGT GGTTGTCCCC CTGCCGGACA TCCGGGGGCG CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT GGGTCCGGAA CGCCCGAGTA TGGTGA
This seems and	to the emine and accuracy SEO ID 1000, ODE (14 )
•	s to the amino acid sequence <seq 1966;="" 614.a="" id="" orf="">:</seq>
a614.pep 1	MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
51	TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101	LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151	KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201	VPFFSISGSD FVEMFVGVGA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 301	GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP GRFDRQVVVP LPDIRGREQI LNVHSKKVPL DKSVDLLSLA RGTPGFSGAD
351	LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*
m614/a614	99.7% identity in 391 aa overlap
	10 20 30 40 50 60
m614.pep	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA
a614	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKGERTDKSTFFTNA 10 20 30 40 50 60
	70 80 90 100 110 120
m614.pep	PLDDNLIKTLLDKNVRVKVTPEEKPSALAALFYSLLPVLLLIGAWFYFMRMQTGGGGKGG
1 1	
a614	PLDDNLIKTLLDKNVRVKVTPEEKPSALAALFYSLLPVLLLIGAWFYFMRMQTGGGGKGG
	70 80 90 100 110 120
	130 140 150 160 170 180
m614.pep	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL
a614	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL
	130 140 150 160 170 180
	190 200 210 220 230 240
m614.pep	AGSPGTGKTLLAKAIAGEAGVPFFSISGSDFVEMFVGVGASRVRDMFEQAKKNAPCIIFI
a614	AGSPGTGKTLLAKAIAGEAGVPFFSISGSDFVEMFVGVGASRVRDMFEQAKKNAPCIIFI
	190 200 210 220 230 240
	250 260 270 280 290 300
m614.pep	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTVIVIAATNRPDVLDPALQRP
a614	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTVIVIAATNRPDVLDPALQRP 250 260 270 280 290 300
	250 260 270 280 290 300
	310 320 330 340 350 360
m614.pep	GRFDRQVVVPLPDIRGREQILNVHSKKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL
a614	CD EDDOUGHED DO DO DE COLL NUMBER MADE DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA DE CADA
a VI4	GRFDRQVVVPLPDIRGREQILNVHSKKVPLDKSVDLLSLARGTPGFSGADLANLVNEAAL

985

```
340
                                                   350
                                                           360
                 310
                         320
                                  330
                         380
                                  390
                 370
           FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX
m614.pep
           FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX
a614
                         380
                                  390
                 370
```

#### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1967>:

```
q615.seq
          ATGTGGAAAC GGCGGCGCG CGGTGtcqqC AGCTTtgaag agcaqcGaAT
       1
          agatgCCGCC GGCAAACCAC AATGCGGAAa gcaggCtgaa gcGGTTgcgC
     51
          GGCagcTTca tGCCGCCTCC TcGTCCaGCC ACGtttGgca gattttggac
          aggcgcAGga ATTTGCcgCc gcgtgcggCA agtatgtcgc gcCAttgtgc
     151
         cacttetteg geggaeggTG cttcgtcgaT getgCATTCG TACageagga
    201
          aatcqaqqqt ttcttcqatg acqqGqatqq AttccqTTTG GataAqCTqc
    251
          ttgagttcgt tcatgactGt TCgGATAcgg aaatcgggaa aatgccgtct
    301
          qAaaqqqctt CAGACGGCat tggATTATTT GCTGTGCAGG AAgcgcgttg
     351
         cctcttccca tttgcCGGAA AtgATGTCGg gtacggcctg cAGGGATttg
         gCGACGGcat cgtcgatttg ccgGcggtgc ttCcgcgctc ggtttGTTca
     451
         agacgtagcc gaCGACGagg ttgcggtcGC CGGGGtggcC GATGCCGAGG
     501
    551
         CGCAGGCGGt aatagtctgC CGTGCCGAGT TTTGCctgAA TGTCTTTCAA
     601
         GCCGTTGTGT CcqcCGttqc cqcCGCCGAG TTTGAATTTq ATCCGTCCGC
         AAGGGATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
     651
         TTGTAGAACT GTGCAAGCGC GGCAACCGCC TGTCCGGAAC GGTTCATGAA
     701
         CGTGGCCGGT TTGAGCAGCC AAACATCGCC GTCGGGCAGG GCGGCGCGGG
     751
         CAACTTCGCC GAAGAATTTT TTTTCTTCTT TAAACGAAGC CTTCCATTTC
         CACGCCAGTT CGTCGAGGAA CCAAAAGCCC GCATTGTGGC GGGTCTGTTC
    851
         GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGttcg
    901
         acatqataTT TtccgtgTTT CTgTCGaatg cggtCtgaAG GCTTCAGacg
    951
         qcatggTtaT TCTTCTTgaT TTtgaACgcg tgtgcggCGC GCTTCTTTGG
    1001
         GGTCGATCAA CAGCGGGCGG TACACTTCGA TGCGGTCGCC GTCGCGCAGC
   1051
         GGCGTGTCGT CTTTGA
   1101
```

### This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```
q615.pep
         MWKRRRGVG SFEEQRIDAA GKPOCGKQAE AVARQLHAAS SSSHVWQILD
         RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
      51
         LSSFMTVRIR KSGKCRLKGL QTALDYLLCR KRVASSHLPE MMSGTACRDL
    101
    151 ATASSICRRC FRARFVQDVA DDEVAVAGVA DAEAQAVIVC RAEFCLNVFQ
    201 AVVSAVAAAE FEFDPSARDV EFVVDDEDFF GFDFVELCKR GNRLSGTVHE
         RGRFEOPNIA VGQGGAGNFA EEFFFFFKRS LPFPRQFVEE PKARIVAGLF
          VFFARVAOAD NHFDCVRHDI FRVSVECGLK ASDGMVILLD FERVCGALLW
         GRSTAGGTLR CGRRRAAACR L*
    351
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1969>:

```
Length: 1116
m615.seq
          ATGCGGAAAA GGCGGTGGCG CGGTTTCGGC AGCTTTGAAA AGCAGTGAGT
         AAATGCTGCC TGCAAACCAC AATGCCGAGA GCAGGATAAA GCGGTTGCGT
         GGCAGATTCA TGCTTGTTCC TCTTCAAGCC ATGTCTGGCA TAGTTTGGAT
         AGGCGCAGGA ATTTTCCGCC GCGTGCGGCC AGCATATCGC GCCAAACGGC
     151
         AATTTCTTCG GCGGAGGGGG CATCGTCTAT GCTGCATTCG TAGAGCAGGA
     201
         AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
     251
         TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
     301
          GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
     351
         CTTCTTCCCA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG
     451 GCGACGGCAT CGTCAATCTG TCGGCGGTGT .TCCGTACTG GGTTTGTTCA
     501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
     551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
     601 GCCGTTGTGT CCGCCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC
     651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
     701 TTGTAGAACT GTGCAAGCGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
         CGTGGCAGGT TTGAGCAGCC AAACGTCGCC GTCGGGCAGG GCGGCACGGG
```

801	CGACTTCGCC	GAAGAATTTT	TTTTCTTCTT	TAAATGAAGC	CTTCCATTTC
851	CACGCCAGTT	CGTCGAGGAA	CCAAAAACCC	GCATTGTGGC	GTGTCTGTTC
901	GTATTCTTTG	CCCGGGTTGC	CCAAGCCGAC	AACCATTTTG	ATTGTGTTTG
951	ACATGATATT	TTCCGTGTTT	CTGTCGAATG	CTGTCTGAAG	GCTTCAGACG
1001	GCATGGTTAT	TCTTCTTGAT	TTTGAACGCG	TTTGCGGCGC	GCTTCTTTGG
1051	GGTCGATCAA	CAGCGGGCGG	TACACTTCGA	TGCGGTCGCC	GTCGCGCAGC
1101	GGCGTGTCGT	CTTTGA			

#### This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

m615.pep Length: 372

1 MRKRRWRGFG SFEKQXVNAA CKPQCREQDK AVAWQIHACS SSSHVWHSLD
51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDPSAGNV EFVVDDEDFF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTGDFA EEFFFFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHDI FRVSVECCLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

# Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

#### m615/g615 86.8% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFE	QXVNAACKP	QCREQDKAVAV	*QIHACSSSSH	IVWHSLDRRR	NFPPRAA
		1::11 11	11:1:11	1:11 11111	11: 11111	1:11111
g615	MWKRRRRGVGSFEE	QRIDAAGKP	QCGKQAEAVAF	RQLHAASSSSH		NLPPRAA
	10	20	30	40	50	60
	70	. 80	90	100	110	120
m615.pep	SISRQTAISSAEGA	SSMLHSXSR	KSRVSSMTGME	SVWISCLSSV	MTVRIWKSG'	TCRLKGL
	1:11:   111:11	11111111	[[]]		11111 111	111111
g615	SMSRHCATSSADGA	SSMLHSYSRI	KSRVSSMTGME	SVWISCLSSF	MTVRIRKSG	KCRLKGI.
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVA	SSHLPARMS	SMACRDLATAS	SICRRCXRTG	FVODIADDE	VAVARVA
	- 111 : 1111111					
g615	QTALDYLLCRKRVA	SSHLPEMMS	STACRDLATAS	SICRRCFRAR	FVODVADDES	JAVAGVA
_	130	140	150	160	170	180
						100
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEF	CLNVFQAVVS	SAVAAAEFEFD	PSAGNVEFVV		TVELCKR
		$\mathbf{H} = \mathbf{H} \cdot \mathbf{H}$		111:1111	11111111	
g615	DAEAQAVIVCRAEF	CLNVFOAVVS	SAVAAAEFEFD	PSARDVEFVV	DDEDEEGEDI	יייוווון מאדוריצס
•	190	200	210	220	230	240
				220	230	240
	250	260	270	280	290	300
m615.pep	GNCLSGTVHERGRF	EOPNVAVGO				TVACIE
	11 11111111111					TANCHE
g615	GNRLSGTVHERGRF	EOPNIAVGOG	GAGNFAEEFF	FFFKRSLPFP	ROFVEEPKAF	TVACTE
-	250	260	270	280	290	300
					230	300
	310	320	330	340	350	360
m615.pep	VFFARVAQADNHFD					
				1111111111	CADMILLIE	ALLILLI LILLI
g615	VFFARVAQADNHFD	CVRHDTFRVS	VECGLKASDG	MVTI.I.DEERV	TCD T T WCD 9 m	וווווו
,	310	320	330	340	350	360
			350	310	330	200
	370					
m615.pep	CGRRRAAACRLX					
• •						
g615	CGRRRAAACRLX					
<b>J</b> - = -	370					
	5.0					

120

120

180

180

240

240

300

987

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1971>:
```

a615.seq ATGCGGAAAC GGCGGCGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT 51 AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC 101 AGGCGCAGGA ATTTGCCGCC GCGTGCGGCA AGTATGTCGC GCCATTGTGC 151 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTCG TACAGCAGGA 201 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC 251 301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT 351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG 401 GCGACGCAT CGTCAATCTG TCGGCGGTG. TTCCGTACTG GGTTTGTTCA 451 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG 501 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA 551 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC 601 651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT 701 TTATAAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG 751 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC 801 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC 851 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG 901 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG 951 1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG GGTCGATCAA CAGCGGGCGG TACACTTCGA TGCGGTCGCC GTCGCGCAGC 1051 GGCGTGTCGT CTTTGA This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>: a615.pep MRKRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC 51 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL 101 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ 151 AVVSTVAAAE FEFDPSAGNV EFVVDDEDFF GFDFIKLRKG GNCLSGTVHE 201 RGRLEOPDIA VGQGSTGDFA EEFFFFFK*S LPFPRQFVEE PKTRIVACLF 251 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW GRSTAGGTLR CGRRRAAACR L* 351 90.3% identity in 371 aa overlap m615/a615 30 MRKRRWRGFGSFEKOXVNAACKPOCREODKAVAWOIHACSSSSHVWHSLDRRRNFPPRAA m615.pep 41141 11 1111:1 :: 11 1111 :: 1111 1: 11 11111: 11111: 11111: 11111: MRKRRRGVGSFEEQRIDAAGKPQCGKQAEAVARQLHAASSSSHVWQILDRRRNLPPRAA a615 10 20 30 40 50 90 70 80 100 110 SISROTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL m615.pep a615 SMSRHCATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL 70 80 90 100 110 130 140 150 160 170 QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA m615.pep 

QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXFRTGFVQDIADDEVAVARVA

DAEAOAVIVCRAEFCLNVFOAVVSAVAAAEFEFDPSAGNVEFVVDDEDFFGFDFVELCKR

DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPSAGNVEFVVDDEDFFGFDFIKLRKG

160

220

220

280

170

230

230

290

150

210

210

270

a615

a615

m615.pep

130

190

190

250

140

200

200

260

PCT/US99/09346 WO 99/57280

```
988
```

```
m615.pep
          GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEEFFFFFKXSLPFPRQFVEEPKTRIVACLF
          GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEEFFFFFKXSLPFPRQFVEEPKTRIVACLF
a615
               250
                       260
                              270
                                     280
               310
                       320
                              330
                                      340
                                             350
         VFFARVAQADNHFDCVXHDIFRVSVECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
m615.pep
          VFFARVAQADNHFDCVXHDIFRVSAECRLKASDGMVILLDFERVCGALLWGRSTAGGTLR
a615
                      320
                              330
                                     340
               370
         CGRRRAAACRLX
m615.pep
         CGRRRAAACRLX
a615
               370
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1973>: g616.seq

```
atgtcgaaCA CAATCAAAAT GGTTGTCGGC TTGGGCAACC CGGGCAAAGA
  51 ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
 101 CGTGGAAATG GAAGGCTTCG TTTAAAGAAG AAAAAAAATT CTTCGGCGAA
 151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
 201 CACGTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
 251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
      CCTTGCGGAC GGATCAAATT CAAACTCGGC GgcggcaaCG gcgGACACAA
 351 CGGCTTGAAA GACATTcagG CAAAACTCGG CACGGcagac tattaCCGCC
 401 TGCGCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
     gtcttgAACa aaccgagcgc gGaagcaccg Ccggcaaatc gacgatgCCG
 451
 501 TCGccaaATC CCTgcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
 551 gaggcaacgc gcTTCCTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
 601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
 651 tcaagcAGGT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCAccgt ccgccgaaga
 751 agtggcacaa TGgcgcgaca tactTGccgc acgcgGcgGC AAATtcCTgc
     gcctgtccaa aatctgcCaa aCGTGGCtGG ACgAGGAGGC GGCatgAAgc
 801
      tGCCGcgcAA CCgcttcaGc ctgctTTCCG CATTGTGGTT TGCCGGCGGc
 901 atctATtCqc tqctcttcaA AGCTGccqaC ACCGCGCCGC CGCCGTTTCC
 951
     ACATTtcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
      tTctGGCCAA AGCATTCAAA ACCGGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGCCCG
1201 gactaa
```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>: g616.pep

```
MSNTIKMVVG LGNPGKEYEO TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
 51 VARAALPDGD VWLLKPATFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101
    PCGRIKFKLG GGNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSAEAP PANRRCRRQI PAGRTRHHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSRFPY PNSHERTQAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPRNRFS LLSALWFAGG
     IYSLLFKAAD TAPPPFPHFD KAAHLALFFA QILFLAKAFK TGKLPIPYRS
    LIAFAFCFAV GSECAQAWFT ATRTGSLGDV LADLTGAALA LFAARSACRP
351
401 D*
```

The following partial DNA sequence was identified in N. meningitidis <SEO ID 1975>: m616.seq

```
ATGTCAAACA CAATCAAAAT GGTTGTCGGC TTGGGCAACC CGGGCAAAGA
 1
    ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTTAAAGAAG AAAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CCGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTCATG AACCGTTCCG GACAGGCAGT TGCCGCGCTT GCACAGTTCT
    ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GGCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAAACTCGG CACGGCAGAC TATTACCGCC
    TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
401
451 GTCCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA
```

```
551
         GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
         TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
    601
         TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
        GATTTCCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
    701
    751
        AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGGCGGA AAATTCCTGC
        GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
        TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
    851
    901
        ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
        GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
    951
        TTCTGACCAA AGCATTCAGA ACCGACAACC GCCCCATCCC CTATCGCAGC
    1001
         CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
        ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
    1101
         TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
    1201
        GACTAA
This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:
m616.pep
         MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
         VARAALPDGD VWLLKPATFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
     51
        PCGRIKFKLG GGNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
    101
        VLNKPSTEXP PTDXRCRRQI PASHTRHPCR QMGRSNPLPA QQMTRCRLKP
        FOTACSRFPY PNSHDRTQAA YPNRIHPRHR RNPRFPALRM QHRRCPLRRR
        NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
    251
        IYSLLFKAAE TAPPPFPHFD KVAHLALFFA QIWLLTKAFR TDNRPIPYRS
        LMVFALCFAL FSECAQAWFT ATRTGSLGDV LADLTGAALA LFTARAACRP
    351
    401
m616/g616 86.0% identity in 401 aa overlap
                           20
                                    30
                                             40
                                                      50
                                                               60
           MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep
           q616
           MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
                           20
                                             40
                  10
                                    30
                  70
                           80
                                    90
                                            100
                                                     110
                                                              120
           VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK
m616.pep
           g616
           VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNGLK
                  70
                                    90
                                            100
                                                     110
                          140
                                   150
                                            160
                                                     170
           DIQAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSTEXPPTDXRCRRQIPASHTRHPCR
m616.pep
           DIOAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSAEAPPANRRCRRQIPAGRTRHHFR
a616
                  130
                          140
                                   150
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                                                              180
                 190
                          200
                                   210
                                            220
                                                     230
                                                              240
           {\tt QMGRSNPLPAQQMTRCRLKPFQTACSRFPYPNSHDRTQAAYPNRIHPRHRRNPRFPALRM}
m616.pep
           QMGRGNALPAQQIIQCRLKPFQTAFSRFPYPNSHERTQAAYPNGIHPRHRRNPRFPAVRM
q616
                          200
                 190
                                   210
                                            220
                                                     230
                                                     290
                 250
                          260
                                   270
                                            280
                                                              300
m616.pep
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                QHRRSTVRRRSGTMARHTCRTRRQIPAPVQNLPNVAGRGGGMKLPRNRFSLLSALWFAGG
q616
                                   270
                 250
                          260
                                                     290
                 310
                          320
                                   330
                                            340
           IYSLLFKAAETAPPPFPHFDKVAHLALFFAQIWLLTKAFRTDNRPIPYRSLMVFALCFAL
m616.pep
           g616
           IYSLLFKAADTAPPPFPHFDKAAHLALFFAQILFLAKAFKTGKLPIPYRSLIAFAFCFAV
                 310
                          320
                                   330
                                            340
                                                     350
                                                              360
                 370
                          380
                                   390
                                            400
m616.pep
           FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX
            q616
           GSECAQAWFTATRTGSLGDVLADLTGAALALFAARSACRPDX
                          380
                                   390
                                            400
                 370
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1977>:

This

a616.seq	
1	ATGTCAAACA CAATCAAAAT GGTTGTCGGC TTGGGCAACC CGGGCAAAGA
51	ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101	CCTCCADATC CARCCOMCA MUNICIPALITY TO GALGAACTGG
151	GTCGCCCGTG CTACCCTGCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201	CACGTTCATG AACCGTTCCG GACAGGCAGT TGCCGCCCTT GCGCAGTTTT
251	ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301	COMMON ACCORDANT ACCORDANT ACCORDANT ACCORDANT ACCORDANT
	CCCTGCGGAC GGATCAAATT CAAACTCGGC GGCGGCAACG GTGGACACAA
351	CGGCTTGAAA GACATTCAGG CAAAACTCGG CACGGCAGAC TATTACCGCC
401	TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451	GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
	GGAA. CACCG CCGACAGATT GACGATGCCG
501	TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551	GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601	TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651	TCAACCACT TATCCAAACC CAATCATTACATCATCATCATCATCATCATCATCATCATC
	TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701	GATTTCCTGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751	AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGGCGGC AAATTCCTGC
801	GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
	GCCTGCAA ACGTGCTGG ACGAGGAGGC GGCATGAAGC
851	TGCCGCGCAA CCGCTTCAGC CTGCTTTCCG CATTGTGGTT TGCCGGCGGC
901	ATCTATTCGC TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951	GCATTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
	TEMPORE ANALYSIS ACCIDENCE GITTICGCA CAAATCTGGC
1001	TTTTGACCAA AGCATTCAAA ACCGGAAAAC TTCCCATCCC CTACCGCAGC
1051	CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101	ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
	MCCGACCARO COMMONOGA COGGAGIII GGGCGAIGII CIIGCCGATA
1151	TGGCAGGTAC GGTTCTCGCA CTCTTTGCCG CCCGCGCCGC CGACCGCCCG
1201	GACTGA
aamaanand	a to the emine eaid converse CECO ID 1070 ODD (1)
correspond	s to the amino acid sequence <seq 1978;="" 616.a="" id="" orf="">:</seq>
a616.pep	
	MONETUMBUC LONDOVENEO EDINACIONE
1	MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51	VARATLPDGD VWLLKPTTFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101	PCGRIKFKLG GGNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151	VI NUMBER D. DEDAR DOT DE CHEROLOGI POLITICA DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDRES DE L'ANDR
	VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QQMTRCRLKP
201	FQTACSRFPY PNSHDRTQAA YPNRIHPRHR RNPRFPAVRM QHRRRTIRRR
251	SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPRNRFS LLSALWFAGG
301	TVCII EVAAD TADDDEDUED MANUALDE ONDERNING BESALWFAGG
	IYSLLFKAAD TAPPPFPHFD KAAHLALFFA QIWLLTKAFK TGKLPIPYRS
351	LMVFALCFAL FSECAQA*FT ATRTGSLGDV LADMAGTVLA LFAARAADRP
401	
	D*
	D*
m616/a616	
m616/a616	90.0% identity in 401 aa overlap
m616/a616	90.0% identity in 401 aa overlap
m616/a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60
	90.0% identity in 401 aa overlap  10 20 30 40 50 60
m616/a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60 MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10
m616.pep	90.0% identity in 401 aa overlap  10
m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10
m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10
m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep a616 m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep a616  m616.pep a616  m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
m616.pep a616 m616.pep a616 m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
m616.pep a616  m616.pep a616  m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
m616.pep a616  m616.pep a616  m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
m616.pep a616  m616.pep a616  m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
m616.pep a616  m616.pep a616  m616.pep a616	90.0% identity in 401 aa overlap  10 20 30 40 50 60  MSNTIKMVVGLGNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!

```
QHRRCPLRRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS
m616.pep
          a616
         QHRRRTIRRRSGTMARHTCRTRRQIPAPVQNLPNVAGRGGGMKLPRNRFSLLSALWFAGG
               250
                       260
                              270
                                      280
               310
                       320
                              330
                                      340
                                             350
                                                     360
         IYSLLFKAAETAPPPFPHFDKVAHLALFFAQIWLLTKAFRTDNRPIPYRSLMVFALCFAL
m616.pep
          IYSLLFKAADTAPPPFPHFDKAAHLALFFAQIWLLTKAFKTGKLPIPYRSLMVFALCFAL
a616
                      320
                              330
                                     340
               370
                      380
                              390
                                     400
         FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX
m616.pep
         a616
         FSECAQAXFTATRTGSLGDVLADMAGTVLALFAARAADRPDX
               370
                      380
                              390
                                     400
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1979>: g619.seq

```
ATGCCGTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
     GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 51
101
     TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCTGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
     TCGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTtcgGC
301
     GGCGTGGGCT ATACATCCCT gccgttgacg gGCAAATTCG GCTTTGAACT
     GGTTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
    AGGGCGGCG CGATTTGCCG CACATGATTT TAATCGGCGT GATTTTCGGG
401
     ATTTTGTTCC GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
    AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
501
551
     GCAGCGAGCT TTTAGGCATA GGCGCGCTGG TCCTGCTCGT CAGCGCGGCG
     GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
601
651
     CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
    TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT TGTCGGCCCG
751 GTGAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
    gtCCGTGCGC CATTCCGTCC GCCTGCcgat gacggtttGC gtcgGcggCATCCTCTTGgt cggCggacaA ACCGTATTCG AACACTTCTT GGGCATGAag
851
901 gCggTATTAA GCGTGGTGGt cgAATTTGCG ggcggactcG TTTTCCTCTA
951 TCTCGTTTTA AAACACAAAA AATGA
```

This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>: g619.pep

```
1 MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLLVFTFG
101 GVGYTSLPLT GKFGFELVVM MGGSLLLFYT LIRQGGRDLP HMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVRSELLGI GALVLLVSAA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVGP
251 VSFFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGO TVFEHFLGMK
```

AVLSVVVEFA GGLVFLYLVL KHKK*

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1981>: m619.seq

```
1
     ATGCCGTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCGTT
    GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCCTG TTTATGACGC
 51
101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCAACTGCG GCTGACCAAA
    CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
    CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
    TCGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCGGC
301 GGCGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
    GGTCGTCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
    AGGGCGGACG CGATTTGTCG CGCATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
    ACAGCGAGCT TTTGGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTTTACCTTT TGGGGCGTGA
    CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
    TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT GGTCGGCCCC
    GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTGTTCG AACACCTGCT CGGTATGCAG
```

```
901
    GCAGTGTTGA GCGTAGTAGT AGAATTTGCC GGCGGACTCG TTTTCCTCTA
    TCTCGTTTTA AAACACAAAA AATGA
```

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>: m619.pep

- MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQLRLTK 1
- LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLLVFTFG 51
- GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGGRDLS RMILIGVIFG 101 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA 151
- VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVGP 201
- VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ 251
- 301 AVLSVVVEFA GGLVFLYLVL KHKK*

m619/g619 95.1% identity in 324 aa overlap

```
20
                                30
                                       40
                                               50
m619.pep
          MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQLRLTKLAALLMVAYA
          MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
g619
                        20
                                30
                                       40
                                               50
                70
                        80
                                90
                                      100
                                              110
                                                      120
          VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLVFTFGGVGYASLPLTGKFGFELVVM
m619.pep
          g619
          VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLVFTFGGVGYTSLPLTGKFGFELVVM
                70
                        80
                                      100
                                              110
                                                      120
               130
                       140
                               150
                                      160
                                              170
          MGGSLLLFYTLIKQGGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
m619.pep
          MGGSLLLFYTLIRQGGRDLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
a619
               130
                       140
                               150
                                      160
                                              170
                                                      180
               190
                       200
                               210
                                      220
                                              230
                                                      240
          NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
m619.pep
          NTVRSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL
q619
               190
                       200
                               210
                                      220
                                              230
                                                      240
               250
                       260
                               270
                                      280
                                              290
                                                      300
          VATATAVVGPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
m619.pep
          VATATAVVGPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
q619
               250
                       260
                               270
                                      280
               310
                       320
         AVLSVVVEFAGGLVFLYLVLKHKKX
m619.pep
          g619
         AVLSVVVEFAGGLVFLYLVLKHKKX
               310
                       320
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1983>:

```
a619.seq
      1
          ATGCCGTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
         GTGGGTTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
      51
          TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG
     101
         CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTTT CGACCCAGCT
     151
         TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
     201
         TCGATTCGCT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCGGC
     251
         GGCGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
     301
         GGTCGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
         AGGGCGGGCG CGATTTGCCG CGTATGATTT TAATCGGCGT GATTTTCGGG
         ATTTTGTTCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA
         AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
         ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
     551
     601
         GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGGCGCGA
         CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
     651
         TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGGCCCG
    701
```

GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC

```
GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
         801
         851
             TCCTCTTGGT CGGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
             GCGGTATTAA GCGTGGTGGT CGAATTTGCG GGCGGACTCG TTTTCCTCTA
         901
         951
             TCTCGTTTTA AGACACAAAA AATGA
This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:
    a619.pep
             MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
             LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLLVFTFG
          51
             GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGGRDLP RMILIGVIFG
ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
         101
         151
             VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVGP
         201
         251
             VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
         301
             AVLSVVVEFA GGLVFLYLVL RHKK*
                97.2% identity in 324 aa overlap
    m619/a619
                       10
                                20
                                         30
                                                  40
                MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQLRLTKLAALLMVAYA
    m619.pep
                a619
                MPSEKNIGFMAGSSRPLWVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
                                         30
                                                  40
                                                           50
                       70
                                80
                                         90
                                                 100
                                                          110
                VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLVFTFGGVGYASLPLTGKFGFELVVM
    m619.pep
                VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLLVFTFGGVGYASLPLTGKFGFELVVM
    a619
                       70
                                80
                                         90
                                                 100
                                                          110
                                                                   120
                      130
                               140
                                        150
                                                 160
                                                          170
                MGGSLLLFYTLIKQGGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
    m619.pep
                {\tt MGGSLLLFYTLIKQGGRDLPRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF}
    a619
                      130
                               140
                                        150
                                                 160
                                                          170
                                                                   180
                      190
                               200
                                        210
                                                 220
                                                          230
                                                                   240
                NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
    m619.pep
                NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
    a619
                      190
                               200
                                        210
                                                 220
                                                          230
                                                                   240
                      250
                               260
                                        270
                                                 280
                                                          290
                                                                   300
               VATATAVVGPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
    m619.pep
                VATATAVVGPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
    a619
                      250
                               260
                                        270
                                                 280
                      310
                               320
   m619.pep
               AVLSVVVEFAGGLVFLYLVLKHKKX
               111111111111111111111111111111
    a619
               AVLSVVVEFAGGLVFLYLVLRHKKX
                      310
                               320
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1985>: g620.seq

```
1 ATGAAGAAAA CCCTGTTGGC AATTGTTGCC GTTTTCGCCT TAAGTGCCTG
51 CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga ttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTCaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGAA GTGGATAGAT GCGCGGAAGAAC CCTTTTACCT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACCATTTTCA AGTAA
```

VVGFDDMPDT YIFK*

```
This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:
g620.pep
          MKKTLLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
          KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
      51
     101 NPNADTEWID AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
     151 VVGFDDMPDA YIFK*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1987>:
m620.seq
         ATGAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCCGCCT TAAGTGCCTG
         CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
     101
         GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
         AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
     151
     201 CACCATCAAG CAGATGTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
     251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
     301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
     351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
     401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
     451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:
m620.pep
         MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
         KAOIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
      51
     101
         NPNADTEWMD AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
         VVGFDDMPDT YIFK*
m620/g620 97.0% identity in 164 aa overlap
                                      30
                                               40
                                                        50
            {\tt MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP}
m620.pep
            g620
            MKKTLLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
                            20
                   10
                                      30
                                              40
                   70
                            80
                                      90
                                              100
                                                       110
            DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
m620.pep
            g620
            DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS
                   70
                            80
                                     90
                                             100
                                                       110
                  130
                           140
                                    150
m620.pep
            GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX
            a620
            GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDAYIFKX
                           140
                                    150
                                             160
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1989>:
     a620.seq
               ATGAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCCGCCT TAAGTGCCTG
            1
           51
               CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
          101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
          151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
          201 CACCATCAAG CAGATGTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
          251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
          301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
          351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
               TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG
               GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:
     a620.pep
               MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
            1
```

KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT

NPNADTEWMD AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK

```
m620/a620
          100.0% identity in 164 aa overlap
                                       40
          MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
m620.pep
          MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
a620
                                       40
                                               50
                70
                        80
                               90
                                      100
                                              110
                                                      120
          DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
m620.pep
          DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
a620
                70
                        80
                               90
                                      100
               130
                       140
                               150
          GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX
m620.pep
          GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX
a620
               130
                       140
                              150
                                      160
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1991>: 9622.seq

```
ATGCAactta ccgctgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
  51
      ACGGGAAAag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccqCA
      ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
 101
      AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAgaaa TCATCCGATG
 151
      GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
 251
     ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCCG CGTTGCCTGC
      GGCTTGGATT CGATGGTTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
 301
 351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
      ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAAGT CCGTACCGAT
 401
      ACCGCTGTCG GCGAAAATTC GGTTTCGATG GCTTCCGCGT CCGTCAAGTT
 451
      GGCGGAACAG ATTTTCCCG ACATCGGCGA TTTGAACGTA TTGTTTATCG
 501
      GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
      CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
 601
 651
     GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
 701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GGCGAGCCAG
 751
     CTTCCGATAG TCGGCAAAGG CATGGTCGAA CGCGCATTGA AACAGCGTCA
     GAGTATGCCG TTGTTCATGC TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTTGAAC GATGCGTATC TTTATACGGT GGACGATATG
 901 GTCAACATCG TCCAAAGCGg caaggaggca aggcagaaag ccgccgcCgc
 951 cgccgaaacg ctggTGTCCG AAAAGGTTGC CGAATTTGTC AGGCAGCAGC
     AGGGCAGGCA GagcgttcCG CTGATTAAGG CCTTGCGGGA CGAGGGCGAG
1001
1051 AAAGCGCGCA AGCAGGTGTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaaCGGCG GAAGaggttt TGgaacggct gtccgtcCAA CTGACCAACA
     AGCTGCTGCA TTCGCCAACT CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1151
     AAAGatttGG TTCATGCCgt cGCGCAGATt tatcatttGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>: g622.pep

```
1 MQLTAVGLNH QTAPLSIREK LAFAAAALPE AVRNLARSNA ATEAVILSTC
51 NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEQESMG AKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDLN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVP LIKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1993>: m622.seq

1 ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51 ACGGGAAAAG CTGGCGTTTG CCGCCGCCG CCTGCCTAAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC

25.	GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351	GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401	ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAGGT CCGTACCGAT
451	ACTGCCGTCG GCGAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAATT
501	GGCGGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551	GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601	CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651	GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701	CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751	TTGCCCATTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801	GAGTATGCCG TTGTTCATGC TTGATTTGGC AGTGCCGCGT GACATTGAAG
851	CGGAAGTCGG CGATTTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901	GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951	CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001	AGGGCAGGCA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGGCGAG
1051	AAAGCGCGCA AACAGGTGTT GGAAAATGCC ATGAAACAGC TTGCCAAAGG
1101	CGCAACGGCA GAAGAGGTTT TGGAACGGCT GTCCGTCCAA CTGACCAACA
1151	AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201	AAAGATTTGG TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
This corr	responds to the amino acid sequence <seq 1994;="" 622="" id="" orf="">:  MOLTAVGLNH QTAPLSIREK LAFAAAALPK AVRNLARSNA ATEAVILSTC</seq>
51	NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMOE TVRHAFRVAC
101	GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151	TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201	PRINTVANRT LARAGELCOK LGVNAEPCLL SDLPAILHDY DVVVSSTASO
251	LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDLN DAYLYTVDDM
301	VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVP LIKALRDEGE
351	KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
351 401	
401	KDLVHAVAQI YHLDK*
m622/g622	98.8% identity in 415 aa overlap
	10 20 30 40 50 60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
g622	MQLTAVGLNHQTAPLSIREKLAFAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD
	10 20 30 40 50 60
	70 80 90 100 110 120
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
	ODDITKWDMDINODE IDDIKE IDIIIDMQDIVKMAFKVACGDDSMVLGEPQILGQIKDAV
	70 80 90 100 110 120
	70 00 00
	70 80 90 100 110 120 130 140 150 160 170 180
m622.pep	70 80 90 100 110 120  130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
m622.pep	70 80 90 100 110 120  130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
m622.pep	70 80 90 100 110 120  130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
	70 80 90 100 110 120  130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
	70 80 90 100 110 120  130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
	70 80 90 100 110 120  130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622	70 80 90 100 110 120  130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV !:!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
g622	70 80 90 100 110 120  130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV !:!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep g622	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep g622	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
g622 m622.pep g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
m622.pep g622 m622.pep g622	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
m622.pep g622 m622.pep g622	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
m622.pep g622 m622.pep g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
m622.pep g622 m622.pep g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
m622.pep g622 m622.pep g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
m622.pep g622 m622.pep g622 m622.pep	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
m622.pep g622 m622.pep g622 m622.pep g622	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :
m622.pep g622 m622.pep g622 m622.pep g622	130 140 150 160 170 180  RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV  :

370 380 390 400 410

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1995>:
```

```
a622.seq
               ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
              ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
           51
              ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
          101
              AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
              GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
          251
              ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
          301
              GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
          3.51
              GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
          401
              ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
              ACTGCCGTCG GCGAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAGTT
          451
              GGCAGAGCAG ATTTTCCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
          501
              GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
          551
          601
              CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
              GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
          651
          701
              CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
              TTGCCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
          751
              GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
          801
              CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
              GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
          901
              CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
         951
         1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
         1051 AAAGCGCGCA AACAGGTCTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
        1101
              CGCAACGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
        1151
              AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
              AAAGATTTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
This corresponds to the amino acid sequence <SEO ID 1996; ORF 622.a>:
     a622.pep
              MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
              NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
              GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
         101
             TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
             PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
             LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDLN DAYLYTVDDM
              VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVP LIRALRDEGE
              KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
              KDLVHAVAQI YHLDK*
    m622/a622
                 98.1% identity in 415 aa overlap
                                  20
                                           30
                                                     40
                 MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
    m622.pep
                 MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD
    a622
                        10
                                  20
                                           30
                                                     40
                                                               50
                        70
                                  80
                                           90
                                                    100
                                                             110
                 SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
    m622.pep
                 a622
                 SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
                        70
                                  80
                                           90
                                                    100
                                                             110
                                 140
                                          150
                                                    160
                                                             170
                                                                       180
                 RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
    m622.pep
                 RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
    a622
                       130
                                 140
                                          150
                                                    160
                                                             170
```

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVAT	YFAAKSPRLI	ITVANRTLAR.	AQELCDKLGVN	AEPCLLSDL	
a622	LFIGAGEMIELVAT	TITITITITI	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	AOET.CDKT.GVN	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
4022	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIV	GKGMVERAL	(QRQSMPLFM)	LDLAVPRDIEA	EVGDLNDAY	LYTVDDM
		111111111		[[]]		
a622	DVVVSSTASQLPIV	GKGMVERALH	(QRQSMPLFM)	LDLAVPRDIEA	EVGDLNDAY	LYTVDDM
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKA	AAAAETLVSE	CKVAEFVRQQ(	QGRQSVPLIKA	LRDEGEKARI	(QVLENA
		111111111		1111111:1	1111111111	
a622	VNIVQSGKEARQKA	AAAAETLVSE	KVAEFVRQQQ	QGRQSVPLIRA	LRDEGEKARF	<b>(QVLENA</b>
	310	320	330	340	350	360
	0.7.0					
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVL	ERLSVQLTNK	LLHSPTQTLN	NKAGEEDKDLV	HAVAQIYHLE	OKX
		1111:1111	111111111		111111111	11
a622	MKQLAKGATAEEVL	ERLSIQLTNK	LLHSPTQTLN	<b>IKAGEEDKDLV</b>	HAVAQIYHLD	XX
	370	380	390	400	410	

The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 1997>: g624.seq

- ATGATCCGTT ATCTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
- GATAATCGGC ATTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTAC 51
- 101 TCTCCGCCGC CTGCTGGGCA AAGGCAtccc cgcgcTTTCa ccgCTGGCTG
- 151 CACCGGCacc gCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
- 201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt 251 cctgcctcat gatctTTtgg CattTTCccc aacnctggtg ggtcGGGGCG
- 301 GTTTCATCGG TTTTTTGTTC CCTTGTcacC ATacggatgt gGcacAGacC
- 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>: g624.pep

- MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
- 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
- 101 VSSVFCSLVT IRMWHRPES*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1999>: m624.seq

- 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TACTGTTGGG
- TATCATCGGC ATTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
- 101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
- 151 CACCGGCACC GCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
- 201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT 251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCG
- 301 GTTTCATCGG TTTTTTGTTC CCTTGTCGCC ATATGGATGT GGCGCAGGCC
- 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>: m624.pep

- MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
- 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
- 101 VSSVFCSLVA IWMWRRPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCI	SLLLGIIGIFLP	LLPTTPFVLLS	SAACWAKASE	RFYRWLHRHR	YFGPMV
		1111111111111	11111111111	111111111	11:111111	111111
g 62 4	MIRYLLIACGGI	SLLLGIIGIFLP	LLPTTPFVLLS	BAACWAKASE	RFHRWLHRHR	YFGPMV
	10	20	30	40	50	60

	·
301	GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351	GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401	ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAGGT CCGTACCGAT
451	ACTGCCGTCG GCGAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAATT
	GGCGGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
501	GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
551	CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
601	CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGT
651	GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701	CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751	TTGCCCATTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801	GAGTATGCCG TTGTTCATGC TTGATTTGGC AGTGCCGCGT GACATTGAAG
851	CGGAAGTCGG CGATTTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901	GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951	CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001	AGGGCAGGCA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGGCGAG
1051	AAAGCGCGCA AACAGGTGTT GGAAAATGCC ATGAAACAGC TTGCCAAAGG
1101	CGCAACGGCA GAAGAGGTTT TGGAACGGCT GTCCGTCCAA CTGACCAACA
1151	AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201	AAAGATTTGG TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
1201	AAAGATIIGG IICAIGCGI GGCGCAGATI IIIGATIIGG AGATATA
·	1 / 4
This corr	esponds to the amino acid sequence <seq 1994;="" 622="" id="" orf="">:</seq>
m622.pep	-
1	MQLTAVGLNH QTAPLSIREK LAFAAAALPK AVRNLARSNA ATEAVILSTC
51	NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
	GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
101	GLDSMVLGEP GILGGIADAV AVAGEGESMG ARDMADERATE I VARAEVATE
151	TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201	PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251	LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDLN DAYLYTVDDM
301	VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVP LIKALRDEGE
351	KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401	KDLVHAVAQI YHLDK*
m622/q622	98.8% identity in 415 aa overlap
,	
	10 20 30 40 50 60
	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
m622.pep	
g622	MQLTAVGLNHQTAPLSIREKLAFAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD
	10 20 30 40 50 60
	70 80 90 100 110 120
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
,	70 80 90 100 110 120
	130 140 150 160 170 180
m622.pep	RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
mozz.pep	[:][][][][][][][][][][][][][][][][][][]
	RAAQEQESMGAKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
g622	130 140 150 160 170 180
	130 140 130 160 170 180
	190 200 210 220 230 240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY
g622	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY
-	190 200 210 220 230 240
	250 260 270 280 290 300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLNDAYLYTVDDM
mozz.pcp	
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLNDAYLYTVDDM
g622	
	250 260 270 280 290 300
	210 200 220 240 250 260
	310 320 330 340 350 360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA
	310 320 330 340 350 360
	370 380 390 400 410
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX
pep	
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX
90	**************************************

390 400 410 370 380

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1995>:

a622.seq ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA 51 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC 101 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT 201 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTAG GACAGATTAA 301 351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT 401 451 ACTGCCGTCG GCGAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAGTT GGCAGAGCAG ATTTTCCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG 501 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT 551 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT 601 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC 651 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG TTGCCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA 751 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG 801 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG 851 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC 901 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC 951 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG 1001 AAAGCGCGCA AACAGGTCTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG CGCAACGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT 1201 AAAGATTTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>: a622.pep 1 MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC 51 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD 101 151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASO LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDLN DAYLYTVDDM VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVP LIRALRDEGE KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED 351 KDLVHAVAQI YHLDK* 401 m622/a622 98.1% identity in 415 aa overlap 20 30 40 MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD m622.pep  ${\tt MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD}$ a622 10 20 30 40 50 80 90 100 110 120 SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV m622.pep SEEIIRWLADYHSLPIEEISPYLYTLGMOETVRHAFRVACGLDSMVLGEPOILGOIKDAV a622 70 80 90 100 110 120 130 140 150 160 170 180 RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV m622.pep RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV a 622 130 140 150 160 170

m622.pep	190 LFIGAGEMIELVAT	200 YFAAKSPRLN	210 MTVANRTLARA	220 AQELCDKLGVI	230 NAEPCLLSDL	240 PAILHDY
a622	LFIGAGEMIELVAT	YFAAKSPRLN	TVANRTLAR.	AQELCDKLGVI	NAEPCLLSDL	PAILHEY
2022	190	200	210	220	230	240
	٥٣٥	260	220	200	290	200
	250	260	270	280		300
m622.pep	DVVVSSTASQLPIV	GKGMVERALF	(QRQSMPLFMI	LDLAVPRDIE	AEVGDLNDAY:	LYTVDDM
• -		11111111111				111111
a622	DVVVSSTASQLPIV	GKGMVERALE	COROSMPLEMI	DLAVPRDIE	AEVGDLNDAY	LYTVDDM
4022	250	260	270	280	290	300
	250	200	270	200	230	500
	210	200	220	240	250	2.60
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKA	AAAAETLVSE	CKVAEFVRQQQ	)GRQSVPLIK <i>i</i>	ALRDEGEKARI	(QVLENA
		11111111111		11111111:		
a622	VNIVOSGKEAROKA	AAAAETI.VSE	KVAEFVROOC	GROSVPLTRA	ALRDEGEKAR	COVLENA
a022	310	320	330	340	350	360
	310	320	330	340	330	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVL	ERLSVQLTN	CLLHSPTQTLN	KAGEEDKDL	JHAVAQIYHLI	OKX
	34714141111111	1111:1111	111111111	111111111		111
			TITUCOMONIN	ועאכבבטאטני		JKX
	MKMLAKCATAFA					
a622	MKQLAKGATAEEVL 370	380 380	390	400	410	XXX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 1997>: g624.seq

1 ATGATCCGTT ATCTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTGG 51 GATAATCGGC ATTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTA 101 TCTCCGCCGC CTGCTGGGCA AAGGCATCGCC CGCGTTTCA CCGCTGGCT 151 CACCGGCAC GCCAAAGCCA AGATTTTCGC CATCACCATG AACAAAACG 201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgCA 251 cctgcctcat gatctTTtgg CattTTCcc aacnctggtg ggtcGGGGC 301 GTTCATCGG TTTTTTGTTC CCTTGTCaCC ATacggatgt gGcacAGac 351 cqaatCTTGA						
101 TCTCCGCCGC CTGCTGGGCA AAGGCAtccc cgcgcTTTCa ccgCTGGCT 151 CACcgGCacc gCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACG 201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcA 251 cctgcctcat gatctTTtgg CattTTCccc aacnctggtg ggtcGGGGC 301 GTTTCATCGG TTTTTTGTTC CCTTGTcacC ATacggatgt gGcacAGac	1	ATGATCCGTT	ATCTTTTAAT	TGCCTGCGGC	GGCATCTCCC	TGCTGTTGGG
151 CACCGGCACC GCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACG 201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcA 251 cctgcctcat gatctTttgg CattTTCccc aacnctggtg ggtcGGGGC 301 GTTTCATCGG TTTTTTGTTC CCTTGTcacC ATacggatgt gGcacAGac	51	GATAATCGGC	ATTTTTTTGC	CGCTGTTGCC	GACCACGCCG	TTCGTACTAC
201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaacegcA 251 cetgeetcat gatetTTtgg CattTTCccc aacnetggtg ggtcGGGGC 301 GTTTCATCGG TTTTTTGTTC CCTTGTcacC ATacggatgt gGcacAGac	101	TCTCCGCCGC	CTGCTGGGCA	AAGGCAtccc	cgcgcTTTCa	ccgCTGGCTG
251 cctgcctcat gatctTTtgg CattTTCccc aacnctggtg ggtcGGGGCC 301 GTTTCATCGG TTTTTTGTTC CCTTGTcacC ATacggatgt gGcacAGac	151	CACcqGCacc	qCTATTTCGG	CCCGATGGTT	CATAACTGGG	AACAAAACGG
301 GTTTCATCGG TTTTTTGTTC CCTTGTcacC ATacggatgt gGcacAGac	201	CGCAGTGCCG	CGCAAAGCCA	AGATTTTCGC	CATCAGCATG	AtaaccgcAt
301 GTTTCATCGG TTTTTTGTTC CCTTGTcacC ATacggatgt gGcacAGac	251	cctqcctcat	gatctTTtgg	CattTTCccc	aacnctggtg	ggtcGGGGCG
351 cqaatCTTGA	301					
	351	cgaatCTTGA				_

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>: g624.pep

- 1 MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
- 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA 101 VSSVFCSLVT IRMWHRPES*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 1999>: m624.seq

- 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TACTGTTGGG
- 51 TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
- 101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
- 151 CACCGGCACC GCTATTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
- 201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
- 251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCG 301 GTTTCATCGG TTTTTTGTTC CCTTGTCGCC ATATGGATGT GGCGCAGGCC 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>: m624.pep

- 1 MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
- 51 HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
- 101 VSSVFCSLVA IWMWRRPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCIS	LLLGIIGIFLP	LLPTTPFVLL	SAACWAKASP	RFYRWLHRHR	YFGPMV
	11111111111111111	11111111111	11111111	111111111	H:HIIII	111111
g624	MIRYLLIACGGIS	LLLGIIGIFLP	LLPTTPFVLL	SAACWAKASP	RFHRWLHRHR	YFGPMV
	10	20	30	40	50	60

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRI					
	1111111111		11111::11:	:111 11111	HEREITHE:	
g624	HNWEQNGAVPRI	KAKIFAISMI	TASCLMIFWE	ifpQxwwvga'	VSSVFCSLVT:	ERMWHRPESX
<b>J</b>	70	80	90	100	110	120

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2001>:

```
1 ATGATACGTT ATCTTTAAT TGCCTGCGGC TGCATTTCCC TGCTGTTGGG
51 TATCATCGGC ATTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCC
301 GTTTCATCGG TTTTTTGTTC CCTTGTCGCC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624.pep
        MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
       HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
       VSSVFCSLVA IWMWRRPES*
    101
m624/a624
          99.2% identity in 119 aa overlap
                                          40
                 10
                         20
                                  30
          MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV
m624.pep
          MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV
a624
                                                           60
                 10
                                          40
                                  90.
                                         100
          HNWEONGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
m624.pep
          HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
a624
                                                          120
                 70
                         80
                                  90
                                         100
                                                 110
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2003>:

```
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACTGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2004>:

```
1 atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGtcTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAGGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACTGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gtal
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>: g625.pep

¹ MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA

```
VLSLGVPFKS PQTKMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
        KLNGMRKSNV QKAVILP*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2006>:
m625.seq
        ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
     1
    51
        ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
        CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
    101
        GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
        TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
    201
        CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
    251
    301
        AAACTGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
    351 GTAA
This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:
m625.pep
        MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
        VLSLGVPFKS POTKMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
     51
       KLNGMRKSNV OKAVILP*
    101
m625/q625 98.3% identity in 117 aa overlap
                  10
                          20
                                   30
                                           40
m625.pep
           MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS
           g625
           MFATRKMKKMTMCTRRVRSWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS
                                   30
                                           40
                  70
                          80
                                   90
                                          100
                                                   110
           POTKMPPEMVYRASSSRMKGMYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX
m625.pep
           PQTKMPPEMVYRASSSRMKGIYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX
g625
                  70
                          80
                                   90
                                          100
                                                   110
This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:
    a625.pep
              MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
           1
          51
              VLSLGVPFKS PQTKMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
              KLNGMRKSNV QKAVILP*
    m625/a625
                 100.0% identity in 117 aa overlap
                         10
                                   20
                                            30
                                                      40
                 MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS
    m625.pep
                 a625
                 MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPMIEASAVPTASRAVLSLGVPFKS
                         10
                                   20
                                                      40
                                                                50
                                                                          60
                                            90
                                                     100
                         70
                                   80
                                                               110
                 PQTKMPPEMVYRASSSRMKGMYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX
    m625.pep
                 a625
                 PQTKMPPEMVYRASSSRMKGMYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX
                         70
                                   80
                                                               110
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2009>:
     g627.seq
              ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
              CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA
         101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
         151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACTCTTCC TCGGCATCTT
         201 CATCACCATC TTCCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
         251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
         301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
         351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
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401 CCTTAATGAC GGGTCCCCTG TTTCATTcgc TGCTGGCGGT TTCTAtgggT 451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

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501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
               ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CAtcgTACAT
          601 ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa
This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:
     g627.pep
               MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
           51
               FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
          101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
               SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
               TLVFFVFKLL *
The following partial DNA sequence was identified in N. meningitidis <SEO ID 2011>:
     m627.sea
               ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
            1
              CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
           51
          101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
          151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACTCTTCC TCGGCATCTT
          201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
          251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
          301 AATGTGATGT ATTTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
          351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
          401 CCTTGATGAC GGGTACCCTG TTTCATTCGC TGCTGGCGGT TTCTATGGGT
          451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
          501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
          551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
          601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA
This corresponds to the amino acid sequence <SEO ID 2012; ORF 627>:
     m627.pep
            1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
           51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
          101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
               SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
               TLIFFVFKLL *
          201
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
```

m627/g627 97.6% identity in 210 aa overlap

m627.pep g627	70 80 90 100 110 120 KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT
m627.pep g627	130 140 150 160 170 180 YLVFFNMAGGDAQALMTGTLFHSLLAVSMGSVFMGALTYIGNAPNFMVKAIAEQRGVPMP
m627.pep	190 200 210 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX                             TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX 190 200 210
The following page 1 1 51 101 151 201	CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACTCTTCC TCGGCATCTT
251 301 351 401 451 501 551 601	CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT AATGTGATGT ATTTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
This correspond	ds to the amino acid sequence <seq 2014;="" 627.a="" id="" orf="">:</seq>
a627.pep 1 51 101 151 201	MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH TLIFFVFKLL *
m627/a627	99.5% identity in 210 aa overlap
m627.pep a627	10 20 30 40 50 60  MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG
m627.pep a627	70 80 90 100 110 120 KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMSGILSAFLDNAPT
m627.pep a627	130 140 150 160 170 180 YLVFFNMAGGDAQALMTGTLFHSLLAVSMGSVFMGALTYIGNAPNFMVKAIAEQRGVPMP

WO 99/57280 PCT/US99/09346

1003

a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX 190 200 210

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2015>:

9628.seq

1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
101 ACACATGGAT TTTACGTTCG GTCAGGCGGC TCAATACCAA CAGGCCGCGT
151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
251 CGGCAGGGAT TTTGCTGAAC GGACGGTGC GAAGCGCAGT CCATAAGCCT
301 GATTGAATCA GGTTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
351 TTCAGGTacq TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep

- 1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRRLNTNRPR
- 51 LKSSAAS<u>LMM TVGSAASGLV SIAL</u>TKMANG SASTAGILLN GRVRSAVHKP
- 101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2017>:

m628.seq

1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
101 AAACATGGAT TTTGCGTTCG GTCAAACGGC TCAATACCAA CAGGCCGCGT
151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG

301 GATTGGATCA GGTTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC

351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep

- 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRPR
- 51 LKSSAAS<u>LIM TVGSAASGLV SIAL</u>TKMANG SASTAGILLN GRVRSAVHKP
- 101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae* 

m628/g628 93.3% identity in 119 aa overlap

30 40 MCVPLKPAGCGPPNSCVSMLAAFSDGTSAPAALQTWILRSVKRLNTNRPRLKSSAASLIM m628.pep q628 MCVPLKPAGCGPPNSCVSILAAFSDGTSAPAALHTWILRSVRRLNTNRPRLKSSAASLMM 10 30 70 80 90 100 TVGSAASGLVSIALTKMANGSASTAGILLNGRVRSAVHKPDWIRLRRTSSPLKFASASGA m628.pep g628 TVGSAASGLVSIALTKMANGSASTAGILLNGRVRSAVHKPDXIRLRRTFSLLNFASASGT 70 80 90 100 m628.pep X g628 X

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2019>:

```
a628.seq
              ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT
              TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
          51
              ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT
          101
              CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGGT CTGCCGCCAG
          151
              CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
              CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG
              GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACGC
              TTCGGGCGCG TAG
This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:
     a628.pep
             MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALHTWILRS VKRLNTSKPR
           1
          51
              LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSAVHKP
         101
              DWIRLRRTSS PLKFANASGA *
                 95.0% identity in 120 aa overlap
    m628/a628
                         10
                                   20
                                                      40
                                                                50
                 MCVPLKPAGCGPPNSCVSMLAAFSDGTSAPAALQTWILRSVKRLNTNRPRLKSSAASLIM
    m628.pep
                 MCVPLKPAGCGPPNSCVSMLAAFSDGTSAPAALHTWILRSVKRLNTSKPRLKSSAASLIT
    a628
                         10
                                   20
                                            30
                                                      40
                                                                50
                                                                          60
                                   80
                                            90
                                                     100
                                                               110
                 TVGSAASGLVSIALTKMANGSASTAGILLNGRVRSAVHKPDWIRLRRTSSPLKFASASGA
    m628.pep
                 TTGSAASGLVSIALTKMANGSASTAGILLNGRVRSAVHKPDWIRLRRTSSPLKFANASGA
    a628
                                                     100
    m628.pep
                 Х
                 1
                 Х
    a628
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2021>:
     g629.seq
              ATGACTGCca aacCTTTTTC CCTCAACCTG GCcaaCCTCC TGCTGCCggc
           1
          51
              ggtatTGTTT GCCGTCAGcc tGtcgqTCGG cattgccgaT TTCCGCTGGT
              CGGATGTGTT TTCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC
         101
         151
              CTGCCGCGCA CGTTTGcgaT TGTGTTGACG GGCgcgtcga tagcgGtggc
         201
              gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTtcta
         251
              tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg
         301
              ctgctgcctg CcgcGccgct gccggtcaAA ATGTCGGtag Ccgccgttgc
         351
              CGCGCTGATC GGGATGTTGG tctTtatgct gctaatccgC Cgcctgccac
              cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG
          401
          451
              GttgaGGCGG TGGCGACGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAT
          501
              GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT
              ACGAGCTGCT TTGGATTACG GGCGGTTTTGG CGGTGTTTGC CTACCTGATT
          601
              GCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATTT
          651
              GGGTTTGAAC CGGACGCGG TGTTGTGGTC GGGTTTGATT ATTGTGGCAC
              TGATTACATC GCTGGTCATT GTAACGGTCG GCAATATTCC GTTTATCGGG
          701
              CTGGTCGTGC CGAATATCGT CAGCCGCCTG ATGGGCGACA GGCTGCGCCA
          751
              AAGCCTGCCT GCGGTCGCCC TCTTGGGCGC GTCTTTGGTT TTATTGTGCG
          801
              ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTCC GGTCTCCACG
          851
              GTTTTTGGTG TGTTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
          901
          951 ACCCGCCTAT GCCGTCTGA
This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:
     g629.pep
              MTAKPFSLNL ANLLLPAVLF AVSLSVGIAD FRWSDVFSLS DSQQVMFISR
           1
          51
              LPRTFAIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLMSL
```

LLPAAPLPVK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGXIFGGV

151	<u>VEAV</u> ATFVAY	EFEMLQMLGV	WQQGDFSSVL	LGRYELLWIT	GGLAVFAYLI
201	ADRLTILGLG	ETVSVNLGLN	RTAVLWSGLI	IVALITSLVI	VTVGNIPFIG
251	LVVPNIVSRL	MGDRLRQSLP	AVALLGASLV	LLCDIIGRMI	VFPFEIPVST
301	VFGVLGTALF	LWLLLRKPAY	AV*		

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2023>:

```
m629.seq
         ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
         GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
         CTGATGTGTT TTCACTGTCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
    151 CTGCCGCGCA CGTTTGCGAT TGTGCTGACG GGCGCGTCGA TGGCGGTGGC
    201 CGGCATGATT ATGCAGATTT TGATGCGCAA CCGTTTTGTC GAACCGTCGA
    251 TGGTGGGCGC AAGCCAAAGC GCGGCTTTAG GTTTGCTGCT GATGACCCTG
    301 CTGCTGCCGG CCGCGCCGCT GCCGGCGAAA ATGTCGGTTG CCGCCGTTGC
    351 CGCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
    401 CGACCGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGTGTG
    451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAAT
    501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGGCGGT
    551 ACGAGCTGCT TTGGATTACG GGCGGTTTGG CGGTGTTTGC CTATCTGATT
     601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT
     651 GGGTTTGAAC CGGACGGCGG TGTTGTGGTC GGGTTTGATT ATTGTGGCTT
         TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
         CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATGGGCGACA GGTTGCGCCA
    801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG
    851 ACATTATCGG ACGCGTGATT GTGTTTCCGT TTGAAATTCC GGTCTCTACG
    901 GTTTTTGGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
    951 ACCCGCCTAT GCCGTCTGA
```

# This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pep

1 MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMVGASQS AALGLLLMTL
101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIFGGV
151 IEAVATFIAY ENEMLQMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI
201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
251 LVVPNIISRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAY AV*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae* 

m629/g629 95.7% identity in 322 aa overlap

m629.pep	10 20 MTAKPFSLNLTNLLLLAVLFAVSL	30 SVGVADFRWSD	40 VFSLSDSQQ 	50 VMFISRLPRT	60 FAIVLT
g629	MTAKPFSLNLANLLLPAVLFAVSL:	SVGIADFRWSD 30	VFSLSDSQQ 40	VMFISRLPRT 50	FAIVLT 60
	70 80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSM		LLMTLLLPA	APLPAKMSVA     :	AVAALI
g629	GASIAVAGMIMQILMRNRFVEPSMI		LLMSLLLPA 100		AVAALI 120
	130 140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVG			LOMLGVWQQG	DESSVL
g629	GMLVFMLLIRRLPPTAQLMVPLVG	:      XIFGGVVEAVA	:       TFVAYEFEM	LQMLGVWQQG	DFSSVL
	130 140	150	160	170	180
	190 200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRL	TILGLGETVSV 	NLGLNRTAV 	LWSGLIIVAI	ITSLVI

g 629	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
	190 200 210 220 230 240
60.0	250 260 270 280 290 300
m629.pep	VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
g 62 9	
9629	250 260 270 280 290 300
	200 200 200 200
	310 320
m629.pep	VFGVLGTALFLWLLLRKPAYAVX
g629	VFGVLGTALFLWLLLRKPAYAVX
	310 320
701 - C-11i	cartial DNIA acqueres was identified in N. maningitidia CEO ID 2025.
• • •	partial DNA sequence was identified in N. meningitidis <seq 2025="" id="">:</seq>
a629.seq	> TO 2 OFFICE A 2 SOUTHWENT OF THE SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOUTH A SOU
1	ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51	GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
101 151	CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GGCGCGTCGA TGGCGGTGGC
201	GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTTGTC GAGCCTTCTA
251	TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTTGCTTCT GATGTCCCTG
301	CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351	CGCGTTAATC GGGATGTTGG TGTTTATGAT GCTTATCCGC CGCCTGCCGC
401	CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451	GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAT
501	GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTTG CTCGGACGGT
551	ATGAACTGTT GTGGGCAACG GGGATTTTGG CTTTGTTTGC CTATTTGATT
601	GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACTT
651	GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701	TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751	CTGGTCGTGC CGAACATCAT CAGCCGCCTG ATAGGCGACA GGCTGCGCCA
801	AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851	ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC GGTATCGACC
901 951	GTCTTCGGCG TATTGGGTAC GGCGTTGTTT TTATGGCTTT TGTTAAGGAA ACCTGCTCAT GCCGTCTGA
321	ACCIDETEAL GCCGTCTGA
This correspond	s to the amino acid sequence <seq 2026;="" 629.a="" id="" orf="">:</seq>
a629.pep	is to the minio acid soquence ADQ ID 2020, Old O27.4
a629.pep	MTAKPFSLNL TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
51	LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLMSL
101	LLPAAPLPVK MSVAAVAALI GMLVFMMLIR RLPPTAQLMV PLVGIIFGGV
151	VEAVATFIAY ENEMLOMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201	ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251	LVVPNIISRL IGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301	VFGVLGTALF LWLLLRKPAH AV*
m629/a629	95.7% identity in 322 aa overlap
	10 20 30 40 50 60
m620 non	10 20 30 40 50 60 MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
m629.pep	
a629	MTAKPFSLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT
4023	10 20 30 40 50 60
	70 80 90 100 110 120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLLMTLLLPAAPLPAKMSVAAVAALI
a629	GASMAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLLMSLLLPAAPLPVKMSVAAVAALI
	70 80 90 100 110 120
	120 140 150 160 120
	130 140 150 160 170 180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMLQMLGVWQQGDFSSVL      ::
	111114-11111111111111111111111111111111

```
GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
a 629
                        140
                               150
                190
                        200
                                210
                                       220
                                                230
                                                        240
          LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
m629.pep
          a629
          LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
                190
                                210
                                       220
                250
                        260
                                270
                                       280
          VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
m629.pep
          a629
          VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
                250
                        260
                               270
                                       280
                                                290
                310
                        320
m629.pep
          VFGVLGTALFLWLLLRKPAYAVX
          a629
          VFGVLGTALFLWLLLRKPAHAVX
                        320
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2027>: g630.seq (partial)

```
aTgatGATTT TGGTGTGGCT ggctttgttt ccccccatgt tttacggcat
    gtacaacgtc GGCGCACAGG CATTCGGTGC CTTAACGCCC GAtttgctqc
101 aacaaagcat cgcccacgac ggcaattacg ccctcgccaa cgctttgggc
151 atcaatatgt cccccgaaGc gggcgtgtTg ggcaaaatgc tgttcgGCGC
    GATttacttc ctgccgattt acgcgaccgt aTTTATTGTG GGcggcttct
251 ggGaagtCTT GTTCGCATCc gtACGCAAAC ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGC
451 GCCTTCCTGT TCTTCGCCTA CCCCGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTT GCCCGCATCG
701 CTtcttgGCG CATTATTGCc ggCGTGATGA TCGGTatGat tGcgatgTCT
751 tcgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 cttggtacat ggcacttggt GGAaagatGa ttAtcactca ctgtacatta
851 aa....
```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>: g630.pep

```
1 MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLQQSIAHD GNYALANALG
51 INMSPEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAS VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
```

- 151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVTGQTIT
- 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
- 251 SLINFIGSDT KAMFAMHLVH GTWWKDDYHS LYIK....

# The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>: m630.seq

```
ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
  1
    GTACAACGTC GGCGCGCAGG CATTCGGTGC GTTAACGCCT GATTTGCTGC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
    ATCAATATGT CGTCTGAAGC GGGCGTGTCG GACAAAATGC TGTTTGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACTGT ATTTGTTGTG GGCGGTTTCT
251 GGGAAGTTTT GTTCGCCACC GTGCGCAAAC ACGAAATCAA CGAAGGTTTC
301 TTCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
    GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCTTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCACTGGCG CAATGGGCGG
    CACACGGTGC AGACGGCCTG AAAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTTATCGG CAAACTGCCC GGCTCCATTG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTT GCCCGCATCG
701 CTTCTTGGCG CATTATTGCC GGCGTGATGA TCGGTATGAT TGCGATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
```

```
TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
        TGGCGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
    851
        TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
        GGCTTACCCC GAAGGCATGA TGTTGGCGAT TCTGTTTGCC AACCTGTTTG
    951
   1001
        CCCCGATTTT CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
        GCGCGCAGCA ATGGCTAA
   1051
This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:
m630.pep
        MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQQNIAND WHYAFANALG
      1
     51
        INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
        FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
    101
    151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVTGQTIT
        WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
        SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
        YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
    351
        ARSNG*
m630/g630 93.5% identity in 275 aa overlap
                  10
                           20
                                    30
           MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQNIANDWHYAFANALGINMSSEAGVS
m630.pep
           MMILVWLALFPPMFYGMYNVGAQAFGALTPDLLQQSIAHDGNYALANALGINMSPEAGVL
q630
                  10
                           20
                                    30
                                             40
                  70
                           80
                                    90
                                            100
                                                     110
                                                              120
           DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
m630.pep
            GKMLFGAIYFLPIYATVFIVGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA
a630
                  70
                           80
                                    90
                                            100
                                                     110
                 130
                          140
                                   150
                                            160
                                                     170
m630.pep
           ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
           ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
g630
                 130
                          140
                                   150
                                            160
                                                     170
                                                              180
                 190
                          200
                                   210
                                            220
m630.pep
           QWAAHGADGLKNAVTGQTITWMDAFIGKLPGSIGEVSTLALLIGGAFIVFARIASWRIIA
           q630
           QWAAHGADGLKNAVTGQTITWMDAFIGKLPGSIGEVSTLALLIGGAFIVFARIASWRIIA
                          200
                                   210
                 190
                                            220
                 250
                          260
                                   270
                                            280
                                                     290
                                                              300
           GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
m630.pep
           \pm 111.1
           GVMIGMIAMSSLINFIGSDTKAMFAM----HLVHGTWWKDDYHSLYIK.
a630
                 250
                          260
                                       270
                                               280
                          320
                                   330
                                            340
m630.pep
           YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
     a630.seq
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2031>:

```
ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
    GTACAACGTC GGCGCACAGG CATTCGGTGC GTTAACGCCC GATTTGCTGC
101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTTG GGCAAAATGC TGTTCGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
251 GGGAAGTTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCCTGT TCTTCGCCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAAACGCCA TAACCGGTCA AACCATCACT
    TGGATGGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
    CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTT GCCCGCATCG
```

701 751 801 851 901 951 1001 1051	CTTCTTGGCG CATTATTGCC GGCGTGATGA TCGGTATGAT TGCCATGTCT TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC TTGGTACTGG CATTTGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA TGGCGACCGA CCCCGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG TACGGCGCAC TGATCGGTG GATGTGCGTA TTAATCCGCG TGGTCAATCC GGCTTACCCC GAAGGCATGA TGTTGGCGAT TCTGTTTGCC AACCTGTTTG CCCCGATTTT CGACTATTC GTCGCACAAG CGAACATCAA ACGCAGAAAG GCGCGCAGCA ATGGCTAA
_	ds to the amino acid sequence <seq 2032;="" 630.a="" id="" orf="">:</seq>
a630.pep 1	MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQQSIAND WHYALANALG
51	INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101	FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 201	AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251	SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301	YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351	ARSNG*
m630/a630	98.3% identity in 355 aa overlap
	10 20 30 40 50 60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQNIANDWHYAFANALGINMSSEAGVS
a630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQQSIANDWHYALANALGINMSSEAGVL
	10 20 30 40 50 60
	. 70 80 90 100 110 120
m630.pep	. 70 80 90 100 110 120 DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
a 630	GKMLFGAIYFLPIYATVFIVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA
	70 80 90 100 110 120
	130 140 150 160 170 180
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA
- 620	
a630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA 130 140 150 160 170 180
	100 100 100
600	190 200 210 220 230 240
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLPGSIGEVSTLALLIGGAFIVFARIASWRIIA 
a 630	QWAAHGADGLKNAITGQTITWMDAFIGKLPGSIGEVSTLALLIGGAFIVFARIASWRIIA
	190 200 210 220 230 240
	250 260 270 280 290 300
m630.pep	250 260 270 280 290 300 GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
a 630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW
	250 260 270 280 290 300
	310 320 330 340 350
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX
n 630	
a 630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX 310 320 330 340 350
	330 330

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2033>: g635.seq

- 1 ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
- 51 GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTTCAGATA CACGATGACG
- 101 GGGATTTTCA ACTGCGCGAG CTGTTCGAAA GACAGGGCAT AGCCTTTCGC
- 151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC 201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
- 251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCGCAGGA

```
301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
         TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
    351
        GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G
This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:
g635.pep
         MTRRRVGKON RIAIHSAQYR KMVVFAVFQI HDDGDFQLRE LFERQGIAFR
         LKTQIGHNAP HILKRRAHLF LTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG
     51
        KIQILLYNIE IPPRFPTLQF DFSVNNRIIV KHRCSIQTIR QGSVPD*
    101
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2035>:
m.635.seq
         ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
        GCAATACCGA GAAATGATCA TCCTTGCGGT ATTTCAGATA CACGATGACG
     51
        GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
    101
        TTCAAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG
    151
    201 GCATCTGCTC CTTATCCAGT TTTTTTAACA CGTCCTCTTC CGTCAGCTTT
        TGCCCGTAAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCGCAGGA
    301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
    351 TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA
This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:
m635.pep
         MTQRRVGKQN RIAVYTAQYR EMIILAVFQI HDDGDLQLCK LLERQGIAFR
        FKTOIRHNAP HILKRRGHLL LIOFF*HVLF ROLLPVKIVO KRHHRSRPAG
     51
        KIQILLYNIE IAPFFPTLHF DFSISNRIIV D*
    101
m635/q635 80.0% identity in 130 aa overlap
                            20
                                     30
                                               40
           MTORRVGKONRIAVYTAOYREMIILAVFOIHDDGDLOLCKLLEROGIAFRFKTQIRHNAP
m635.pep
            MTRRRVGKQNRIAIHSAQYRKMVVFAVFQIHDDGDFQLRELFERQGIAFRLKTQIGHNAP
g635
                                              40
                                                        50
                   10
                            20
                                     30
                            ឧក
                                     90
                                             100
           HILKRRGHLLLIQFFXHVLFRQLLPVKIVQKRHHRSRPAGKIQILLYNIEIAPFFPTLHF
m635.pep
            HILKRRAHLFLTQFFQHFFFRQLLPVKIVQKRRHRSRPAGKIQILLYNIEIPPRFPTLQF
g635
                   70
                                             100
                                                       110
                            80
                                     90
                  130
m635.pep
            DFSISNRIIVDX
            1111::1111
           DFSVNNRIIVKHRCSIQTIRQGSVPDX
g635
                  130
                           140
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2037>:
     a635.seg
               ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC
               GCAATACCGA GAAATGATCA TCCTTGCGGT ATTTCAGATA CACGATGACG
          101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCGC
          151 CTCAAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC
          201 GCATCTGCTC CTTATCCAGC TTTTTCAACA CGTCCTCTTC CGTCAGCTTT
          251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCGCAGGA
          301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC
               TCTGCACTTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA
This corresponds to the amino acid sequence <SEO ID 2038; ORF 635.a>:
     a635.pep
               MTQRRVGKQN RIAVYTAQYR EMIILAVFQI HDDGDLQLCK LLERQGIAFR
            1
               LKTQIRHDAP HILKRRAHLL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
           51
          101 KIOILLYNIE IAPFFPTLHF DFSISNRIIV D*
                   95.4% identity in 131 aa overlap
     m635/a635
                                                          40
                                                                     50
                                                                               60
                           10
                                     20
                                                30
```

```
{\tt MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIAFRFKTQIRHNAP}
m635.pep
          a 635
          MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIAFRLKTQIRHDAP
                70
                        80
                                90
                                       100
          HILKRRGHLLLIQFFXHVLFRQLLPVKIVQKRHHRSRPAGKIQILLYNIEIAPFFPTLHF
m635.pep
          a635
          HILKRRAHLLLIQLFQHVLFRQLLPVKIVQKRRHRSRPAGKIQILLYNIEIAPFFPTLHF
                        80 .
                               90
               130
          DFSISNRIIVDX
m635.pep
          111111111111
          DFSISNRIIVDX
a 635
               130
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2039>: g638.seq

```
ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
 1
    TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
 51
     TTGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
101
151
    TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
    ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCqccqqq CqcqtTCCAA ACGGTAACGC CATTGCCGCG CTCATTCACG
401 CGCAAGGTCG CatCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
    AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGC GCTTTTTCGA GATAAATACC GGCATCCATT
    GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTTGTCC CCTTCGATGG
    TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GGCGCGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CGGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCACG
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGGTAT GGCCGAACAA AATAAAGCAT CATTCAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCCTGAAA CGGTACGGCA AGCGGTTTGG CTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```
1 MIGGQFIVVG IVGKNALARF VDN<u>IVVNIGI VDIVEHDALI</u> AAADGDIVEH
51 FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGKNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 RTMKVYAERI IKNIVVFNQG ARGGFFEINT GIHCWQAHTG TGNGQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNFF VDIKFGLIYA GSQFDRIARP
251 GAGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIAK PPETVRQAVW L*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2041>: m638.seq

```
ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
    TGCCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
 51
    TTGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
101
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTG TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTCACG
    CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCCAAAATA TTGTTGTGTT
    CAATCAGGGC GCGCGGGCA GTTTCTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTCG CCTTCGATGG
    TTGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
651
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA
```

```
This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:
m638.рер
        MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
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     51
        FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFVGVVRAG
        IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
    101
    151
        RTMQIYADRI IQNIVVFNQG ARGSFFEINT GIHCGQAHTG TGNGQVAERY
        VRRVYGYGTP APVAFDGCGT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
    201
        GAGKCGIPIS IIGS*
    251
m638/g638 88.2% identity in 254 aa overlap
                                             40
                                                     50
           MIGEKFIVVGIIGKYALACLVDNVVVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHQHI
m638.pep
           MIGGQFIVVGIVGKNALARFVDNIVVNIGIVDIVEHDALIAAADGDIVEHFEPFGKHQHI
q638
                  10
                           20
                                    30
                                             40
                                                    110
                                                              120
                  70
                           80
                                    . 90
                                            100
m638.pep
           AHIVAHGNIAADFAVVGVHIVDGETQIAEAVVFVGVVRAGIGKNAVPPFGNVVADDLRTG
           AHIVAHGNIAADFAVVGVHIVDGETQVAEAVVFIGVVRAGIGKNAVPPFGNVVADDLRAG
g638
                  70
                           80
                                    90
                                            100
                                                     170
                                                              180
                 130
                          140
                                   150
                                            160
           CVPNGNAVAALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIVVFNQGARGSFFEINT
m638.pep
            RVPNGNAIAALIHAQGRIADDFILAHHRIGRTMKVYAERIIKNIVVFNQGARGGFFEINT
g638
                          140
                                   150
                                            160
                                                     170
                                                              180
                 130
                                                              240
                 190
                          200
                                   210
                                            220
                                                     230
           GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCGTVGRPFNRNRFVNVKFGFIYA
m638.pep
           GIHCWQAHTGTGNGQVAERYVRRVYGYGTPALVPFDGCGTVGRPFNRNRFVDIKFGLIYA
q638
                                   210
                                                    230
                 190
                          200
                                            220
                          260
                 250
           GSQFERIARPGAGKCGIPISIIGSX
m638.pep
           1111:111111111
           GSQFDRIARPGAGKNFGKVVLRGNVDDGCRCRLKNAAGGKYQHGLQPYTERGCVHSVPLF
a638
                                            280
                                                     290
                 250
                          260
                                   270
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2043>:
     a638.seq
               ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
           51
               TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
               TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
               TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCCACGG
               AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
          201
               AAACGCAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
          251
              ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
               GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTCACG
          351
               CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
          401
          451
               AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
          501
               CAATCAGGGC GCGCGGGCA GTTTCTTCGA GATAAATACC GGCATCCATT
               GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
               GTCCGGCGCG TGTACGCCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
          601
               TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
               AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
          701
               GGCGCGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA
This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:
     a638.pep
               MIGGOFIVVG IVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
            ī
               FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
           51
               IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
          101
               RTMQIDADRI IQNIIVFNQG ARGSFFEINT GIHCGQAHTG TGNGQVAERY
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VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGLIYA GSQFERIARP

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251 GAGKCGIPIS IIDSW*
                  91.3% identity in 264 aa overlap
     m638/a638
                          10
                                    20
                                              30
                                                        40
                                                                  50
     m638.pep
                  MIGEKFIVVGIIGKYALACLVDNVVVNIGIVDIVEHNALIAAADGDIVEYFEPLGKHOHI
                  MIGGQFIVVGIVGKNALARFVDNVVVNIGIVDIVEHDALVAAADGDIVKHFEPLGKHQHI
     a 638
                                    20
                                                        40
                                             30
                                                                 50
                                              90
                                                      100
                                                                110
     m638.pep
                  AHIVAHGNIAADFAVVGVHIVDGETQIAEAVVFVGVVRAGIGKNAVPPFGNVVADDLRTG
                  AHIVAHGNIAADFAVVGVHIVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNIVADDLRAG
     a638
                          70
                                   80
                                             90
                                                      100
                                                                110
                                                                          120
                         130
                                   140
                                            150
                                                      160
                                                                170
     m638.pep
                  CVPNGNAVAALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIVVFNQGARGSFFEINT
                   RVPNGNAIAALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQGARGSFFEINT
     a 638
                         130
                                   140
                                            150
                                                      160
                                                                170
                                                                          180
                         190
                                   200
                                            210
                                                      220
                                                                230
                                                                          240
                  GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCGTVGRPFNRNRFVNVKFGFIYA
     m638.pep
                  GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGCRTVGRPFNRNRFVDVKFGLIYA
     a638
                         190
                                   200
                                            210
                                                      220
                                                                230
                         250
                                   260
     m638.pep
                  GSQFERIARPGAGKCGIPISIIGSX
                  GSOFERIARPGAGKCGIPISIIDSWX
     a 638
                         250
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2045>:
g639-1.seq
      1 ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
        GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
        ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
    101
        GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGAA
        CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCAAA GGGCGGGACG
    251
        GCATTTTTC CAATACCAGC ACGCACAACA CCTATAAAAA CAACCGCTTC
        AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
        CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
    351
        CCGAACGGCT CAAAGTGTTC GACAATATCG CCGTCGGCAG CCGCGATTAG
    451
        GGCATCATGC TCAACTATGT CAACTATTCC GATATTCACG ACAATATTAT
    501
        CAACAAAGCG GGCAAGTGCG TTTTTGCCTA CAATGCCAAC TACGATAAAC
        TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
    601
        GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
    651
        CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
        ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
    701
        TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
        GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
    801
        TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
        GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
    901
        TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
        AACGGGGCAG GGCGGAAAAC GGTTCTTTGA ACTAG
This corresponds to the amino acid sequence <SEO ID 2046; ORF 639-1.ng>:
g639-1.pep
        MSLPAMDAGI YLEKAAPRAL VEHNNIFDNS FGVYLHGSAD AMVRENKIVG
      1
     51
        DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
    101 SDLRFAVHYM YTNDSEVSGN ISVGNNMGYV LMFSERLKVF DNIAVGSRD*
        GIMLNYVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
    201 AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYWSD NSPFDLNGDG
        FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAQ FPAVLPGGVV
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2047>:

DSKPLMKPYA PKIQTRYQAM KDELLKEAET RQSERGRAEN GSLN*

```
m639-1.seq
      1 ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAACTGCCCC
     51
         GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
         ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
    101
    151
         GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
         CGCACCCGGT GCGCAGGTCG TCGGCAACGA CATTTCCAAA GGGCGGGACG
    201
         GCATTTTTC CAATACCAGC ACGCACAACA CCTACAAAAA CAACCGCTTC
    251
    301
         AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
         CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
    351
         CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
    401
         GGCATTATGC TCAACTATGT CAACTATTCC GATATTCACG ACAACATTAT
    451
    501
         CAACAAGGCA GGCAAGTGCG TATTTGCCTA TAATGCCAAC TACGATAAAC
    551
         TTTTCGCCAA TCATTTTGAA AACTGTCAAA TCGGCATACA CTTTACCGCC
         GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
    601
         CCAGGTCAAA TACGTCAGCA CGCGCTTTCT CGATTGGAGC GAGGGCGGAC
    651
         ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
    701
         TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
    751
         GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
    851
         TCAAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCTGG CGGCGTGGTG
         GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
    901
         TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
    951
         AATGGGGCAG GGCGGAAAAC GGTTCTTTGA ACTAG
This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:
m639-1.pep
        MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
        DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
     51
    101
         SDLRFAVHYM YTNDSEISGN ISVGNNMGYV LMFSERLKVF DNIAVGSRDQ
         GIMLNYVNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
    201
         AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYWSD NSAFDLNGDG
         FGDSAYRPNG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAQ FPAVLPGGVV
    251
         DSKPLMKPYA PKIQTRYQAM KDELLKEVET RQSEWGRAEN GSLN*
g639-1/m639-1
               95.9% identity in 344 aa overlap
                   10
                            20
                                     30
                                              40
                                                       50
g639-1.pep
           MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG
            MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG
m639-1
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                                     30
                                              40
                                                       50
                                                                60
                            80
                                     90
                                             100
                                                      110
g639-1.pep
           NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEVSGN
            m639-1
           NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEISGN
                            80
                                     90
                                             100
                                                      110
                  130
                           140
                                    150
                                                      170
                                             160
                                                               180
           ISVGNNMGYVLMFSERLKVFDNIAVGSRDXGIMLNYVNYSDIHDNIINKAGKCVFAYNAN
g639-1.pep
           m639 - 1
           ISVGNNMGYVLMFSERLKVFDNIAVGSRDQGIMLNYVNYSDIHDNIINKAGKCVFAYNAN
                  130
                           140
                                    150
                  190
                           200
                                    210
                                             220
           YDKLSANHFENCQIGMHFTAAIEGTSLHDNSFINNGSQVKYVSTRFLDWSEGGHGNYWSD
g639-1.pep
            YDKLFANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYWSD
m639-1
                  190
                           200
                                    210
                                             220
                                                      230
                  250
                           260
                                    270
                                             280
           NSPFDLNGDGFGDSAYRPDGIIDQIIWRAPVSRLLMNSPAISIVKWAQAQFPAVLPGGVV
g639-1.pep
           m639-1
           NSAFDLNGDGFGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAQFPAVLPGGVV
                  250
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                                             280
                                                      290
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                  310
                           320
                                    330
                                             340
g639-1.pep
           DSKPLMKPYAPKIQTRYQAMKDELLKEAETRQSERGRAENGSLNX
           m639 - 1
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                  310
                           320
                                    330
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The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2049>: a639-1.seq

1	ATGAGCCTGC	CCGCAATGGA	TGCCGGTATT	TATCTCGAAG	AAACTGCCCC
51	GCGCGCCCTG	ATTGAACACA	ATAATATTTT	GGATAATTCG	GTCGGCGTCT
101	ATCTGCATGG	TTCTGCCGAT	GCGATGGTGC	GGGAGAATAA	AATCGTCGGC
151	GACGCGACTT	TGCGCGTGAA	CGAGCGCGGC	AATGGCGTTA	CCGTTTGGAA
201	CGCGCCCGGC	GCGCAGGTCG	TCGGCAACGA	TATTTCCAAA	GGGCGGGACG
251	GCATTTTTTC	CAATACCAGC	ACGCACAACA	CCTATAAAAA	CAACCGCTTC
301	AGCGATTTGC	GTTTCGCCGT	CCACTATATG	TACACCAACG	ACAGCGAAAT
351	CAGCGGCAAT	ATTTCCGTGG	GCAACAATAT	GGGCTATGTG	CTGATGTTTT
401	CCGAGCGGCT	CAAAGTGTTT	GACAATATCG	CCGTCGGCAG	CCGCGACCAA
451	GGCATCATGC	TCAACTATGT	CAACTATTCC	GATATTCACG	ACAACATTAT
501	CAACAAAGCG	GGCAAGTGCG	TTTTTGCCTA	CAATGCCAAC	TACGATAAAC
551	TGTCCGCCAA	TCATTTTGAA	AACTGCCAAA	TCGGCATACA	CTTTACCGCC
601	GCCATCGAAG	GCACGTCCCT	GCACGACAAT	TCCTTTATCA	ACAACGAAAG
651	CCAGGTCAAA	TACGTCAGCA	CGCGCTTTCT	CGACTGGAGC	GAGGGCGGAC
701	ACGGCAACTA	TTGGAGCGAC	AACAGCGCGT	TCGATTTGAA	CGGCGACGGC
751	TTCGGAGACA	GCGCGTACCG	TCCCAACGGC	ATCATCGACC	AAATCATCTG
801	GCGCGCACCC	GTATCGCGCC	TCTTGATGAA	CAGTCCCGCA	ATCAGCATCG
851	TCAAATGGGC	GCAGGCGCAA	TTTCCCGCCG	TTTTGCCTGG	CGGCGTGGTG
901	GACAGCAAAC	CGCTGATGAA	GCCTTATGCC	CCCAAAATTC	AAACCCGTTA
951	TCAGGCGATG	AAGGACGGGC	TGCTCAAAAA	AGTCGAAACG	CGGCAGTTGG
1001	AATGGGGCAG	GGCGGAAAAC	GGTTCTTTGA	ACTAG	

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>: a639-1.pep

```
1 MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
```

- 51 DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
- 101 SDLRFAVHYM YTNDSEISGN ISVGNNMGYV LMFSERLKVF DNIAVGSRDQ
- 151 GIMLNYVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
- 201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYWSD NSAFDLNGDG 251 FGDSAYRPNG IIDOIIWRAP VSRLLMNSPA ISIVKWAQAQ FPAVLPGGVV
- 301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

a639-1/m639-1 98.8% identity in 344 aa overlap

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                        20
                               30
                                       40
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         MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG
a639-1.pep
          m639-1
          MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG
                10
                       20
                               30
                                       40
                                                      60
                       80
                               90
                                      100
                                             110
         NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEISGN
a639-1.pep
          NGVTVWNAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEISGN
m639-1
                70
                        80
                               90
                                      100
                                              110
                                                      120
               130
                       140
                              150
                                      160
                                              170
                                                      180
          ISVGNNMGYVLMFSERLKVFDNIAVGSRDQGIMLNYVNYSDIHDNIINKAGKCVFAYNAN
a639-1.pep
          ISVGNNMGYVLMFSERLKVFDNIAVGSRDOGIMLNYVNYSDIHDNIINKAGKCVFAYNAN
m639-1
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                                      160
                                                      180
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                                      220
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a639-1.pep
          YDKLSANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYWSD
          m639-1
          YDKLFANHFENCQIGIHFTAAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYWSD
               190
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                                      220
                                              230
                                                      240
               250
                       260
                              270
                                      280
                                              290
          NSAFDLNGDGFGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAQFPAVLPGGVV
a639-1.pep
          m639 - 1
          NSAFDLNGDGFGDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAQFPAVLPGGVV
               250
                       260
                              270
                                      280
                                              290
               310
                       320
                              330
          DSKPLMKPYAPKIQTRYQAMKDGLLKKVETRQLEWGRAENGSLNX
a639-1.pep
          m639-1
          DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX
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WO 99/57280 PCT/US99/09346

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2051>:
     q640.seq
              ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
           1
             TATGTCCTGT TTTTCAATCC GGCGTATGTC TGCGTTTCGG GCGCGGATAA
           51
          101 CGGCGTTTTT TACCGCCTTT GTCTTTTTGA CGGcggcACT GCCCGCTTAT
              GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
              TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
          251
              GCqtttaCAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
          301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
          351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
          401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTCGA TAAGTTCATC
          451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
          501 GGCGCCGGGC GACATCATCA GcggtGCGAC TgttaCACTG ATGGTGGTTA
          551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
          601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
          651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
          701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
              CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
          801 GGCCGGCGTG GCCGATCACG CCGAACAGGG CGATCCTGAC GATACCTTTA
         851 TTGATTTGTA TGTTGCCTTG GTCAGCCAGC CTTCCATCGG TAAAAGCCTG
         901 CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCGGGCA
         951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCGG
         1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
         1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
         1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAAGT TTCTTGGTTT ACCATCCCTG
         1151 AAGGCGTAGC GTTTGACGGT GCGGAGCCGT GGCGGCTGTA A
This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:
     g640.pep
              MIHIISILKS IGISGIAMSC FSIRRMSAFR ARITAFFTAF VFLTAALPAY
              AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
              AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
              DKYIGLNFIK NPPTPSVAPG DIISGATVTL MVVNDSIQRS YKVIANQYRL
              GSDKALQTAS ASDVREAAPA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
          251 LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
          301 LGEDGWAHLQ KRLKPGQQAV LVAGEGRYSW KGSGYVRGGI FDRIEMIQGE
          351 NSFRFTDAQH ERVVELSAAD APRFKEVSWF TIPEGVAFDG AEPWRL*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2053>:
     m640.seg (partial)
              ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
              CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
              CGGCGTTTTT TGCCGCCTTT GTCTTTTTGA CGGCGGCACT GCCCGCTTAT
              GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
              TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
          251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
          301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
          351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
          401 AACCGATTAT GCTGATCGGT ATCCCGCAT...
This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:
    m640.pep
               (partial)
              MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
              AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
              AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...
m640/g640 96.5% identity in 143 aa overlap
                                             30
                 MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
     m640.pep
                 q640
                 MIHIISILKSIGISGIAMSCFSIRRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK
                         70
                                   80
                                             90
                                                      100
                                                               110
```

```
IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDAVNTRGYSSKPIDTLMVLAN
    m640.pep
                 q640
                 IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDAVNTRGYSSKPIDTLMALAN
                        70
                                  80
                                                    100
                        130
                                 140
                 DGTIAGAKLVDHHEPIMLIGIPH
    m640.pep
                 DGTIAGAKLVDHHEPIMLIGIPOSRVDKFIDKYIGLNFIKNPPTPSVAPGDIISGATVTL
     q640
                                 140
                                          150
                                                    160
                                                             170
                                                                       180
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2055>:
     a640.seq
              (partial)
              ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
           1
              CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
              CGGCGTTTTT TGCCGCCTTT GTCTTTTTGA CGGCGGCACT GCCCGCTTAT
              GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
              TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
              GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
         251
              GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
              GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
             AGTCGATTAT GCTGATCGGT ATCCCGCAT...
This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:
     a640.pep
              (partial) Length: 143
              MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
              AERLPDFLAK IOPSEIVPGA DRYSKPEGKP MVARVYKGDE OLGLVYITTD
              AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHHESIMLIG IPH...
m640/a640 96.5% identity in 143 aa overlap
                                  20
                                                     40
                        10
                                           30
                 MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
    m640.pep
                 MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFVFLTAALPAYAERLPDFLAK
     a640
                        10
                                  20
                                           30
                                                     40
                                                              50
                                                                        60
                                                                       120
                        70
                                  RΛ
                                           90
                                                    100
                                                             110
                 IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDAVNTRGYSSKPIDTLMVLAN
    m640.pep
                 a640
                 IOPSEIVPGADRYSKPEGKPMVARVYKGDEOLGLVYITTDAVNTRGYSSKPIDTLMALAK
                        70
                                  80
                                           90
                                                    100
                                                             110
                       130
                 DGTIAGAKLVDHHEPIMLIGIPH
    m640.pep
                 1111111111111111
                 DGTIAGAKLVDHHESIMLIGIPH
     a640
                        130
                                 140
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2057>:
     q642.seq
              ATGCGGTATC CGCCGCAATC GGCGGTTTTG CAGAATGCCG CGCGTTGCCT
              TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
              TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
              GGTGTCTTCG TGTTCCTCCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
              TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
         201
              TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
         251
              GGcaaagcgG ACatcggtTT Gcacggcgtc gagCAGGGtt tggtTTTTGT
         301
              CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAACTGG
         351
              TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
         401
              GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
         451
              CCTTCGCGCC CAAGAGTTTT TGCAACATTT GCGCGGCGGC GTAAGTGTAT
         551 TCCGTGGCGa ggGTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
              ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCGG
              AAACCTGATG GCGGCGTTGG ATTTCGCGGC GTTCGTAATC GACGAATCTG
```

```
701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
     GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
     GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
 851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGCGCG
 901 CAGGCCTTCG GATGCGAGGG TTTCGCAGCG GATGTATGTT TTGGGGACGA
 951 GCAGCAGGTC GATGactttg gcgagtttgC Cgtttttgcg ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTCGCGGC
1051 GttgACGTAA ATGGTTtgtt cgtcggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAt cgCcgcgccg gaggtTtcgg gttcggtaAc gcccaaacgg
1151 cggctttcgc ctTTGAAAAT CATGTCCAAA CCTTGTGCGA CTTGCgcttc
     gccgccgaac tCTTGCAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251
     TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG
```

## This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```
g642.pep
         MRYPPQSAVL QNAARCLLRR PKSACRRICP LSAISAVQYI FADVVQQEGC
     51 GVFVFLLYED KKSGDDFADE DFLQGAGVGQ GVFLQEAADV FGQSVVAGNG
    101 GKADIGLHGV EQGLVFVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
    151 GADIDGDIAG WVSAFKTLRA QEFLQHLRGG VSVFRGEGFD DVRLHQLMGD
```

- 201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFHN 251 AVRHADQLQA AADKDVLERA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
- QAFGCEGFAA DVCFGDEQQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG VDVNGLFVGI FVAGLHFACN RRAGGFGFGN AQTAAFAFEN HVQTLCDLRF
- 401 AAELLQRLQH QRAFDAGTQR NGHAVMPRNP *

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2059>:

```
m642.seq (partial)
         GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
         CTTTGCGGAT GTCGTTCAGC AGGAAGGCTG CGGTGTCTTC GTGTTTCGCC
         TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTG
    151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
        CTTCAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
         TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACTTCA TGCCTGCTTC
         TTTTTCTTCG GCGGTGGCGC GGACAAACTG GTCGTAAATT TCGGCATAAA
         GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
         ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
         TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
    451
         CGATGTTCGC CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
    501
        GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCCG
    551
    601
         GATTTCGCGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
         GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
    651
    701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
    751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTGCAGGC ATTTCGGCAT
         CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
    851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
    901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
    951 TTTGCGAGTT GCCCTGCCAG TATTTCGCGG CGTTGACGTA AATGGTTTGT
   1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
   1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAAA
```

TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCAGT GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC

# This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

GCCGTAATGC CCCGCAATCC G

1101

```
m642.pep
         (partial)
         ACRRICPLPA ISAVQYIFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
     51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEOG LVFVQLHACF
    101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRTQEF
    151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
    201 DFAAFVIDEF DVVADVSFQI FKDVFHNAVR HADQLQAAAD KDVLERAQTG
     251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEOOVDDF
     301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRRA
     351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQRA FDAGTQRNGH
     401 AVMPRNP
```

### m642/g642 90.4% identity in 407 aa overlap

```
10
                                           20
m642.pep
                             ACRRICPLPAISAVQYIFADVVQQEGCGVFVFRLYED
                             MRYPPQSAVLQNAARCLLRRPKSACRRICPLSAISAVQYIFADVVQQEGCGVFVFLLYED
q642
                 10
                         20
                                 30
                                         40
                                                 50
                                                         60
           40
                   50
                           60
                                   70
                                           8.0
                                                   90
          KESGDDFADKDFLQGAGIGQGVFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLH
m642.pep
          KKSGDDFADEDFLQGAGVGQGVFLQEAADVFGQSVVAGNGGKADIGLHGVEQGLVFVQLN
g642
                 70
                        80
                                90
                                       100
                                                110
          100
                  110
                          120
                                  130
                                          140
                                                  150
          ACFFFFGGGADKLVVNFGIKHIVRAFKNREGADVDSDIAGGVSAFKTLRTQEFLQHLRGG
m642.pep
          g642
          ACFFFFGGGADELVVNFGIKHIVRAFKNREGADIDGDIAGWVSAFKTLRAQEFLQHLRGG
                130
                        140
                                150
                                       160
                                                170
          160
                  170
                          180
                                  190
                                          200
                                                  210
          VSVFRGEGFDDVRLHQLMGDGGNRRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVS
m642.pep
          g642
          VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDESDIVADIS
                190
                        200
                                210
                                       220
                                                230
          220
                  230
                          240
                                  250
                                          260
                                                  270
          FQIFKDVFHNAVRHADQLQAAADKDVLERAQTGSVALGEFHHGGCRHFGIDAVDGVTDGA
m642.pep
           VQVVKDVFHNAVRHADQLQAAADKDVLERAQTGSVAPGEFHHGGCRHFGIDAVDGVTDGA
q642
                250
                        260
                               270
                                       280
                                                290
                                                       300
          280
                  290
                          300
                                  310
                                          320
                                                  330
m642.pep
          QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVDI
          QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRGVDVNGLFVGI
q642
               310
                        320
                               330
                                       340
                                                350
                                                       360
          340
                  350
                          360
                                  370
                                          380
                                                  390
          {\tt FVVGLHFACNRRAGGFGFGNTQTAALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQR}
m642.pep
          q642
          FVAGLHFACNRRAGGFGFGNAQTAAFAFENHVQTLCDLRFAAELLQRLQHQRAFDAGTOR
               370
                        380
                               390
                                       400
                                                410
                                                        420
          400
          NGHAVMPRNP
m642.pep
          111111111
          NGHAVMPRNPX
a642
                430
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2061>:

42.seq	(partial)				
1	GCCTGCCGCC	GTATTTGCCC	GCTATCCGCA	ATATCGGCAG	TCCAATATGT
51	CTTTGCGGAT	GTCGTTCAGC	AGGAAGGCTG	CGGTGTCTTC	GTGTTCCGCC
101	TGTACGAAGA	CAAAGAGTCG	GGCGATGATT	TTGCCGATAA	AGACTTTTTG
151	CAGGGCGCAG	GCATCGGTCA	GGGTGTGTTC	CTGCAGGAAG	CTGCGGATGT
201	CTTCGGGCAA	AGTGTAGTCG	CGGGCGACGG	CGGCAAAGCG	GGCATCGGTT
251	TGCAGGCGGT	CGAGCAGGGT	TTGGTTTTTG	TCCAACTTCA	TGCCTGCTTC
301	TTTTTCTTCG	GCGGTGGCGC	GGACAAACTG	GTCGTAAATT	TCGGCATAAA
351	GCATATCGTT	CGGGCCTTCA	AAAATCGTGA	AGGGGCGGAT	GTCGATAGCG
401	ATATTGCCGG	CGGTGTGTCC	GCGTTCAAAA	CCCTTCGCGC	CCAAGAGTTT
451	TTGCAACATT	TGCGCGGCGG	CGTAAGTGTA	TTCCGTGGCG	AGGGTTTTGA
501	CGATGTTCGC	CTCCATCAGT	TGATGGGCGA	CGGGTGCAAC	GGGCGAAACG
551	GAATGGCAGA	CGTAGCGGTA	AAGAATCTCG	GAAACCTGAT	GGCGGCGCCG
601	GATTTCGCGG	CGTTCGTAAT	CGACGAATCT	GATGTCGTTG	CGGACGTATC
651	GTTCCAGGTT	TTCAAGGGTG	TATTCCATAA	TGCCGTGCGT	CATGCCGATC

701 751 801 851 901 951 1001 1051 1101 1151	AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTGCAGGC ATTTCGGCAT CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC TTTGCGAGTT GCCCTGCCAG TATTTCGCGG CGTTGACGTA AATGGTTTGT CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGC GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCAGT GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC GCCGTAATGC CCCGCAATCC G
This correspond	s to the amino acid sequence <seq 2062;="" 642.a="" id="" orf="">:</seq>
a 642.pep  1 51 101 151 201 251 301 351 401	Length: 407  ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP DFAAFVIDES DVVADVSFQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
m642/a642 95.8	% identity in 407 aa overlap
m642.pep	10 20 30 40 50 60 ACRRICPLPAISAVQYIFADVVQQEGCGVFVFRLYEDKESGDDFADKDFLQGAGIGQGVF
a 642	ACRRICPLSAISAVQYVFADVVQQEGCGVFVFRLYEDKESGDDFADKDFLQGAGIGQGVF  10 20 30 40 50 60
m642.pep a642	70 80 90 100 110 120 LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFFGGGADKLVVNFGIKHIV
m642.pep a642	130 140 150 160 170 180 RAFKNREGADVDSDIAGGVSAFKTLRTQEFLQHLRGGVSVFRGEGFDDVRLHQLMGDGGN
m642.pep a642	190 200 210 220 230 240 RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVSFQIFKDVFHNAVRHADQLQAAAD
m642.pep a642	250 260 270 280 290 300  KDVLERAQTGSVALGEFHHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
m642.pep a642	310 320 330 340 350 360 GEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVDIFVVGLHFACNRRAGGFGFGNTQT
m642.pep a642	370 380 390 400  AALAFENHLQTLRDLRFIAELLQWLQHQRAFDAGTQRNGHAVMPRNP

WO 99/57280 PCT/US99/09346

1021

370 380 400 390 The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2063>: q643.seq ATGGTGTTGC CTTTGATGTT GTTGGCGACA ATCAGGTcgg CTACGCTGAc 51 gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTCGCCGTC GGCAGCTTTG 101 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCGG CGGCAACGGT 151 201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC CGATGACGGC GGagaTGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG 251 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAt 301 GACCTGCGCg aGTGtTGCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT 351 401 TTTcggTTTG a This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>: q643.pep MVLPLMLLAT IRSATLTLXR LAMLNRVSPS TTRWMLAWSG EVSASPSAAL 1 ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR 51 101 ATSCMSSSAA CMSFGGMTCA SVAVWVSDGM AVCFSV* The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2065>: m643.seq ATGGTGTTGC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC 1 51 GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT 101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT 151 ATGTTGCGGA GATGCGGAAA TTTTGTGTTC GGCAACTGTG TCAGGCGTGC 201 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTTCGG 251 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT GATCTGCGCG AGTGTTGCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT 351 TTTCGGTTTG A 401 This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>: m643.pep MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL 1 ATRVSKRTRR LPSAAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR 51 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV* Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. meningitidis menA with menB ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from N. gonorrhoeae: m643/g64310 20 30 40 MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR m643.pep  ${\tt MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR}$ g643 10 20 30 40 70 80 90 100 m643.pep LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFGGMTCA g643 70 80 90 100 110 120 130

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2067>:

m643.pep

g643

```
a643.seq
              ATGGTGTTGC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
           1
             GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
          51
              GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCGCCGTC GGCAGCTTTG
         101
         151
201
              GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
              ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
              CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTTCGG
         251
              GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
         301
              GATCTGCGCG AGTGTTGCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
         351
         401 TTTCGGTTTG A
This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:
    a643.pep
              MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
              ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
         101 ATSCMSSSAA CMSFWGT<u>ICA SVAVWVSDGM AVC</u>FSV*
    m643/a643
                 97.1% identity in 136 aa overlap
                                                              50
                                           30
                                                    40
                        10
                                 20
                 MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR
    m643.pep
                 MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR
    a 643
                                                              50
                                 20
                                           30
                                                    40
                                                             110
                                                                      120
                                           90
                                                   100
                        70
                                  80
                 LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA
    m643.pep
                 LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGTICA
     a643
                                 80
                                           90
                                                   100
                        70
                       130
                 SVAVWVSDGMAVCFSVX
     m643.pep
                 11111111111111111
                 SVAVWVSDGMAVCFSVX
     a643
                       130
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2069>: 9644.seq

```
ATGCCGTCTG AAAGGCCGGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
     GTTTAGAAAA TTAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
 51
     TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
101
     CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
201 ATTCCCCCGC ATTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
     AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
251
     GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
301
     CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
351
     TCGAAGGCGC GCTGGTGTTG CAGCCTCTGC AAGagttcgg cggcgaagcG
     CAAGTCGCAC AAGGTTTGGA CATGATTTTC AAaggcgaaa gccgccgttt
451
     gggcgTtacc gaacccgaAa cctccggcgc gGcgaTTGCA CGCGAAAtgc
     agtoctgota cgaatatacc gacgaacaAA CCATTTACGT caaCGCCGCG
551
601 AAATACTGGC AGGGCAATTC GCAAAGCGAC TTCCTcctcg ttgccgccaa
     agagegeaaa aacGGeaaac tegeeaaagt CATCGACCTG CTGCTCGTCC
651
     CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
701
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCCGGGGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
     TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
851
     GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
901
     CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCCATCAG GTTTCCGAAA
951
     TCCTTTACCG CTACGTCTGC CATTCCGTTT CGcccgtcgC GCccgTCGCC
1001
     CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
1051
     TTACGCCGCC GCGCAAATGT TGCAAAAACT CTTGGGCGCG AAGGGTTTTG
1101
     AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1151
     ATTTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1201
     CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
1251
1301 accaaaCCCT Gctcgacgcc gtgCAAaccg atGTCcgctt tgCCGCCGTT
     GCCcgcGacT ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GACGCCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA
```

```
TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
    1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
    1551 ATAG
This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:
         MPSERPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
         QPSTMDTAAF LKHIESAFPR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
      51
     101
         DKKHGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGGEA
     151 QVAQGLDMIF KGESRRLGVT EPETSGAAIA REMQSCYEYT DEQTIYVNAA
         KYWQGNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
     251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIFIRSRL QLIGMTHGIM
     301 EYILDNLNRY VRNDIRFVDY ERREIQRRHQ VSEILYRYVC HSVSPVAPVA
         HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
     401 IFEGPNDMLY AEIYDQFVRA TAEEKEAGIK LDKNQTLLDA VQTDVRFAAV
     451 ARDYALPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQEEHEDTTA
        FLLNDIRKDI LDCRYCG*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2071>:
m644.seg
         ATGCCGTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
         GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
     51
     101
         TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
         CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
         ATTCCGCCGC ATTTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
         AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
         GACAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAGT
         CCTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
         TCGAAGGCGC GCTGGTGTTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
         CAAGTCGCGC AAGGTTTGGA GATGATTTTC AAAGGCGAGG GCGGCGGTTT
         GGGTGTTACC GAACCCGAAA CCTCCGGCGC GGCGATTGCA CGCGAAATGC
     501
         AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
     601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
        AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
         CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
         GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
    751
     801 GATGAAACTC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
        TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
    851
         GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
         CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCCGAGA
    951
   1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCTGTTGC CCCCGTCGCC
   1051 CATCAGCTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
         TTACGCCGCC GCGCAAATGT TGCAAAAACT CTTGGGTGCG AAGGGTTTTG
   1151 AACGCGGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
   1201 ATTTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
   1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
        ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
   1351 GCCCGCGACT ACACTTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
   1401 CACCCTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
         TCGCCCGACT CTTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
   1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:
      1 MPSERSADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
         QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL
    101 DKKYGGRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGDEA
    151 QVAQGLEMIF KGEGGGLGVT EPETSGAAIA REMQSYYEYI DGQTIYVNAA
         KYWQGNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
         VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIFIRSRL QLIGMTHGIM
     301 EYILENLERY VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
     351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
     401 IFEGPNDMLY AEIYDQFVRA TAEEKEAGMK LDKNQTLLDR LQTDARFAAV
         ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAKHEDTAA
     501 FLLNDIRKDI LDCRYCG*
m644/g644 94.6% identity in 517 aa overlap
                              20
                                        30
            MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep
            g644
            MPSERPADCCPVHFVVKFRKLTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
```

	10	20	30	40	50	60
m644.pep	70 LKHIESAFRRIFSD !!!!!!!! !!!!! LKHIESAFPRIFSD 70	1111111111	нинін	111111111:	111111111111111111111111111111111111111	111111
m644.pep g644	130 AGHYGVPVTLRTGI             AGHYGVPVTLRTGI 130	111111111		11:111111:	1111111	
m644.pep	190 REMQSYYEYIDGQT               REMQSCYEYTDEQT 190	шшші	пішп	11111111111	111111111111111111111111111111111111111	111111
m644.pep	250 ETLASEGLRAVRYA !!!!!!!!!!!! ETLASEGLRAVRYA 250		111111111111111111111111111111111111111	шшін	пинийн	
m644.pep	310 EYILENLERYVRND     :  :      EYILDNLNRYVRND 310	1:1111111	1:11111111	шшш	111111111	111111
m644.pep	370 TLATEYTYAAAQML           TLATEYTYAAAQML 370		111 11111	нини	11111111111	11111
m644.pep	430 TAEEKEAGMKLDKN !!!!!!!! TAEEKEAGIKLDKN 430	1111: 1111	1111111111	:111111111	ÎH III II II II	111111
m644.pep g644	490 GKIIARLFVFVQAK            : GKIIARLFVFVQEE 490	1111:1111	ПППППП	1111		

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2073>:

```
a644.seq
         ATGCCGTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
         GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
     51
    101
         TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
     151
         CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
     201
         ATTCCGCCGC ATTTTTGCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
         AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
     251
         GACAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
     301
     351
         CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
         NNGAAGGCGC GCTGGTGTTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
     401
         CAAATCGCAC AGGGTTTGGA CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
     451
         AGGCGTTACC GAACCCGAAA CCTCCGGCGC GGCGATTGCC CGAGAAATGC
         AGTCTTACTA CGAATATACC GACGGACAAA CCATTTACGT CAACGCCGCG
         AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
         AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
     651
         CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
     701
    751
         GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
         GATGAAACTC TCCCAGAGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
     801
```

851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG 901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT

901	
951	
1001	TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051	CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101	
1151	
1201	
1251	TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301	ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351	
1401	
1451	TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501	TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551	
	ds to the amino acid sequence <seq 2074;="" 644.a="" id="" orf="">:</seq>
a644.pep	
1	MPSERSADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
51	QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101	
151	
. 201	KYWQGNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251	VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIFIRSRL QLIGMTHGIM
301	
351	
401	IFEGPNDMLY AEIYDQFVRA TAEEKEAGMK LDKNQTLLDR LQTDARFAAV
451	ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501	
301	FILINDIKKDI IDCKICG
m644/a64	4 97.3% identity in 517 aa overlap
	10 20 30 40 50 60
m644 non	
m644.pep	${\tt MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF}$
m644.pep	
m644.pep	${\tt MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF}$
	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
a644 m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644 m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644  m644.pep a644  m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644 m644.pep a644 m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644  m644.pep a644  m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
m644.pep a644  m644.pep a644  m644.pep a644	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF

	310	320	330	340	350	360
	370	380	390	400	410	420
m644.pep	TLATEYTYAAAQML	QKLLGAKGF	ERGHTAGNIAI	DIRPFTIFE	GPNDMLYAEI	/DQFVRA
	11111111111111111	11111111	11111111111			
a644	TLATEYTYAAAQML	OKLLGAKGE	ERGHTAGNIAI	DIRPFTIFE	GPNDMLYAEI:	YDQFVRA
4011	370	380	390	400	410	420
	430	440	450	460	470	480
m644.pep	TAEEKEAGMKLDKN	OTLLDRLQT	DARFAAVARD	TLPEDIRSF:	LQEHTLTDACA	ALQKVFI
MO11.PGP		THILLIA	1111111111		111111111	
a644	TAEEKEAGMKLDKN	OTLLDRLOT	DARFAAVARD	TLPEDIRSE	LQEHTLTDAC	ALQKVFI
2011	430	440	450	460	470	480
	490	500	510			
m644.pep	GKIIARLFVFVQAK	HEDTAAFLL	NDIRKDILDC	RYCGX		
ollvF-F						
a 644	GKIIARLFVFVQAE	HEDTAAFLL	NDIRKDILDC	RYCGX		
4011	490	500	510			

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2075>:

```
g645.seq
         ATGATGATGG TGTTGGCGTT GGGGATGTCG ATGCCGGTTT CGATGATGGT
         GGAACAGAGC AACACATTGA ATCTTTGCTG CAAAAAGTCG CGCATGACTT
      51
         GTTCCAGCTC GCGCTCACGC AGTTGTCCGT GCGCCACGCC GATACGGGCT
    151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
     201 TTCATTGTGC AGGAAAAata cCTGTCCTCC GCGTTTGAGT TCGCGCAACA
         CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTCACG
     301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
     351 TTCGAGCGCC ATGCTGAGGG TGCGCGGAAT CGGCGTGGCG GTCATGGTTA
     401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGTCGCACG
         CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTTGAATTT
     501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
     551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTTGAAA
     601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTCGGCGAA
     651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTCGGGGCG AGTACGGCGA
     701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GGCGACTTCG
     751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
     801 CTGCGTCAAA TCTTTAATCA CGGcggcgat ggcggcggcC TGGTCTTCGG
     851 TTTCCTCGTA G
```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>: g645.pep

```
1 MMMVLALGMS MPVSMMVEQS NTLNLCCKKS RMTCSSRSR SCPCATPIRA
51 SGSRVSSRSR IFSIVSTSLC RKNTCPPRLS SRNTASRTLP SLNGLTKVFT
101 ARRRLGAVVI SEKSRRPSSA MLRVRGIGVA VMVRMSTLAR RRLSCSFCRT
151 PKRCSSSIIN KPKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSAKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2077>: m645.seq

```
ATGATGATGG TGTTGGCGTT GGGGATATCG ATACCGGTTT CGATGATGGT
 1
51 GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
    TTCATTGTGC AGGAAAAATA CCTGTCCTCC GCGTTTGAGT TCGCGCAACA
251 CGGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTAA
    GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTTGAATTT
501 GATGTCGTCC TGCACCAGTT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTCGGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAAGCGT GGTCGGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GGCGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
    TTGCGTCAAA TCTTTAATCA CGGCGGCGAT GGCGGCGGCC TGGTCTTCGG
```

```
851 TTTCCTCGTA G
```

```
This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:
m645.pep
        MMMVLALGIS IPVSMMVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA
      1
        SGSRVSSRSR IFSIVSTSLC RKNTCPPRLS SRNTASRTLP SLKGLTKVLT
     51
        ARRRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
    101
        PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
        RERLATFICK SAKRSAKFCA CCSTKSVVGA STATCLPPIT ATNAARRATS
    201
        VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*
    251
m645/g645 93.7% identity in 286 aa overlap
                                  30
                                          40
                          20
                 10
           MMMVLALGISIPVSMMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
m645.pep
           MMMVLALGMSMPVSMMVEQSNTLNLCCKKSRMTCSSSRSRSCPCATPIRASGSRVSSRSR
q645
                                  30
                                          40
                 10
                                                  110
                                                           120
                                          100
                  70
                          80
                                  90
           IFSIVSTSLCRKNTCPPRLSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
m645.pep
           []]]]]]
           IFSIVSTSLCRKNTCPPRLSSRNTASRTLPSLNGLTKVFTARRRLGAVVISEKSRRPSSA
a645
                                          100
                                  90
                  70
                          80
                                          160
                                 150
                 130
                         140
           ILKVRGIGVAVMVRISTLARRRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
m645.pep
           MLRVRGIGVAVMVRMSTLARRRLSCSFCRTPKRCSSSIINKPKFLNFMSSCTNLCVPITI
g645
                                 150
                                          160
                 130
                         140
                                                  230
                                 210
                                          220
                 190
                         200
           STVPSAMPSSAALVALLLLKRERLATFTGKSAKRSAKFCACCSTKSVVGASTATCLPPIT
m645.pep
           STVPSAMPSSVALVALLLLKRERLATFTGKSAKRSAKFCACCSTRSVVGASTATCLPPIT
g645
                                          220
                                                  230
                                                           240
                                 210
                         200
                 190
                                          280
                         260
                                  270
                 250
           ATNAARRATSVLPKPTSPHTRRSIGFACVKSLITAAMAAAWSSVSSX
m645.pep
           ATNAARRATSVLPKPTSPHTSRSIGFACVKSLITAAMAAAWSSVSSX
a 645
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2079>:

280

270

260

250

```
a645.seq
         ATGATGATGG TGTTGGCGTT GGGAATGTCG ATACCGGTTT CGATGATGGT
      1
         GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
         GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
         TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
         TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
     201
         CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
         GCGAGGCGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
     301
         TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
     351
         GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
          CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
     451
          TATGTCGTCC TGCACCAGTT TGTGCGTACC GATAACAATA TCGACCGTGC
          CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTTGAAA
     551
          CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTCGGCAAA
     651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTCGGTGCG AGTACGGCAA
         CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GGCGACTTCG
         GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
          CTGCGTCAAA TCTTTAATCA CGGCGGCGAT GGCGGCTGCC TGGTCTTCGG
     801
          TTTCTTCGTA G
     851
```

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep

1 MMMVLALGMS IPVSMMVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA

51 101 151 201	SGSRVSSRSR MFSMVS ARRRLGAVVI SEKSRS PKRCSSSIIT KPTFLN RERLATFTGK SAKRSA	PSSA ILKVI FMSS CTSLO	RGIGVA VMVF CVPITI ST <u>VF</u>	RMSTLAR RRI PSAMPSS AAI	SCSF*RT VALLLLK	
251	VLPKPTSPHT RRSIGE				THE WOOD IN	
m645/a645	96.9% identity	in 286 aa	overlap			
m645.pep	10 MMMVLALGISIPVS:        :					
a645	MMMVLALGMSIPVSI 10					
m645.pep	70 IFSIVSTSLCRKNT					
a645	:  :           MFSMVSTSLCRKNT( 70					
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVR	: 111111111		1111111111	11:111111	
a645	ILKVRGIGVAVMVRI 130	MSTLARRRLS 140	SCSFXRTPKRC 150	SSSIITKPTF 160	LNFMSSCTSI 170	LCVPITI 180
m645.pep	190 STVPSAMPSSAALVA		210 .ATFTGKSAKR		230 KSVVGASTAT	
a645	STVPSAMPSSAALVA	<i></i>				
m645.pep	250 ATNAARRATSVLPKI	260 PTSPHTRRSI	270 GFACVKSLIT	280 AAMAAAWSSV	SSX	
a645				 AAMAAAWSSV 280		

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2081>: g647.seq

- 1 ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA 51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTTAAAGAG CGTGCACGCT
- 101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
  151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
- 201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
- 251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
- 301 CTGATAATCT AA

### This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>: g647.pep

- 1 MQRLAADGIQ IFFVGVDGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
- 51 GFKGTVGQTE RGTVAVADTV FRQIVGVVDD TDAERTAVHS RGTRGFYRIS

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2083>: m647.seq

- 1 ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTCGA 51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTTAAAGAG CGTGCACGCA
- 101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
- 151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
- 201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
- 251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
- 301 CTGATAATCT AA

## This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>: m647.pep

¹ MQRLAADGIQ IFFVSVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```
51 GFKGTVGQTE RGTVAVADTV FRQIISIVNH ADAERTAAHS RGTRGFYRIS
    101 LII*
m647/g647 91.3% identity in 103 aa overlap
                           20
                                    30
                                            40
                                                     50
                  10
           {\tt MQRLAADGIQIFFVSVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE}
m647.pep
           MQRLAADGIQIFFVGVDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE
q647
                                    30
                                            40
                                                     50
                           20
                  70
                           80
                                    90
           RGTVAVADTVFRQIISIVNHADAERTAAHSRGTRGFYRISLIIX
m647.pep
           RGTVAVADTVFRQIVGVVDDTDAERTAVHSRGTRGFYRISLIIX
a647
                                    90
                  70
                           80
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2085>:
     a647.seq
               GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCGA
            1
               TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTTAAAGAG CGTGCACGCA
           51
               CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
          101
               GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC
          151
               GGACACCGTT TTTCGCCAAA TAATACGCAT AGTTGATCAC GCCGATACCG
               AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
          251
               CTGATAATCT AA
          301
This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:
     a647.pep
               VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
              GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAAHS GGTRGFYRIS
           51
          101
               LII*
                  87.4% identity in 103 aa overlap
     m647/a647
                                              30
                                                        40
                                    20
                  MQRLAADGIQIFFVSVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE
     m647.pep
                  VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE
     a647
                                    20
                                                        40
                                                                  50
                          10
                                                       100
                          70
                                    80
                                              90
                  RGTVAVADTVFRQIISIVNHADAERTAAHSRGTRGFYRISLIIX
     m647.pep
                  RGAVAVADTVFRQIIRIVDHADTERTAAHSGGTRGFYRISLIIX
     a647
                          70
                                    80
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2087>:
g648.seq
         ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
         CGACGTTTTG AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC
     51
         GTGGAAAACA GGTCGGCAGC CGGAATGATA CGCTTGCGTA TGTTCGGGTC
        TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
    151
     201 ACGCTTCGTA CAACCCCGAA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
     251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCATA
         ATCAAGCTGG CGGATACGGT TGTCTTCCAC GCCCCGGTTG TTTTTCAACA
     351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC
         GCGCCGCCGC GCACGCCACC TTGCGAACAA GATTTGACCG CCGCCTGAAA
         CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGGCTTCA CCGCCCCGGA
     451
         TTTCGCTGTC CAGCCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCG
         CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
     551
        CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>: g648.pep

```
MNRRNARIER AVRIAVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV
      1
         LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVDLHAI
     51
         IKLADTVVFH APVVFQHQQA FGFNMPQGVE QGCRAAAHAT LRTRFDRRLK
    101
        HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
    151
        QTIVAFNQHT A*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2089>:
         ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
         CGACGTTTTG AATGTAGATG CGCCCGGTTC CGGCACGCTC CTGCATCAGC
     51
         GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
    101
        TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
    151
        ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
    251
        CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
        ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCGCGGTTG TTTTTCAACA
    301
         CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
         GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTTGACCG CCGCCTGAAA
    401
        CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCCGGA
    451
    501
        TTTCGCTGTC CAAACCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
        CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
    551
        CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA
This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:
m648.pep
        MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
        LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
     51
         IKLTDTVVFH TAVVFQHQQA FGFDMPQGVE QGCRAAAHAA LRTGFDRRLK
    101
         HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
    151
        QTIVAFNQHT A*
m648/g648 91.5% identity in 211 aa overlap
                            20
                                     30
                                                        50
           \verb|MNRRDARIERAVRIAVIDVL| NVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK|
m648.pep
            {\tt MNRRNARIERAVRIAVIDVLNVDAPGPGTLLHQRGKQVGSRNDTLAYVRVLLVFRIEPLK}
q648
                   10
                                               40
                                                        50
                            80
                                     90
                                             100
           FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHTAVVFQHQQA
m648.pep
            FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQAVDLHAIIKLADTVVFHAPVVFQHQQA
a648
                   70
                            80
                                     90
                                             100
                                                       110
                                                                120
                                                       170
                                                                180
                  130
                           140
                                    150
                                             160
            FGFDMPQGVEQGCRAAAHAALRTGFDRRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA
m648.pep
            q648
            FGFNMPQGVEQGCRAAAHATLRTRFDRRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA
                  130
                           140
                                    150
                                             160
                                                       170
                                                                180
                  190
                           200
           DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX
m648.pep
            g648
            DARALGNVFHNRAGSGIDGIQTIVAFNQHTAX
                  190
                           200
                                    210
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2091>:
     a648.seq
               ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
            1
               CGACGTTTTG AATGTAGATG CGCCCGGTTC CGGCACGCTC CTGCATCAGC
           51
               GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
          101
          151
               TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
          201
               ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
          251
               CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCGTA
               ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCCCCGGTTG TTTTTCAACA
          301
               CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
          351
               GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTTGACTG CCGCCTGAAA
          401
```

CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCCGGA

```
TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCA
              CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
              CAGGCTGTCG TCGCATTCGA TCAATACGCA GCTTGA
This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:
     a648.pep
              MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
              LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
           51
              IKLTDTVVFH APVVFQHQQA FGFDMPQGVE QGCRAAAHAT LRTGFDCRLK
          101
          151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
              QAVVAFDQYA A*
                  93.8% identity in 211 aa overlap
     m648/a648
                                                                 50
                                             30
                         10
                                   20
                  MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK
     m648.pep
                  MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK
     a648
                                                                 50
                                                       40
                                             30
                         10
                                                      100
                                                                110
                          70
                                   80
                                             90
                  {\tt FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHTAVVFQHQQA}
     m648.pep
                  FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVDLHAVIKLTDTVVFHAPVVFQHQQA
     a648
                                                                         120
                                                      100
                                                                110
                          70
                                   80
                                             90
                                                      160
                                            150
                                  140
                         130
                  FGFDMPQGVEQGCRAAAHAALRTGFDRRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA
     m648.pep
                  FGFDMPQGVEQGCRAAAHATLRTGFDCRLKHFKEGNAAGMPCFAAPDFAVQSADTSGIDA
     a648
                                                      160
                                                                         180
                                   140
                                            150
                         130
                         190
                                   200
                  DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX
     m648.pep
                  DARTLGNVFHNRAGSGVDGIQAVVAFDQYAAX
     a648
                                            210
                         190
                                   200
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2093>:
g649.seq
         ATGCTTGCCA TACTGTTGTC TGCAATACTG GGACTGGTAT CAACAACTGC
      1
      51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG ACATACCAAA CATATCAGCA
     101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
     151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
         CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA
         TCCAATGCCG GGCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
     251
     301 TTCCGCCGTT AA
This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:
 g649.pep
         MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
       1
         RAAWYRSQGN VQELRENKKA RKAFRTLPYA EQKIQCRAAY EAFDDFDGGR
      51
 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2095>:
 m649.seq
         ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
       1
         CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
      51
         AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
     101
     151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
     201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA
         TCCAATGCCG GGCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
     251
         TTCCGCCGTT AA
```

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>: m649.pep

```
MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKOML HPECRKYLER
        RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
     51
    101
m649/q649 96.1% identity in 103 aa overlap
                                                      50
                                             40
           MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN
m649.pep
           MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERRAAWYRSQGN
a649
                           20
                                    30
                                             40
                  10
                  70
                           80
                                    90
           VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
m649.pep
           VQELRENKKARKAFRTLPYAEQKIQCRAAYEAFDDFDGGRFRRX
g649
                  70
                           80
                                    90
                                            100
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2097>:
     a649.seq
               ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
            1
               CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
           51
          101
               AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
               CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
          151
               CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
               CCCAATGCCG GGCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
               TTCCGCCGTT AA
          301
This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:
     a649.pep
               MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKOML HPECRKYLER
            1
               RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
           51
          101
               FRR*
                  96.1% identity in 103 aa overlap
     m649/a649
                                                        40
                                                                  50
                                              30
                                    20
                          10
                  MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN
     m649.pep
                  MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERRAAWYRSQGN
     a649
                                                        40
                                                                  50
                          10
                                    20
                          70
                                    80
                                              90
                                                       100
     m649.pep
                  VOELRENKKARKAFRSLPYAEOKIOCRAAYEAFDDFDGGSFRRX
                  VQELRENKKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX
     a 649
                                    80
                                              90
                                                       100
                          70
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2099>:
g650.seq
        ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
         TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
     51
         CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
        TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
    151
    201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
        CAAGCCGCAG CTATTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
    251
         TACCATATCG CCAACGAAGT CAAAAAACGC AATATGCCCG CCGAAGCCGC
    301
    351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
    401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
    451 GGCTTGGAAA AAACaccgGT TTACGacggc aggcacGacg TTtacgcaGc
         taccgatgcc gcacTCAACT AtctGcAATA TCTCTAtggA CTGTTCGGCG
    501
    551 ACTGGCCGCT CGCCTTTGCC GCCTACAACT GGGGTGAAGG CAACGTCGGA
     601 CGCGCCGTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
         CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
     651
    701 TGCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC
```

```
751 ATAGACAACA AACCCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
     801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
     851 CCCTGAATCC TGCATTCAAC GTCCCCGCgt tcatCCCCAA AAAcaaacgc
     901 aaacTGCTGC TTCCTGTCGC GTCCGTCCAA ACCTTccaaa gcaACTACCT
     951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
    1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
    1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCA ACGCAGGACG
    1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAAt
    1151 CCGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
    1201 ATGCcggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccgc
    1251 cgcaCAGACA gcggacatta ccgtcgcacc tttgccgcaa gaaaccgtcc
    1301 gtacgggaac ccgatccct tgtccgcaTt accgaacccg ccctTGCGAC
    1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA
This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:
g650.pep
          MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ VGLAIMRLNS SILDLPPTKQ
          YFQSGSLWDE LRQGFRMGEV NPELVRRHES KFIASRSYFD RVVNRSRPYM
      51
     101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
     151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEGNVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
     251 IDNKPYFQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
     301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
     351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDTYRSN
     401 MPAGTVNVSI ARIOPAAAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
     451 SRSATSNRKT DCHAV*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2101>:
          ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
       1
          TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
     101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
     151 TATTTCCAAT CCGGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
     201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
     301 TACCATATCG CCAACGAAGT CAAAAAACGC AATATGCCCG CCGAAGCCGC
     351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
     401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
     451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACG TTTACGCCGC
     501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCGGCG
     551 ACTGGCCGCT TGCCTTTGCC GCCTACAACT GGGGTGAAGG CAACGTCGGA
     601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
     651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
     701 TGCGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
     751 ATAGACAACA AACCCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
     851 CCCTAAACCC CGCATTCAAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
     901 AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
    1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
    1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCA ACGCAGGACG
    1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
    1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
    1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
    1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
    1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA
This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:
m650.pep
       1 MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
      51 YFQSGSLWGE LRQGFRMGEV NPELVRRHES KFIASHSYFN RVINRSRPYM
          YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
     151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEGNVG
```

```
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
    KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNING NIVNAGRSIL VAKNGKTLOT ASESVVSIDI DNTPDTYRSN
401 MPAGTVNVGI ARIRPAAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*
```

		10	20	30	40	50	60
m650.pep	MSKLKT	IALTASGLSV	CPGFLYAQNT	SSHQIGLAIM	RLNSSILDLP	PTKQYFQSGS	LWGE
						1111111111	
g650	MSKLKT.	IALTASGLSV 10	CPGFLYAQNT 20	SSHQVGLAIM 30	40	PTKQYFQSGS 50	7MDF
		10	20	30	40	30	00
		70	80	90	100	110	120
m650.pep						VKKRNMPAEA	
	111111		111111111:	111:11:111			
g650	LRQGFRI	MGEVNPELVR 70	RHESKFIASR 80	SYFDRVVNRS 90	RPYMYHIANE 100	VKKRNMPAEA 110	ALLP 120
		70	80	90	100	110	120
		130	140	150	160	170	180
m650.pep						ATDAALNYLQ	
g650	FIESAF		SGLWQFMPAT 140	GRHYGLEKTP 150	VYDGRHDVYA. 160	ATDAALNYLQ 170	YLYG 180
		130	140	150	160	170	100
		190	200	210	220	230	240
m650.pep	LFGDWP	LAFAAYNWGE	GNVGRAINRA	RAQGLEPTYE	NLRMPNETRN	YVPKLLAVRN	IIAT
						131111111	
g650	LFGDWP					YVPKLLAVRN	
		190	200	210	220	230	240
		250	260	270	280	290	300
m650.pep	POSEGMI					PAFNVPAFIP	
	111111	11111111	HILLIHII III	1111111111	11111111	11111111111	1:11
g650	POSFGMI					PAFNVPAFIP	
		250	260	270	280	290	300
		310	320	330	340	350	360
m650.pep	KLLLPV					MSIADIKRLN	
	111111	шініш	1111111111	1111111111	111111111	F1 F1 F1 F1 F1 F1	$\Pi\Pi$
g650	KLLLPV					MSIADIKRLN	
		310	320	330	340	350	360
		370	380	390	400	410	420
m650.pep	NIVNAG					NVGIARIRPA	
шозо.рер	111111		11:111111			11:1111:11	1111
g650	NLVNAG	RSILVAKNGK	TLHTASESVV	SIDIDNTPDT	YRSNMPAGTV	NVSIARIQPA	AAQT
,		370	380	390	400	410	420
			4.40	450	4.50		
650	3 D.T.M(*3*	430	440 ••••••••••	450 CPCDSRSATS	460 NDVTDDUXVV		
m650.pep		-					
g650				RPCDSRSATS			
3+00		430	440	450	460		

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2103>: a650.seq

• •		-			
50.seq					
1	ATGTCCAAAC	TCAAAACCAT	CGCCCTGACC	GCGTCAGGTC	TGTCCGTTTG
51	TCCGGGTTTC	CTATACGCCC	AAAACACCTC	ATCACACCAA	ATCGGTTTGG
101	CGATTATGCG	CTTAAACTCT	TCAATACTCG	ACCTGCCACC	GACAAAACAA
151	TATTTCCAAT	CCGGCAGCCT	GTGGAGCGAG	CTGCGCCAAG	GCTTCCGGAT
201	GGGCGAAGTC	AATCCCGAAC	TGGTACGCCG	CCACGAAAGC	AAATTCATCG
251	CAAGCCACAG	CTATTTCAAC	AGGGTCATCA	ACCGGAGTAG	ACCCTATATG
301	TACCATATCG	CCAACGAAGT	CAAAAAACGC	AATATGCCCG	CCGAAGCCGC
351	CCTGCTTCCC	TTCATCGAAA	GCGCGTTCGT	CACCAAAGCC	AAATCACACG
401	TCGGCGCATC	GGGCCTGTGG	CAGTTCATGC	CCGCTACCGG	CAGGCATTAC
451	GGCCTGGAAA	AAACACCGGT	TTACGACGGC	AGGCACGACA	TTTACGCCGC
501	CACCGATGCC	GCACTCAACT	ATCTGCAATA	CCTCTATGGA	CTGTTCGGCG
551	ACTGGCCGCT	CGCCTTTGCC	GCCTACAACT	GGGGTGAAGG	CAACGTCGGA
601	CGCGCCATCA	ACCGCGCCCG	CGCCCAAGGG	CTCGAACCGA	CCTACGAAAA
651	CCTGCGTATG	CCCAACGAAA	CGCGCAACTA	TGTTCCCAAG	CTGCTCGCCG
701	TGCGCAACAT	CATTGCCGCC	CCCCAATCTT	TCGGCATGAA	TATCAGCGAC
751	ATAGACAACA	AACCGTATTT	TCAGGCAGTC	GAACCGGACC	GTCCGCTCGA
801	CAACGAAGCC	ATCGCCCGGC	TTGCCGGCAT	CACGCAAAGC	GAGCTGCTCG
851	CCCTAAACCC	CGCATTCAAC	GTCCCCGCGT	TCATCCCCAA	AAGCAAACGC

a650

	•
901	AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951	CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001	CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
	GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCA ACGCAGGACG
1051	
1101	CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151	CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201	ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251	CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301	GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351	AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA
	•
This correspond	s to the amino acid sequence <seq 2104;="" 650.a="" id="" orf="">:</seq>
	s to the annie dold sequence SEQ IS STORY, STA OSCIA.
a650.pep	NOTE THAT A COLUMN OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
1	MSKLKTIALT ASGLSVCPGF LYAQNTSSHQ IGLAIMRLNS SILDLPPTKQ
51	YFQSGSLWSE LRQGFRMGEV NPELVRRHES KFIASHSYFN RVINRSRPYM
101	YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151	GLEKTPVYDG RHDIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEGNVG
201	RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251	IDNKPYFOAV EPDRPLDNEA IARLAGITOS ELLALNPAFN VPAFIPKSKR
301	KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351	DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPNTYRSN
	MPAGTVNVGI ARIRPAAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
401	
451	SRSATSNRKT DRHAV*
m650/a650	99.1% identity in 465 aa overlap
	10 20 30 40 50 60
m650.pep	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
a 650	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
a 0 3 0	10 20 30 40 50 60
	10 20 30 10 30
	70 80 90 100 110 120
	70 00 20 ==-
m650.pep	LRQGFRMGEVNPELVRRHESKFIASHSYFNRVINRSRPYMYHIANEVKKRNMPAEAALLP
a650	LRQGFRMGEVNPELVRRHESKFIASHSYFNRVINRSRPYMYHIANEVKKRNMPAEAALLP
	70 80 90 100 110 120
	·
	130 140 150 160 170 180
m650.pep	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
moso.pep	
65.0	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG
a650	
	130 140 150 160 170 180
	240
	190 200 210 220 230 240
m650.pep	LFGDWPLAFAAYNWGEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
a650	LFGDWPLAFAAYNWGEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA
	190 200 210 220 230 240
	250 260 270 280 290 300
-CEO non	POSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR
m650.pep	
a 650	PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR
	250 260 270 280 290 300
	310 320 330 340 350 360
m650.pep	KLLLPVASVQTFQSNYLNAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
a650	KLLLPVASVQTFQSNYLNAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
2000	310 320 330 340 350 360
	240 250 230 240 250 200
	370 380 390 400 410 420
	0,0
m650.pep	NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDTYRSNMPAGTVNVGIARIRPAAAQT
	να τικί του στι τι του καισκατί του συνείτες της Ευτορίας Ευτορίας Ευτορίας Ευτορίας Ευτορίας Ευτορίας Ευτορία

NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPNTYRSNMPAGTVNVGIARIRPAAAQT

```
410
                                                       420
                                       400
                370
                       380
                               390
                       440
                               450
                430
          ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRHAVX
          ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRHAVX
a650
                               450
                430
                       440
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2105>:

```
g652.seq
         ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
         GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
     51
     101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
     151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
     201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
     251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
     301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
         CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
     401 AAGCCGCCGG CTACAAGGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
     451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
         CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATACTTGGAA GGCTTGGTTA
     551 ACGAATTCCC GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
     601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
     651 CGGCGACGAC TTGTTCGTAA CCAATCCGAA AATTCTTGCC GAAGGCATCG
     701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
     751 TTAAGCGAAA CCCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
     801 cagCGTGATG AGCCAccgct ccggCGAAAC CGAAGACAGT Accattgccg
     851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTAAAAACCGG TTCTTTGAGC
          CGTTCCGACC GCATGGCGAA ATACAACCAA CtGCTGCGTA TCGAGGAAGA
     951 ATTGGCGGAA GCCGCCTACT ACCCCGGCAA AGCCGCATTC TACCAACTGG
    1001 GCAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>: q652.pep

```
MIELDGTENK GNLGANATLA VSMAVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
201 EGWKLLTEKL GKKVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEEELAE AAYYPGKAAF YQLGK*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2107>:

```
ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
     GACTTTGGCG GTTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
 51
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
     GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAAGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
     GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGTAGAG TTCAATTGGT
601
     TGGCGACGAC TTGTTCGTAA CCAATCCAAA AATCTTGGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
     TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
     CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
 901
     ATTGGCGGAA GCCGCCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>: m652.pep

1 MIELDGTENK GNLGANATLA VSMAVARAAA EDSGLPLYRY LGGAGPMSLP 51 VPMMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC

```
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
       ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
        EGWKLLTEKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
       LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
    251
    301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK*
m652/g652 98.2% identity in 335 aa overlap
                 10
                         20
                                 30
                                         40
                                                 50
                                                          60
          MIELDGTENKGNLGANATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMMNVINGG
m652.pep
          MIELDGTENKGNLGANATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMMNVINGG
g652
                 10
                         20
                                 30
                                         40
                 70
                         80
                                 90
                                        100
                                                110
                                                         120
          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
m652.pep
          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
g652
                                 .90
                                        100
                130
                        140
                                150
                                        160
                                                170
          SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLĖ
m652.pep
          SHKEALQLMVEAAEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
a652
                130
                        140
                                150
                                        160
                                                170
                                                         180
                190
                        200
                                210
                                        220
                                                230
                                                         240
          GLVNEFPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
m652.pep
          GLVNEFPIISIEDGMDENDWEGWKLLTEKLGKKVQLVGDDLFVTNPKILAEGIEKGVANA
g652
                190
                        200
                                210
                                        220
                        260
                                270
                                        280
          LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
m652.pep
          LLVKVNQIGTLSETLKAVDLAKCNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
g652
                250
                        260
                                270
                                        280
                                                290
                310
                        320
                                330
          RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX
m652.pep
          RSDRMAKYNQLLRIEEELAEAAYYPGKAAFYQLGKX
q652
                310
                        320
                                330
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2109>: a652.seq

```
ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
  1
     GACTTTGGCG GTTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
 51
     GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
     GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
     GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
     CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
351
401
     AAGCCGCCGG CTACAAAGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
     GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
451
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGAA GGCCTGGTCA
     ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
     GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGCAAAG TCCAACTCGT
601
     TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
     TTGAGTGAAA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
     ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
     CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
901
     ATTGGCGGAA GCCGCCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
951
1001 GCAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>: a652.pep

- 1 MIELDGTENK GNLGANATLA VSMAVARAAA EDSGLPLYRY LGGAGPMSLP
- 51 VPMMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
- 101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```
ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPIIS IEDGMDENDW
    151
        EGWKLLTEKL GGKVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
        LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
    251
        RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK*
    301
          99.7% identity in 335 aa overlap
m652/a652
                 10
                         20
                                 30
                                                 50
                                         40
          MIELDGTENKGNLGANATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMMNVINGG
m652.pep
          a652
          MIELDGTENKGNLGANATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMMNVINGG
                                         40
                 70
                         80
                                 90
                                        100
                                                110
          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
m652.pep
          EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN
a652
                 70
                         80
                                 90
                                        100
                                                110
                                                        120
                130
                        140
                                150
                                        160
                                                170
                                                        180
          SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
m652.pep
          SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
a652
                        140
                                150
                                        160
                                                170
                                                        180
                190
                        200
                                210
                                        220
                                                230
          GLVNEFPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
m652.pep
          a652
          GLVNEFPIISIEDGMDENDWEGWKLLTEKLGGKVQLVGDDLFVTNPKILAEGIEKGVANA
                                                        240
                190
                        200
                                210
                                        220
                                                230
                250
                        260
                                270
                                        280
                                                290
                                                         300
          LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
m652.pep
          a652
          LLVKVNQIGTLSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
                250
                        260
                                270
                310
                        320
          RSDRMAKYNQLLRIEEELAEAADYPSKAAFYOLGKX
m652.pep
          RSDRMAKYNQLLRIEEELAEAADYPSKAAFYQLGKX
a 652
                310
                        320
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2111>: g652-1.seq

```
ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
     CAACCCCACA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
     GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
101
     CTTCGCGACG GCGACAAATC CCGCTATTCC GGCAAAGGCG TATTGAAGGC
151
     CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
     CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
251
     GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TCTCTATGGC
301
 351
     GGTTGCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
     TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
 401
     AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
 451
     501
     AAATTTTCCA CGCCTTGAAA AAACTGTGCG ACAGTAAAGG CTTCCCGACC
 551
     ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
 601
     AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
     GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
 701
     GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
 751
     ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTCCCG ATTATTTCCA
801
     TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
     GAAAAATTGG GCAAAAAAGT TCAATTGGTC GGCGACGACT TGTTCGTAAC
 901
     CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
 951
     TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1001
     GTCGATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1051
1101
     CGGCGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
     GTATGCAGAT TAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1151
     TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1201
     CCCCGGCAAA GCCGCATTCT ACCAACTGGG CAAATAA
```

This corresponds to the amino acid sequence <SEO ID 2112; ORF 652-1.ng>:

```
g652-1.pep
         MSAIVDIFAR EILDSRGNPT VECDVLLESG VMGRAAVPSG ASTGQKEALE
      1
        LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
     51
         ENKGNLGANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMMNVI
    151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
         TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
    251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
    301 EKLGKKVQLV GDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSETLKA
         VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
    351
         YNOLLRIEEE LAEAAYYPGK AAFYQLGK*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2113>:
m652-1.seq
         ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
      1
        CAACCCCACA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
     51
        GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
         CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
    201 GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
    251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
    301 GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
         GGTTGCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
         TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
         AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
         551 AAATTTTCCA CGCCTTGAAA AAACTGTGCG ACAGCAAAGG CTTCCCGACC
     601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
         AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGGC TACAAAGCGG
         GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
         GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
     751
         ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
         TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
     851
         GAAAAACTGG GCGGTAGAGT TCAATTGGTT GGCGACGACT TGTTCGTAAC
     901
         CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
     951
    1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
         GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
    1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
         GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
         TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
         CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA
This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:
m652-1.pep
      1 MSAIVDIFAR EILDSRGNPT VECDVLLESG VMGRAAVPSG ASTGQKEALE
      51 LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
         ENKGNLGANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMMNVI
     151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
         TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
         DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
         EKLGGRVQLV GDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSETLKA
         VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
     351
     401 YNQLLRIEEE LAEAADYPSK AAFYQLGK*
                98.6% identity in 428 aa overlap
m652-1/g652-1
                                                         50
                    10
                                       30
                                                40
             MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRYS
m652-1
             MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRYS
 g652-1
                            20
                                                         50
                                       30
                                                40
                    10
                                               100
                                                        110
                                       90
                             80
             GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGANATLAVSMAVAR
 m652-1
             GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGANATLAVSMAVAR
 g652-1
                                               100
                    70
                             80
                                       90
                                               160
                   130
                             140
                                      150
             AAAEDSGLPLYRYLGGAGPMSLPVPMMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
 m652-1
             AAAEDSGLPLYRYLGGAGPMSLPVPMMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
 g652-1
                                                         170
```

160

130

140

150

```
240
                                             220
                                                       230
                           200
                                    210
                  190
           CGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
m652 - 1
            CGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEAAEAAGYKAGEDVLFA
g652-1
                                                       230
                                                                240
                                    210
                                             220
                           200
                                                       290
                                    270
                                             280
                           260
           LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
m652 - 1
            LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
g652-1
                                                       290
                                                                300
                           260
                                    270
                                             280
                                                       350
                                                                360
                                    330
                                              340
                  310
                           320
            EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
m652-1
            EKLGKKVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKCNRYA
q652-1
                  310
                           320
                                    330
                                             340
                           380
                                    390
                                              400
                  370
            SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAKYNQLLRIEEELAEAADYPSK
m652-1
            SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAKYNQLLRIEEELAEAAYYPGK
g652~1
                                     390
                                              400
                                                       410
                           380
                  370
                 429
m652-1
            AAFYQLGKX
            111111111
g652-1
            AAFYQLGKX
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2115>:
a652-1.seq
      1 ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
         CAACCCCACA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
         GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
     101
         CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
         GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
     201
         CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
     251
         GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
         GGTTGCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
         TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
         AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
     451
         551 AAATTTTCCA CGCCTTGAAA AAACTGTGCG ACAGCAAAGG CTTCCCGACC
         ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
         AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCCGGC TACAAAGCGG
     651
         GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
         GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
     751
         ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
     801
         TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
     851
         GAAAAACTGG GCGGCAAAGT CCAACTCGTT GGCGACGACC TCTTCGTTAC
     901
         CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
         TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
    1001
         GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
    1051
         CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
    1101
         GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
    1151
         TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
    1201
    1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA
This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:
 a652-1.pep
       1 MSAIVDIFAR EILDSRGNPT VECDVLLESG VMGRAAVPSG ASTGQKEALE
         LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
         ENKGNLGANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMMNVI
          NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
          TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
          DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
          EKLGGKVQLV GDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLSETLKA
          VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLSRSDRMAK
          YNQLLRIEEE LAEAADYPSK AAFYQLGK*
```

m652-1/a652-1 99.8% identity in 428 aa overlap

m652-1	MSAIVDIFAREILDSRG					
a652-1	MSAIVDIFAREILDSRG					
m652-1	70 GKGVLKAVEHVNNQIAQ	80 ALIGIDANE	90 QSYIDQIMIE	100 LDGTENKGNL	110 GANATLAVSM	120 AVAR
a652-1						 AVAR 120
m652-1	130 AAAEDSGLPLYRYLGGA	140 GPMSLPVPM	150 MNVINGGEHAI	160 NNSLNIQEFM	170 IMPVGAKSFR	180 EALR
a652-1			 MNVINGGEHAI 150	 NNSLNIQEFM 160	 IMPVGAKSFR 170	IIII EALR 180
m652-1	190 CGAEIFHALKKLCDSKG	200	210	220	230 FAAGYKAGED	240 VI.FA
a652-1			ПППППП	11111111111	111111111	1111
	250	260	270	280	290	300
m652-1 a652-1	LDCASSEFYKDGKYHLE	11111111	1111111111	111111111	1111111111	HII
	250 310	260 320	270 330	280 340	290 350	300 360
m652-1	EKLGGRVQLVGDDLFVT	NPKILAEGI	EKGVANALLVI	KVNQIGTLSE	TLKAVDLAKR	NRYA
a652-1	EKLGGKVQLVGDDLFVT 310	'NPKILAEGI 320	EKGVANALLVI 330	340	350	360
m652-1	370 SVMSHRSGETEDSTIAD					
a652-1	SVMSHRSGETEDSTIAD 370					
m652-1	429 AAFYQLGKX					
a652-1	AAFYQLGKX					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2117>: g653.seq

```
1 ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTTCCGG
51 ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGCt ttgcccaAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaacgTGGC TTTCGGTGCG GCCGGAAAcg atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTTCACTTGT TTTGCGTATT
251 GTTTGAACtC GGGTTGCaac gcttctTTAA acgctACGGC TttgGCGGCG
```

- 251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgGCGGCG 301 ATAACGTgca tcaACGGAcc gCCTTGCAGG CTTGGGAAGA TGGAAGAGTT
- 351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAAATCACA CCGCCGCGAG
- 401 GGCCGCGTAG GGTTTTGTGG GTGGTAGTGg ttACgaaGTc GCAGAatggc
- 451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>: g653.pep

- 1 MAAEPMRMPE VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
- 51 KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
- 101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
- 151 TGLGYSPPAT SPA*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2119>: m653.seq

- 1 ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTTCCGG
- 51 ATCGTTCGGA ATGGCGTTTT TGTTGACGGT GATGTGCGCT TTGCCCAAAG
- 101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```
151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
    201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACTTGT TTTGCGTATT
    251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
    301 ATAACGTGCA TCAGCGGACC GCCTTGCAGG CTTGGGAAGA TGGAAGAGTT
    351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
    401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
    451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG
This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:
m653.pep
        MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
        KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
     51
        ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
    101
        TGLGYSPPAT RPA*
m653/g653 96.9% identity in 163 aa overlap
                                             40
           MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
m653.pep
            MAAEPMRMPEVTYGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
g653
                                             40
                                    30
                           20
                                                              120
                            80
                                     90
                                            100
                                                     110
                   70
            MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
m653.pep
            MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
g653
                                                     110
                  70
                           80
                                    90
                                            100
                           140
                  130
            SWVLSRHKITPPRGPRRVLWVVVVTKSQNGTGLGYSPPATRPAX
m653.pep
            SWVLSRHKITPPRGPRRVLWVVVVTKSQNGTGLGYSPPATSPAX
g653
                                    150
                           140
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2121>:
a653.seq
         ATGGCGGCGG AACCGATGCG GATGCCGGAG GTAACGAAGG GTTTTTCCGG
         ATCATTCGGG ATGGCGTTTT TGTTGACAGT GATGTGCGCT TTGCCCAAAG
      51
         CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG
     101
     151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
     201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACTTGT TTTGCGTATT
     251 GTTTGAACTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
         ATAACGTGCA TCAGCGGGCC ACCTTGCAGG CTTGGGAAGA TGGAAGAGTT
        CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
     351
         GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
     451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG
This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:
a653.pep
         MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
      51 KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
         ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
     101
         TGLGYSPPAT RPA*
            100.0% identity in 163 aa overlap
m653/a653
                            20
                                     30
                                              40
                                                       50
            MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
m653.pep
            MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
 a 653
                                                                60
                                              40
                                                       50
                   10
                                             100
                                                      110
                            80
                                     90
            MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
m653.pep
            MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
 a 653
                                             100
                                                      110
                                                               120
                                     90
                   70
                           140
                                    150
                  130
            SWVLSRHKITPPRGPRRVLWVVVVTKSQNGTGLGYSPPATRPAX
 m653.pep
            SWVLSRHKITPPRGPRRVLWVVVVTKSQNGTGLGYSPPATRPAX
 a653
```

WO 99/57280 PCT/US99/09346

1043

150 160 130 140 The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2123>: q656.seq ATGCCGCGTT TCTCCGGTTC GATTTCTTCG ATGATTTCCA TCGCGCGGAC TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT 51 CCATATTGGT AACGCCCTCT TTCAAACAGC CLTCGACGTT GGAAACGATG 101 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TGACTTTGAC TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA GCATAACGTG TTCGGCGatt TCTTTGGCGT CGCTTAACAA ATCTTGTTCG TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCGGGCG AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG

## This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

g656.pep

1 MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM

51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSISITCSAI SLASLNKSCS

101 LARSSAGVLP RRRVPAMGRT MTSSRSRRTR ISGEEPTMWK SPKS*

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2125>:

### ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCA TGGCGCGGAC

| TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT TGCATTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
| TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACTTTGAC
| TTCGCCGGTT TTACTGATGC GGCCGACGTC GTTGCGTCCT AAGTCAATCA
| ACATGACGTG TTCGGCGGT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
| ACATGACGTG CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
| TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG TCGGACGAGG ATTTCGGCGCG
| AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

m656.pep

1 MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPS FRRPSTLETM

51 CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS

101 LARSSAGVLP RRRVPAMGRT ITSLRSRRTR ISGEEPTMWK SPKS*

# Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

#### m656/g656 91.0% identity in 144 aa overlap

50 40 20 30 MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPSFRRPSTLETMCITWEYFSIT m656.pep MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPSFKQPSTLETMCITWEYFSIT g656 60 50 30 40 20 10 90 100 80 70 ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLPRRRVPAMGRT m656.pep ILSVTLTSPVLLMRPTSLRPKSISITCSAISLASLNKSCSLARSSAGVLPRRRVPAMGRT g656 100 120 90 80 70 140 130 ITSLRSRRTRISGEEPTMWKSPKSX m656.pep MTSSRSRRTRISGEEPTMWKSPKSX g656 140 130

PCT/US99/09346 WU 99/57280

1044

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2127>:
a656.seq
         ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCA TGGCGCGGAC
      1
         TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
     51
        CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
    101
         TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCGG TAACTTTGAC
    151
         TTCGCCGGTT TTACTGATGC GGCCGACGTC GTTGCGTCCT AAGTCAATCA
    201
        ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
         TTGGCAAGGT CTTCGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
    301
         GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTCGGGCG
    351
        AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:
a656.pep
         MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPS FRRPSTLETM
         CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
     51
         LARSSAGVLP RRRVPAMGRT MTSSRSRRTR ISGEEPTMWK SPKS*
    101
            98.6% identity in 144 aa overlap
m656/a656
                                     30
                                              40
                            20
                   10
            MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPSFRRPSTLETMCITWEYFSIT
m656.pep
            MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPSFRRPSTLETMCITWEYFSIT
a656.
                                              40
                                     30
                   10
                            20
                                     90
                                             100
                            80
            ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLPRRRVPAMGRT
m656.pep
            ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLPRRRVPAMGRT
a656
                                                       110
                                     90
                                             100
                            80
                           140
                   130
            ITSLRSRRTRISGEEPTMWKSPKSX
m656.pep
            MTSSRSRRTRISGEEPTMWKSPKSX
a656
                           140
                   130
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2129>:
      q657.seq
                ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
             1
                CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
            51
                AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
           151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
```

```
201 GGCAAAATGC GCGGCGGTta cgACCGAATT TGAAAacgtc aaTGCCGACG
    CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
     GTGTCCATTG CACAAAACCG CATTCAGGAA AAAGCGTGGA TACGCAAAGC
    AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
     CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
     GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
     AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
     TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
    AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
601
     GGCTTattcC ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
651
     CGCGGCAGAC GGCGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
701
     TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACACATGAAT TGCTCGTCAA
751
     TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
801
     GCGCCGCAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAACCTGCCG
851
     CCCGCCGACA CCAAATTATT aTCCCCttgC TGTATGGCGA ATATTTTGGG
901
     CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
951
     GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAAC CGCACAGAAA
1001
     GGTCGGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgC
     ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
DRHLCAPEDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
USTAONRIOE	KAWIRKAGLO	TAPYOAVCKA	EDITEASAQF	LPGILKTATL
CYDCKGOTRV	KTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
NVOTEDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADELDYVGV
	DRHLCAPFDD VSIAQNRIQE	DRHLCAPFDD RAALDELAKC VSIAQNRIQE KAWIRKAGLQ GYDGKGOIRV KTLDELKAAF	DRHLCAPFDD RAALDELAKC AAVTTEFENV VSIAQNRIQE KAWIRKAGLO TAPYQAVCKA GYDGKGOIRV KTLDELKAAF AEHGGVDCVL	MNTPPILPPA MLGILGGGQL GRMFAVAAKT MGYKVTVLDP DRHLCAPFDD RAALDELAKC AAVTTEFENV NADAMRSLAK VSIAQNRIQE KAWIRKAGLQ TAPYQAVCKA EDITEASAQF GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRGEI NVOTFDPAEN IHENGILAYS IVPARLSADV QQQARQTAQR

WU 99/57280 PCT/US99/09346

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251	LAVEMFVVGD	THELLVNETA	PRTHNSGHHT	IDACAADQFQ	QQVRIMCNLP
301	PADTKLLSPC	CMANILGDVW	QEDGGEPDWL	PLQSRPNAHL	HLYGKKTAQK
351	GRKMGHFTVL	TTDSDTAFQE	AKKLHQSL*		

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2131>:

```
m657.seq
         ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG
      1
         CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA
     51
     101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC
     151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
    201 GGCAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG
    251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCCTAG CGGCGATTGT
    301 GTGGCGATTG CACAAAACCG CATTCAGGAA AAGGCATGGA TACGCAAAGC
     351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
     401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
     451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACTCAA
    501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
         TGGATTTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC
     601 AACGTGCAAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
         GGCTTATTCC ATCGTCCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG
         CGCGGCAGAT GGCGCAACGC TTGGCGGACG AATTGGATTA TGTCGGCGTA
     751 TTGGCGGTAG AAATGTTTGT TGTCGGTGAC ACGCATGAAT TGGTCGTCAA
    801 CGAAATCGCC CCGCGCCCGC ACAATTCCGG ACACCATACG ATAGATGCCT
    851 GCGCAGCAGA CCAGTTCCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
    901 CCTGCCGATA CCAAATTACT GAGTTCTTGC TGTATGGCAA ATATTTTGGG
    951 CGACGTTTGG CAGGAAGACG GCGCGAACC GGATTGGCTG CCCTTGCAAA
    1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
    1051 GGGCGGAAAA TGGGACACTT TACCGTTTTA ACCACCGATT CGGACACCGC
    1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

#### This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep					
1	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	DPDAPAAEFA
51	DRHLCAPFND	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC
101	VAIAQNRIQE	KAWIRKAGLQ	TAPYQVVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL	EKMVDLRSEI	SVIVCRLNND
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQMAQR	LADELDYVGV
251	LAVEMFVVGD	THELVVNEIA	PRPHNSGHHT	IDACAADQFQ	QQVRIMCNLP
301	PADTKLLSSC	CMANILGDVW	QEDGGEPDWL	PLQSHPNAHL	HLYGKKTAHK
351	GRKMGHFTVL	TTDSDTAFQE	AKKLHQSL*		
351	GRKMGHFTVL	TTDSDTAFQE	AKKLHQSL*		

## Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

#### m657/g657 93.9% identity in 378 aa overlap

m657.pep	10 MKNISLSPPAMLGI				50 PAAEFADRHI	
g657	MNTPPILPPAMLGI	<i>.</i>	:           AVAAKTMGYK		IIIIIIIII PAAEFADRHI	CAPEDD
9037	10	20	30	40	50	60
		•			4.10	100
	70	80	90	100	110	120
m657.pep	QAALDELAKCAAVT'	TE FENVNADA	MRFLAKHTNV	SPSGDCVAIA	QNRIQEKAW:	IRKAGLQ
	:	111111111	11 1111111	11111111:11		111111
q657	RAALDELAKCAAVT	TEFENVNADA	MRSLAKHTNV	SPSGDCVSIA	ONRIGEKAW:	IRKAGLO
5	70	80	90	100	110	120
	130	140	150	160	170	180
m657.pep	TAPYOVVCKAEDIT	EASAOFLPGI	LKTATLGYDG	KGQIRVKTLD	ELKAAFAEHO	GGVDCVL
	11111:1111111		1111111111	111111111	111111111	111111
g657	TAPYQAVCKAEDIT	FASAOFT.PGT	TKTATLGYDG	KGOTRVKTLD	ELKAAFAEHO	GVDCVI
9001	130	-	150	160	170	180
	130	140	100	100	1/0	100

WU 99/57280 PCT/US99/09346

1047

	190 200 210 220 230 240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR
moo, vp-p	
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR
-	190 200 210 220 230 240
	250 260 270 280 290 300
m657.pep	LADELDYVGVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
g657	LADELDYVGVLAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP
	250 260 270 280 290 300
	310 320 330 340 350 360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNAHLHLYGKKTAHKGRKMGHFTVL
moo7.pep	
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAQKGRKMGHFTVL
9057	310 320 330 340 350 360
	370 379
m657.pep	TTDSDTAFQEAKKLHQSLX
g657	TTDSDTAFQEAKKLHQSLX
	370
The following p	partial DNA sequence was identified in N. meningitidis <seq 2133="" id="">:</seq>
a657.seq	
1	ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGGCGG
51	CGGACAATTA GGCAGAATGT TTACTGTTGC TGCCAAAACC ATGGGCTACA
101	AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151	GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201	GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251	CGATGCGTTT TCTCGCCAAA CATACCAATG TTTCCCCCAG CGGCGACTGC
301	GTTGCCATCG CGCAAAACCG CATTCAGGAA AAGGCATGGA TACGCAAAGC
351	AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401	CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451	GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501	AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551	TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
601 651	CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701	CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 751	TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACGCATGAAT TGGTCGTCAA
801	CGAAATCGCG CCGCGTCCGC ACAATTCCGG CCACCATACC GTCGACGCCT
851	GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901	CCTGCTGACA CCAAATTGCT GAGTTCTTGC TGTATGGCGA ATATTTTGGG
951	CGACGTTTGG CAGGAAGACG GCGCCGAACC GGATTGGTTT CCCCTGCAAA
1001	
1051	GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101	ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
This correspond	ds to the amino acid sequence <seq 2134;="" 657.a="" id="" orf="">:</seq>
a657.pep	
i	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51	
101	VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151	GYDGKGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201	
251	
301	
351	GRKMGHFTIL STDSDTAFQE AKKLHQSL*
m657/a657	94.2% identity in 378 aa overlap
	10 20 20 40 50 60
mcE7	10 20 30 40 50 60 MKNISLSPPAMLGILGGGOLGRMFTVAAKTMGYKVTVLDPDPDAPAAEFADRHLCAPFND
m657.pep	LIVIA TO TO L LYMING I DOGOČITOVALI I AVVATAGO I VA I A PDE DE DREAVET VOKUTĆA LEDI

a657	
m657.pep	70 80 90 100 110 120 QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ  : : :  :
m657.pep	130 140 150 160 170 180 TAPYQVVCKAEDITEASAQFLPGILKTATLGYDGKGQIRVKTLDELKAAFAEHGGVDCVL     :  ::
m657.pep	190 200 210 220 230 240 EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR
m657.pep	250 260 270 280 290 300 LADELDYVGVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
m657.pep	310 320 330 340 350 360 PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNAHLHLYGKKTAHKGRKMGHFTVL
m657.pep a657	370 379 TTDSDTAFQEAKKLHQSLX :                   STDSDTAFQEAKKLHQSLX 370

## The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2135>:

nowing p	artial Divilo	oquoisso		J	
g658.seq					7 CC7 CC7 7 TT
1	ATGGTGGCCG	GAATTGTGCG	TGCGCGGGGC	GGTTTCATTG	ACGAGCAATI
51	CATGTGTGTC	GCCGACAACA	AACATTTCTA	CCGCCAAtac	GCCGACATAA
101	TCCAATTCGT	CCGCCAagcG	TTGCGCCGTC	TGCCGCGCCT	GTTGCTGCAC
151	GTCGGCACTC	AGCCGCGcgg	gGACGATGga	atAAGCCAAG	ATGCCGTTTT
201	CGTGGATGTT		TCGAAGGTTT	GCACGTTTTC	
251	CGGCATACGA	TCACGGAAAT	CTCGCCGCGC	AAGTCCACCA	
301		ACGCCGCCGT			
351		GCGGATTTGA		CGTAGCCCAA	
401		CGGGCAAAAA		GCTTCAGTAA	
451		GCCTGATACG		CAAGCCTGCT	TTGCGTATCC
501		CTGAATGCGG			GTCGCCGCTG
551		TGGTATGCTT			CGGCAttgac
601		TCGGTcgtaA			TCGTCCAACG
	gtilleanni	GTCAAACGGC	TAAAAAAA	GGCGGTCGGC	AAATTCCGCC
651	CGGCCCGGTC				
701	GCCGGCGCAT		ATCGAGAACG		AGCCCATGGT
751	TTTAGCGGCA	ACGGCAAACA	TTctgcctAA		

## This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

g658.pep

1 MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRRLPRLLLH 51 VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

101	NAIHAAVFGK	RGFEFVQRFD	ADLTFAVVAQ	RSRFQDAGQK	LRACFSNVFG
	LANRLIRRGL				
201	VFKFGRNRRA	FCQFVQRGPV	VKRRAQMAVG	KFRRRRIRVG	IENGYFVAHG
251	FSGNGKHSA*				

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2137>:

```
ATGGTGTCCG GAATTGTGCG GGCGCGGGGC GATTTCGTTG ACGACCAATT
    CATGCGTGTC ACCGACAACA AACATTTCTA CCGCCAATAC GCCGACATAA
51
    TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
101
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CGGCATACGA TTACGGAAAT TTCACTGCGC AAATCCACCA TTTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTAC GCGGATTTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTTG CAATCCCGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
601
    CAGCTTGGTC GTTAAACGGC GCGCACAAAT GGCGGTCGGC AAATTCTGCT
651
    GCCGGCGCT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
    TTTGGCGGCA ACGGTAAACA TTCTGCCTAA
```

### This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

m658.pep					
1	MVSGIVRARG	DFVDDQFMRV	TDNKHFYRQY	ADIIQFVRQA	LRHLPRLLLH
51	VGTQSRGDDG	ISQDAVFVDV	FGRVESLHVV	IVQTAYDYGN	FTAQIHHFFQ
101	NAIHAAVFGK	RGFEFIOCFY	ADLTFAVVAQ	RSRFQDAGQK	LRACFSDVFS
151	LTNHLIRRGL	OSRFAYPCLF	LNAVLCNRHT	IAARGNIGMF	CQKAHRIGID
201	VFKFSGHRRA	FCOFVOSSLV	VKRRAOMAVG	KFCCRRVRIG	VENGYFVAHG
	FGGNGKHSA*		~		

## Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

#### m658/g658 82.2% identity in 259 aa overlap

moso, good	<u> </u>		•			
m658.pep	10 MVSGIVRARGDFVD	20 DOFMRVTDNK	30 HFYROYADII	40 OFVROALRHL	50 PRLLLHVGTQ	60 SRGDDG
moso.pep	11:11111111111111	·			111111111	11111
cro	MVAGIVRARGGFID					
g658	MVAGIVRARGGIID	20	30	40	50	60
	10	20	50		•	
	70	80	90	100	110	120
m658.pep	ISQDAVFVDVFGRV	ESLHVVIVQT	AYDYGNFTAQ	IHHFFQNAIH	AAVFGKRGFE	EFIQCEY
• •				: [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [		
g658	ISQDAVFVDVFGGV	EGLHVFIVQT	AYDHGNLAAÇ	VHHFFQNAIH	AAVFGKRGFE	EFVQRFD
9	70	80	90	100	110	120
	130	140	150	160	170	180
m658.pep	ADLTFAVVAQRSRF	ODAGOKLRAC	FSDVFSLTNE	HLIRRGLQSRE	'AYPCLFLNA	/LCNRHT
moso.pep			11:11:1:1:		111:111	
q658	ADLTFAVVAQRSRF	ODAGOKLRAC	FSNVFGLANE	RLIRRGLOACE	AYPRFFLNA	/LCNGHA
9636	130	140	150	160	170	180
	130	110	200			
	190	200	210	220	230	240
45.0	IAARGNIGMFCQKA				BAOMAVGKEC	CRRVRIG
m658.pep	:     :  :  :	UKIGIDALKE	SGIIKKAE CQI			11:1:1
	:         :     :     :	11:111111				
g658	VAAGGNVGMLCQRA			220	230	240
	190	200	210	220	230	240
	466	0.50				
	. 250	260				
m658.pep	VENGYFVAHGFGGN	IGKHSAX				

**IENGYFVAHGFSGNGKHSAX** g658 250 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2139>: a658.seq ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT 1 51 CATGCGTGTC GCCGACAACA AACATTTCTA CCGCCAATAC GCCGACGTAG TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT 101 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT 151 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTTGTC ATTGTTCAGA 201 CGGCATACGA TAACGGAAAT TTCGCCGCGC AAGTCCACCA TTTTTTCCAA 251 AACGCAATCC ACGCCGCGT GTTCGGCAAA CGCGGCTTTG AGTTCATCCA CCGTTTTGAC GCGGATTTGG CCTTTGCCGT CATAGCCCAA TGTAGCGGTT 351 401 TTCAGGATGC CGGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC TTTGCAAATT GCTTGATACG GCGCGGTTTG CAGGCCTGCT TTGCGTATCC 451 ATGCCTTTTC CTGAATGCGG TTTTGCGCGA TGGCAACGCA GTCGCCGCTG 501 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCCAAAG 601 CGGTTTGGTT GTCAAACGGC GCACACAAAT GGCGGTCGGC AAATTCCGCT 651 GCCGGCGCAT TCGGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT 701 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA 751 This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>: a658.pep MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN VGTQSGWDDG VGEDTVFVNV FGRIESLHVV IVQTAYDNGN FAAQVHHFFQ 51 NAIHAAVFGK RGFEFIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG 101 151 FANCLIRRGL QACFAYPCLF LNAVLRDGNA VAAGGNIGMF GEKTHRIGID VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFRCRRIRVG IEYGYFVAHG FGSNSKHSA* 251 m658/a658 75.3% identity in 259 aa overlap 30 MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTQSRGDDG m658.pep MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVVQFIGQTLRHLSRLLLNVGTQSGWDDG a658 10 20 30 40 50 60 70 80 90 100 110 120 ISQDAVFVDVFGRVESLHVVIVQTAYDYGNFTAQIHHFFONAIHAAVFGKRGFEFIOCFY m658.pep VGEDTVFVNVFGRIESLHVVIVQTAYDNGNFAAQVHHFFQNAIHAAVFGKRGFEFIHRFD a658 70 80 90 100 130 140 150 160 170 ADLTFAVVAQRSRFQDAGQKLRACFSDVFSLTNHLIRRGLQSRFAYPCLFLNAVLCNRHT m658.pep ADLAFAVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRGLQACFAYPCLFLNAVLRDGNA a658 130 140 150 160 170 1.80 190 200 210 220 230 m658.pep IAARGNIGMFCQKAHRIGIDVFKFSGHRRAFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG VAAGGNIGMFGEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFRCRRIRVG a658 190 200 210 220 230 250 VENGYFVAHGFGGNGKHSAX m658.pep 

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2141>:

260

**IEYGYFVAHGFGSNSKHSAX** 

250

a658

```
q661.seq
               ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
           51 GGCGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
          101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
          151 ACCGGAAAAA CCCtgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT
          201 TGCCGTGCAG ATTGCCGGCA GCGACCccga acaGATGGCG Gatgcggcgc
          251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
               cccgccaaGA AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
          351 CGAGccgctg gttgcCgcca tTTtggaggc ggtggtcAAG GCGGCGGgcg
          401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
          451 ctgcCcgccg tcgccaaaat cgccgaagat tgcggcattg ccgccCttgc
          501 cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGCqcGTTAC
          551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
          601 CGGCGACATC actTCgccgc AAAAAGCCGC CGccgTCCTC AAACAAACCG
          651 CCGCCGACGG CATCATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTT
          701 TTCCGCGATT TGAAGCATTA TGCCGAACAC GGCGTTTTAC CGCCTGCCTT
          751 GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
          801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
          851 GGCTGGTACA TCGGCGAAAT GCCCGACGGC GAACAGGCGC GGCGTGA
This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:
     g661.pep
               MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
               TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AOVIDINMGC
          101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDDQN
          151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
               RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
          251 EFGRMQSRHF EPHPRHARVL WXDRRCAHRT QTHRLVHRRN ARRRTGAA*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2143>:
     m661.seq
              ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
            1
           51 GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
          101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
          151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
          201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
          251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
          301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
          351 CGAGCCGCTG GTTGCCGCCA TTTTGGAAGC CGTCGTCCGT GCGGCAGGCG
          401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
              CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
               CGTCC.ACGG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
              GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
          601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCCTC AAACAAACCG
          651 CCGCCGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG GCCGTGGTTC
          701 TTCCGCGATT TGAAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
          751 GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
          801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
          851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA
This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:
    m661.pep
              MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
              TRKTLHRSDF ADEGGIVAVQ IAGSDPQQMA DAARYNVSLG AQLIDINMGC
              PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
              LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae* 

RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFAACL EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*

	10 20 30 40 50 60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
1	
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF 10 20 30 40 50 60
	10 20 30 40 , 30 80
	70 80 90 100 110 120
m661.pep	ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL
•	70 80 90 100 110 120
	130 140 150 160 170 180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
661	
g661	VAAILEAVVKAAGVPVTLKTRLGWHDDDQNLPAVAKIAEDCGIAALAVPRARAHANVQRR 130 140 150 160 170 180
	130 140 130 100 170 180
	190 200 210 220 230 240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPRFETL
,	
g661	GALRTHRRDQKPSEHPGLGQRRHHFAAKSRRRPQTNRRRRHHDRARRARQAVVFPRFEAL
•	190 200 210 220 230 240
	<b>250 260 270 280 290 299</b>
m661.pep	CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRRHRRCAHRTQTHRLVHRRNARRRTDTSX
g661	CRTRRFTACLEFGRMQSRHFEPHPRHARVLWXDRRCAHRTQTHRLVHRRNARRRTGAAX
	250 260 270 280 290
TP1 C 11	ential DNIA appropriate identified in N manimalidia CCTO ID 2145
	partial DNA sequence was identified in N. meningitidis <seq 2145="" id="">:</seq>
a661. <b>s</b> eq	
1	ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51	GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101	CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151	ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
201 251	GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301	CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351	CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAAA GCGGCGGGCG
401	TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451	CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501	CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551	GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601	CGGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCCTC AAACAAACCG
651	CCGCAGACGG CATTATGATA GGGCGCGGCG CGCAAGGCAG ACCGTGGTTC
701	TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTTAC CGCCTGCCTT
751	
801	
851	GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA
	0TO TD 0446 ODD 664
This correspond	Is to the amino acid sequence <seq 2146;="" 661.a="" id="" orf="">:</seq>
a661.pep	
1	MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51	
101	
	LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
	RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPRFETL RRTRCFTACL
251	EFGRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRRTDTS*
	04.60 14.44.44.44.000
m661/a661	94.6% identity in 298 aa overlap
	10 20 30 40 50 60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF

a661	MHIGGYFIDNPIAL			• • • • • • • • • • • • • • • • • • • •		
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGS	DPQQMADAAR	YNVSLGAQLI	DINMGCPAKE	(VCNVQAGSA	LMQNEPL
		1111111111	111111111	1111111111		
a661	ADEGGIVAVQIAGS	DPQQMADAAR	YNVSLGAQLI	DINMGCPAKE	(VCNVQAGSA	LMQNEPL
	70	80	90	100	110	120
	•					
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGV	PVTLKTRLGW	HDDHQNLPVI	AKIAEDCGIA	AALAVXRTHA	YANVQRR
		11111111		1111111111		:
a661	VAAILEAVVKAAGV		-			_
	130	140	150	160	170	180
	4.00	000	0.1.0	000		0.40
	190	200	210	220	230	240
m661.pep	SALRTHRRNOMPSE		_		-	
	1 - 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					
a661	SGLRPDCRNQMPSE 190	несьсукки: 200	210	220	CARRARQTVV. 230	
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAACLEFGR	MRRRYFEPHP	RHTRVLRRHR	RCAHRTQTHE	RLVHRRNARR	RTDTSX
	11111:111111	1:11111	1:111111	111111111	111111111	HIHI
a661	RRTRCFTACLEFGR	МҮКНҮБЕРНР	SHARVLRRHR	RCAHRTQTHE	LVHRRNARR	RTDTSX
<del></del>	250	260	270	280	290	

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2147>:

```
q663.seq
         ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
      1
      51 TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
    101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTTGGCA
    151 AAATGTTTC CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTTGAAACA
    201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
         ACGCGtctGC CAAATGCCTG AAATCGCTGG TGCGCTACCG CAATAAGCAT
         TATTTGGACG ACGCGCTGGC GGCGGGGGAA AAAGTCATCA TCCTGTACCC
         GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
     401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
    451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
    501 CGAagggctg cgCGCCCtcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
     551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTTGTG
     601 GATTTTTCG GCATtcaqaC GGCAACGATT ACCGGCTTGA GCCGCATTGC
     651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
    701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGGAAATC CTTTCCGAGT
     751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTTA TCGAAGAACG
     801 CGTGCGCGAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
     851 CCCGTCCGGA AGGCAGCCCC GATTTTTACT GA
```

### This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

9663.pep

1 MCTEMKFIFF VLYVLQFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51 KCFPEWDEEK RKTVLKQHFK HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNNSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTLQ FYPAWKSFPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2149>:

m663.seq

1 ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT

51 TCTGCCGTTT GCGCTGCC ACAAGATTGC CGACCTGACG GGTTTGCTTG

101 CCTACCTTCT GGTCAAACCG CGCCGCGTA TCGGCGAAAT CAATTTGGCA

151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTTGAAACA

201	GCATTTCAAA	CACATGGCGA	AACTGATGTT	GGAATACGGT	TTATATTGGT
251	ACGCGCCTGC	CGGACGTTTG	AAATCGCTGG	TGCGCTACCG	CAATAAGCAT
301	TATTTGGACG	ACGCGCTGGC	GGCGGGGGAA	AAAGTCATCA	TCCTGTATCC
351	GCACTTCACC	GCGTTCGAGA	TGGCGGTGTA	CGCGCTTAAT	CAGGATATCC
401	CGCTGATCAG	TATGTATTCC	CATCAAAAAA	ACAAGATATT	GGACGAACAG
451	ATTTTGAAAG	GCCGCAACCG	CTATCACAAC	GTCTTCCTTA	TCGGGCGCAC
501	CGAAGGGCTG	CGCGCCCTCG	TCAAACAGTT	CCGCAAAAGC	AGCGCGCCGT
551	TTCTGTATCT	GCCCGATCAG	GATTTCGGAC	GCAACGATTC	GGŤTTTTGTG
601	GATTTTTTCG	GTATTCAGAC	GGCAACGATT	ACCGGATTGA	GCCGCATTGC
651	CGCGCTTGCA	AATGCAAAAG	TGATACCCGC	CATTCCCGTC	CGCGAGGCAG
701	ACAATACGGT	TACATTGCAT	TTCTACCCTG	CTTGGAAATC	CTTTCCGGGT
751	GAAGACGCGA	AAGCCGACGC	GCAGCGCATG	AACCGTTTTA	TCGAAGACAG
801	GGTGCGCGAA	CATCCGGAAC	AATATTTTTG	GCTGCACAAG	CGTTTTAAAA
851		AGGCAGCCCC			

## This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

m663.pep 1 MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA 51 KCFSEWSEEK RKTVLKQHFK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH 101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ

151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV 201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWKSFPG

251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

Computer analysis of this amino acid sequence gave the following results:

## Homology with a predicted ORF from N. gonorrhoeae

#### m663/q663 94.9% identity in 293 aa overlap

m663.pep g663	10 MCIEMKFIFFVLYVI               MCTEMKFIFFVLYVI 10	11111111	111 1 1 11	11111111111	11:111
m663.pep g663	70 RKTVLKQHFKHMAKI           RKTVLKQHFKHMAKI 70		1 1 11111		
m663.pep	130 AFEMAVYALNQDIPI             AFEMAVYALNQDVPI 130	[	1111111111	111111111	
m663.pep	190 SAPFLYLPDQDFGRI              SAPFLYLPDQDFGRI 190	1:1111111	111111111		
m663.pep	250 FYPAWKSFPGEDAK          :   : FYPAWKSFPSEDAQ 250	1111111111	1:1111111	111111111	1

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2151>: a663.seq

- 1 ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
- 51 TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
- 101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA

```
151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAAACCG TGTTGAAACA
         GCATTTCAAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
        ACGCGCCCGC CGGGCGTTTG AAATCACTGG TGCGCTACCG CAACAACAT
    251
        TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
    301
        GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
    351
        CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
    401
        ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTTCCTTA TCGGGCGCAC
        CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
    501
        TTCTGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTTGTC
    551
        GATTTCTTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
    601
        CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
    651
        ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGGAATC CTTTCCGAGT
        GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTTA TCGAGGAACG
    751
        CGTGCGCGAA CATCCCGAGC AGTATTTTTG GCTGCACAAG CGTTTCAAAA
    801
        CCCGTCCGGA AGGCAGCCCC GATTTTTACT GA
This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:
a663.pep
        MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA KCFPEWDGKK RKTVLKQHFK HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
      1
     51
        YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
    101
        ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
        DFFGIRTATI TGLSRIAALA NAKVIPAIPV READNTVTLH FYPAWESFPS
    201
        EDAOADAORM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*
    251
           96.2% identity in 293 aa overlap
m663/a663
                            20
                                              40
           MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK
m663.pep
           MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFPEWDGKK
a663
                            20
                                     30
                                              40
                                                       50
                   70
                            80
                                     90
                                             100
                                                      110
                                                                120
           RKTVLKQHFKHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT
m663.pep
           RKTVLKQHFKHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT
a663
                   70
                            80
                                     ٩n
                                             100
                                                      110
                                                                120
                                             160
                                                      170
                           140
                                    150
                                                                180
                  130
           AFEMAVYALNQDIPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
m663.pep
            AFEMAVYALNQDVPLISMYSHQKNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS
a663
                  130
                                             160
                           200
                                    210
                                             220
           {\tt SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPVREADNTVTLH}
m663.pep
           {\tt SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALANAKVIPAIPVREADNTVTLH}
a663
                           200
                  190
                                    210
                                             220
                  250
                           260
                                    270
                                             280
           FYPAWKSFPGEDAKADAQRMNRFIEDRVREHPEOYFWLHKRFKTRPEGSPDFYX
m663.pep
            FYPAWESFPSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX
a663
                  250
                           260
                                    270
                                             280
                                                      290
```

#### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2153>:

```
g664.seq
      1
         ATGATACATC CGCACCACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
     51
         AGAAATTGTT CATCTCCTCA TAGCTGACqq qGCGCACCGG ATGGGCGGTC
         GGGCCTGCGT CTTCGGGGAA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
    101
     151 GATGCGCGC ACGGCGCGGC CGGCGGGTC GCCGGAAAAC TCTTGGTCGC
    201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
    251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
    301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
         CGAACTTGGT GTTAAAAATG TTCAAACCCT TGTTTTCCAT CGCGCCCATA
    351
         TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
     401
     451
         cCcgaagcgc gtttcgtcCc acttcatcgC gtTTTTCAA cgaTTCCACG
         GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAAA ACTCGATTTT
```

```
WO 99/57280
                                        1056
          551 GA
This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:
               MIHPHHFRAF FINGHGVEIV HLLIADGAHR MGGRACVFGE LVLAQQADVL
           51 DAAHGAAGAV AGKLLVAEHG QPFLQRKLEP VAAGYAVARP VVEIFVSDHG
          101 FNAFEIGIGG GAAVGEDELG VKNVQTLVFH RAHIEIAYGD DHENIQVIFQ
          151 PEARFVPLHR VFSTIPRQSR PWVCPLRWCK TRF*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2155>:
     m664.seq
               GTGATACATC CGCACTACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
            1
           51 AGAAATTGTT CATCTCCTCA TAGCTGGCGG GGCGCACCGG ATGGGCGGTC
          101 GGGCCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTC
          151 GATGCGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAAAAT TCTTGGTCGC
          201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
          251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAA TACTCGTGTC CGACCACGGA
          301 TTCGATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCAAGGA
          351 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCGCCCATA
          401 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
          451 ACCGAAGCGC GTTTCGTCCC ATTTCATCGC GTTTTT.CAA CGATTCCACG
          501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAA ACTCGATTTT
          551 GA
This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:
     m664.pep
               VIHPHYFRAF FINGHGVEIV HLLIAGGAHR MGGRACVFGE LVLAQQADVF
               DAAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGYAVARP VVEILVSDHG
           51
               FDAFEIGIGG GAAVGKDELG VKDVQTLVFH RAHIEIAHGD DHENIQVVFQ
           151 TEARFVPFHR VFXTIPRQSR PWACPLRWCK TRF*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
     m664/g664 91.8% identity in 183 aa overlap
```

m664.pep g664	10 VIHPHYFRAFFINGI :    :        MIHPHHFRAFFINGI 10	[11]]]]	1 11111111	1111111111	11111:111	
m664.pep	70 AGKFLVAEHGQPFL    :          AGKLLVAEHGQPFL 70		11111111111	:111111:11		:
m664.pep g664	130 VKDVQTLVFHRAHII   :          VKNVQTLVFHRAHII 130	1111:1111		111:111	1111111111	111111
m664.pep g664	TRFX      TRFX					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2157>:

```
a664.seq
1 GTGATACATC CGCACCACTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TATCGGGCGG GGCGCACCGG ATGTGCGGTC
101 GGACCTGCGT CTTCGGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTC
```

151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGGAAAAT TCTTGGTCGC

```
GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
         201
             GTCACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
         251
             TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
         301
             CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCACCCATA
             TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
         401
             ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
         451
             GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAA ACTCGATTTT
         501
         551
This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:
    a664.pep
             VIHPHHFRAF FINGHGVEIV HLLISGGAHR MCGRTCVFGE LVLAQQADVF
             DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
          51
             FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
         101
             TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*
             92.9% identity in 183 aa overlap
m664/a664
                                         30
                                                  40
                       10
                                20
                VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRACVFGELVLAQQADVFDAAHGAAGAV
    m664.pep
                VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTCVFGELVLAQQADVFDTAHGAAGAV
    a664
                                         30
                                                  40
                                                           50
                       10
                                         90
                                                 100
                                                          110
                                                                   120
                        70
                                80
                AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG
    m664.pep
                AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
     a664
                                80
                                         90
                                                 100
                                                          110
                                                                   120
                       70
                                        150
                                                 160
                                140
                      130
                VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVFXTIPRQSRPWACPLRWCK
    m664.pep
                VKDVQTLVFHRTHIEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
     a664
                                                 160
                       130
                                140
                                        150
```

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2159>:

TRFX

|||| TRFX

m664.pep

a664

```
q665.seq
          atgaagtgGg acgaaacgcg cttcgGgttg GAAtatgact tggatatttT
          CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
          GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
          ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
          CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
          CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
     251
          CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
     301
          GAACCAGTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
     351
          TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
     401
          GGCGCGGAAG TGGTGCGGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
     451
          CCAAAAAGGC ATGAAGCTAT ATTTCcaacg CCACGACGGA CAGGCAGTGA
     501
          CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
          GACCAGTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAGC
          CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
     651
          TGCCGCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
     701
          AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
     751
          GGGCAAACGC GCAACCGAAG CCGTGTTGCT GATGACCGAA GCCGAACagg
     801
          CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
     851
          GGGTTCAGCG CGCCAGTGTA TCTGAACTAT CCGTACAGCG ACGACGACCT
     901
          GCTGCTCCTG CTCGCCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG
```

```
1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAa ctGTGGGACG GCACGGAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
1251 CttcctqcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCAggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTtcgt cctGCGCGCC GACCCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
     GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
     CTGGCGCAGT TTGCCGAcaa gTtttcAGAC GACGCGCTGG TGATGGACAA
     ATATTTCGCC CTTATCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
     TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
     GCCCGTTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTTCACGC
1651
     ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1701
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
     TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTCGG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA
```

#### This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

```
g665.pep
         MKWDETRFGL EYDLDIFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
         TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
      51
         RAGRAVRRIE NIRLLRQNQF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
    101
        GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
    201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPPTPDM ADKQPMMIPV
    251 KVGLLNRNGE AVAFDYQGKR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
    301 GFSAPVYLNY PYSDDDLLLL LAHDSDAFTC WEAAQTLYRR AVAANLAALS
    351 DGIGLPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
    401 LRYHQAREAL LDTLAVRFLP KWHELDRQAA KQENQSYEYS PETADWRTLR
    451 NVCRAFVLRA DPAHIETVAE KYGEMAQNMT HEWGILSAVN GNESDTRNCL
    501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLENPNK
    551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
     601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2161>:

```
m665.seq
          ATGAAATGGG ACGAAACGCG CTTCGGTTTG GAATACGACT TGGATATTTT
      51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
     101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
     151 ACCGATACCG ATTTCGAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
     201 CCACAACTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
     251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
     301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
          GCACCAGTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCCCCG
         CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
     451 GGCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
     501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
     551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
     601 GACCAGTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAGC
     651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
     701 TGCCGCCCAC GCCCGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
     751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
     801 GGGCAAACGC GCGACCGAAG CCGTGTTGCT GCTGACCGAA GCCGAACAGA
     851 CCTTCCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCCTC GCTGCTGCGC
     901. GGGTTCAGCG CGCCGGTGCA TCTGAACTAT CCGTACAGCG ACGACGACCT
     951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTCACGCGC TGGGAAGCCG
    1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
    1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
    1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
    1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
    1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
    1251 CTTCCTGCCG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC
```

1351	AACGTCTGCC	GCGCCTTTGT	CCTGCGCGCC	GACCCCGCGC	ACATCGAAAC
1401	CGTTGCCGAA	AAATACGGCG	AAATGGCGCA	AAACATGACC	CACGAATGGG
1451	GCATCCTGTC	CGCCGTCAAC	GGCAACGAAA	GCGATACGCG	CAACCGCCTG
1501				GACGCGCTGG	
1551				CAGCGACACC	
1601				GCCTCGAAAA	
1651	GCCCGTTCGC	TCATCGGCAG	CTTCAGCCGC	AACGTCCCGC	ATTTCCACGC
1701	AGAAGACGGC	AGCGGCTACC	GCTTCATCGC	CGACAAAGTC	ATCGAAATCG
1751	ACCGCTTCAA	CCCGCAGGTC	GCCGCCCGCT	TAGTGCAGGC	GTTCAACCTC
1801				TTGGTGAAAC	
1851	GCGCATTCGG	GCGCAGGAAG	GATTGTCGAA	AGACGTGGGC	GAAATCGTCG
1901	GCAAAATTTT	GGATTGA			

## This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

				AARLVQAFNL
CNKLEPHRKN	LVKQALQRIR	AQEGLSKDVG	EIVGKILD*	
	TDTDFEGIES RASRAVRRIE GAEVVRMYHT DQFALWYSQA KVGLLNRNGE GFSAFVHLNY DGVELPKHEK LRYHQAREAL NVCRAFVLRA LAQFADKFSD ARSLIGSFSR	TDTDFEGIES VVGHEYFHNW RASRAVRRIE NIRLLRQHQF GAEVVRMYHT LLGEEGFQKG DQFALWYSQA GTPVLEAEGR KVGLLNRNGE AVAFDYQGKR GFSAPVHLNY PYSDDDLLLL DGVELPKHEK LLAAVEKVIS LRYHQAREAL LDTLAVHFLP NVCRAFVLRA DPAHIETVAE LAQFADKFSD DALVMDKYFA ARSLIGSFSR NVPHFHAEDG	TDTDFEGIES VVGHEYFHNW TGNRVTCRDW RASRAVRRIE NIRLLRQHQF PEDAGPTAHP GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG DQFALWYSQA GTPVLEAEGR LKNNIFELTV KVGLLNRNGE AVAFDYQGKR ATEAVLLLTE GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LRYHQAREAL LDTLAVHFLP KWHELNRQAA NVCRAFVLRA DPAHIETVAE KYGEMAQNMT LAQFADKFSD DALVMDKYFA LVGSSRRSDT ARSLIGSFSR NVPHFHAEDG SGYRFIADKV	MKWDETRFGL EYDLDIFMVV AVGDFNMGAM ENKGLNIFNT TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT RASRAVRRIE NIRLLRQHQF PEDAGPTAHP VRPASYEEMN GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPPTPDM KVGLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLEGV GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LRYHQAREAL LDTLAVHFLP KWHELNRQAA KQENQSYEYS NVCRAFVLRA DPAHIETVAE KYGEMAQNMT HEWGILSAVN LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

# Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m665/g665 96.1% identity in 637 aa overlap

m665.pep	10 MKWDETRFGLEYDL	шшш	30 FNMGAMENKG           FNMGAMENKG	11111111111		
g665	MKWDETRFGLEYDL 10	20	30	40	50	60
m665.pep	70 VVGHEYFHNWTGNR             VVGHEYFHNWTGNR	VTCRDWFQLS			 AVRRIENIRI	:   LLRQNQF
•	70 130	80 140	90 150	100 160	110 170	120 180
m665.pep	PEDAGPTAHPVRPA	1111111111	1111111111	1111111111		ПППП
g665	PEDAGPTAHPVRPV 130	SYEEMNNFYT 140	MTVYEKGAEV 150	VRMYHTLLGE 160	EGFQKGMKLY 170	YFQRHDG 180
m665.pep	190 QAVTCDDFRAAMAE             QAVTCDDFRAAMAE 190	1111111111	4111111111	[[]]]]	:1111:111	
m665.pep	250 TDKQPMMIPVKVGI :          ADKQPMMIPVKVGI 250	11111111111		1111:11111:		HHHHH

m665.pep g665	310 GFSAPVHLNYPYSD       :        GFSAPVYLNYPYSD 310	111111111		1111111	:   :	11111
m665.pep	370 LLAAVEKVISDDLL             LLAAVEKVISDDLL 370	1.1441111111111	1111111111	:		111:11
m665.pep	430 KWHELNRQAAKQEN      :        KWHELDRQAAKQEN 430	11111111:1	111111111	11111111111		111111
m665.pep	490 HEWGILSAVNGNES           HEWGILSAVNGNES 490	1111 11111	11111111111			1:1111
m665.pep g665	550 PKFSLENPNKARSI            PKFSLENPNKARSI 550	11111111111	111:11111		[	11111
m665.pep	610 CNKLEPHRKNLVK(            CNKLEPHRKNLVK( 610			1111		

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2163>:

nowing be	muai Divito	oquence	1001111111111		•
665.seq				CD D MD CCD CM	መራሮችሞአሞሞሞሞ
1	ATGAAGTGGG	ACGAAACGCG	CTTCGGTTTG	GAATACGACT	TGGATATITI
51	CATGGTCGTC	GCCGTGGGCG	ATTTCAATAT	GGGTGCGATG	GAAAACAAGG
101	GTTTGAACAT	CTTTAACACC	AAGTTCGTCC	TTGCCGACAG	D.GCD.A.M.D.M.M.
151	ACCGATACCG	ATTTTGAAGG	CATCGAATCC	GTGGTCGGAC	ACGAATATTT
201	CCACAACTGG	ACGGGCAACC	GCGTGACCTG	CCGCGACTGG	TTCCAGCTTT
251	CGCTGAAGGA	AGGGTTGACC	GTGTTCCGCG	ACCAAGAATT	TTCCGGCGAC
301	CGCGCCAGCC	GCGCCGTGCG	CCGTATCGAA	AACATCCGCC	TGCTGCGCCA
351	GCACCAGTTC	CCCGAAGACG	CAGGTCCGAC	CGCACATCCG	GTGCGCCCCG
401	CCCGATATGA	GGAGATGAAC	AATTTCTACA	CCATGACCGT	TTATGAAAAA
451	GGCGCGGAAG	TGGTGCGGAT	GTATCACACC	TTGCTCGGCG	AAGAGGGCTT
501	CCAAAAAGGT	ATGAAGCTCT	ATTTCCAACG	CCACGACGGA	CAGGCTGTTA
551	CCTGCGACGA	TTTCCGCGCG	GCGATGGTGG	ACGCGAACGG	CATCAACCTC
601	GACCAATTCG	CCTTGTGGTA	CAGCCAAGCA	GGTACGCCGG	TTTTAGATGC
651	TCAAGGGCGT	CTGAAAAACA	ATGTGTTCGA	GTTAACCATC	AAACAAACCG
701	TGCCGCCCAC	GCCCGATATG	GCGGACAAAC	AGCCGATGAT	GATTCCCGTC
751	AAAATCGGGC	TGCTGAACTG	CAACGGCGAA	GCGGTGGCAT	TTGATTATCA
801	GGGCAAACGC	GCGACCGAAG	CCGTGTTGCT	GCTGACCGAA	GCCGAACAGA
851	CCTTCCAGTT	CGAAAGCGTA	ACCGAAGCCG	TCGTTCCCTC	GCTGCTGCGC
901	GGGTTCAGCG	CGCCGGTGCA	TCTGAACTAT	CCGTACAGCG	ACGACGACCT
951	GCTGCTTCTG	CTCGCCCATG	ACAGCGACGC	CTTCACGCGC	TGGGAAGCCG
1001	CACAAACGCT	CTACCGCCGT	GCCGTCGCCG	CCAACCTTGC	CGCGCTTTCA
1051	GACGGCGTCG	AGTTGCCGAA	ACACGAAAAA	CTGCTTGCCG	CCGTCGAAAA
1101	AGTCATTTCA	GACGACCTCT	TAGACAACGC	TTTCAAAGCC	CTGCTTTTGG
1151	GTGTGCCGTC	TGAAGCCGAG	CTGTGGGACG	GCGCGGAAAA	CATCGACCCG
1201	CTGCGCTACC	ATCAGGCGCG	CGAAGCCTTG	TTGGATATAC	TTGCCGTCCG
1251	CTTTCTGCCG	AAATGGCACG	AATTGAACCG	TCAGGCGGCG	AAGCAGGAAA
1301	ACCAAAGCTA	CGAGTACAGC	CCCGAAGCCG	CCGGTTGGCG	CACGCTGCGC
1351	AATGTCTGCC	GCGCCTTCGT	CCTGCGCGCC	GATCCCGCGC	ACATCGAAAC

1401		AAATACGCCG			
1451		CGCCGTCAAC			
1501		TTGCCGACAA			
1551		CTCGTCGGCT			
1601	TTCAAACCGC	CTTGCAGCAT	CCGAAGTTCA	GCCTCGAAAA	TCCCAACAAA
1651				AACGTCCCGC	
1701	AGAAGACGGC	AGCGGCTACC	GCTTCATCGC	CGACAAAGTC	ATCGAAATCG
1751	ACCGCTTTAA	CCCGCAGGTC	GCCGCCCGCC	TGGTGCAGGC	GTTCAACCTC
1801	TGCAACAAGC			TTGGTGAAAC	
1851	GCGCATTCGG	GCGCAGGAAG	GATTGTCGAA	AGACGTGGGC	GAAATCGTCG
1901	GCAAAATTTT	GGATTGA			
This correspond	s to the amin	o acid seque	nce <seq ii<="" th=""><th>O 2164; ORI</th><th>₹ 665.a&gt;:</th></seq>	O 2164; ORI	₹ 665.a>:
a665.pep					
1	MKWDETRFGL	EYDLDIFMVV	AVGDFNMGAM	ENKGLNIFNT	KFVLADSRTA
51	TDTDFEGIES	VVGHEYFHNW	TGNRVTCRDW	FQLSLKEGLT	VFRDQEFSGD
101	RASRAVRRIE	NIRLLRQHQF	PEDAGPTAHP	VRPARYEEMN	NFYTMTVYEK
151	GAEVVRMYHT	LLGEEGFQKG	MKLYFQRHDG	QAVTCDDFRA	AMVDANGINL

151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL 201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPPTPDM ADKQPMMIPV

251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR 301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLAALS 351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP

401 LRYHQAREAL LDILAVRFLP KWHELNRQAA KQENQSYEYS PEAAGWRTLR NVCRAFVLRA DPAHIETVAE KYAEMAQNMT HEWGILSAVN GNESDTRNRL LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK

551 ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL

601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

97.3% identity in 638 aa overlap m665/a665

m665.pep	10 MKWDETRFGLEYDLDI					
a665	MKWDETRFGLEYDLDI					
m665.pep	70 VVGHEYFHNWTGNRVI             VVGHEYFHNWTGNRVI 70	1111111111	1111111111	111111111	1111111111	1111
m665.pep	130 PEDAGPTAHPVRPASY !!!!!!!!!!!!! PEDAGPTAHPVRPARY 130		1111111111	11111111111	111111111	1111
m665.pep	190 QAVTCDDFRAAMADAN             QAVTCDDFRAAMVDAN 190		111111111:	1:111111:1	111:111111	1111
m665.pep	250 TDKQPMMIPVKVGLLM :          ADKQPMMIPVKIGLLM 250	1 11111111	1111111111	HITHIII	:1:111111	1111
m665.pep	310 GFSAPVHLNYPYSDD            GFSAPVHLNYPYSDD 310	111111111	1111111111	1111111111	1:11111111	1111

m665.pep	370 LLAAVEKVISDDLLI	380 NAFKALLLG	390 VPSEAELWDG	400 AENIDPLRYI	410 IQAREALLDT	420 LAVHFLP
moos.pep		11111111	1111111111	1111111111	1111111	111:111
a665	LLAAVEKVISDDLLI	NAFKALLLG	VPSEAELWDG	AENIDPLRY	IQAREALLDI	LAVRFLP
8000	370	380	390	400	410	420
		_			470	480
	430	440	450	460	470	
m665.pep	KWHELNRQAAKQEN(	OSYEYSPEAR	AGWRTLRNVCR	AFVLRADPA	HIETVAEKIG	EMAQNMI
				111111111		
a665	KWHELNRQAAKQEN				ILETVAEKYA	EMAQNM1
	430	440	450	460	470	480
		500	E10	520	530	540
	490	500	510	•		
m665.pep	HEWGILSAVNGNES	DTRNRLLAQI	ADKISDDALV	MDKYFALVG	SSKKSDILQQ	VKIALQR
	111111111111111111111111111111111111111					11111:
a665	HEWGILSAVNGNES				SSKKSDTLQQ	IVQTALQH
	490	500	510	520	530	540
	5.50	560	570	580	590	600
	550 PKFSLENPNKARSL					
m665.pep	PKESLENPNKARSL	IGSESKNVPI	TENALUGSGIF	(LIMDKATET)	TITLITITI TKENEQVAAN	1111111
a665	PKFSLENPNKARSL				JRENPQVAAR 590	TNAWAT
•	550	560	570	580	590	000
	610	620	630	639		
	610		•	000		
m665.pep	CNKLEPHRKNLVKQ					
a665	CNKLEPHRKNLVKQ			PVITDY		
	610	620	630			

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2165>: g665-1.seq

-1.000	1				
1	ATGAGCAAAA	CCGTCCGTTA		TACCAAACGC	
51	CATTCTTGAA	ACCGAACTGC	ATTTCGACAT		CAAACCGTCG
101	TGAAGTCGCG	TTTGACGGTC	GAGCCGCAGA	GGGCGGCGA	
151	TTGGACGGTT	CGGCAAAACT	CTTGTCCGTC		GCGCGGCGGC
201	GGATTATGTG	TTGGAAGGCG	AGACGCTGAC	GATTGCAGAC	
251	AACGCTTCAC	CGTCGAAGTG	GAAACCGAAA	TCCTGCCGGC	
301	TCGCTGATGG	GGCTGTATGC	TTCCGGCGGC		CCCAGTGCGA
351	GCCGGAGGGC	TTCCGCAAAA	TCACGTTCTA	CATCGACCGT	CCGGATGTGA
401	TGTCCAAGTT	CACGACCACC	ATCGTCGCGG	ACAAAAAACG	CTATCCCGTT
451	TTGCTTTCCA	ACGGCAACAA	AATCGACGGC	GGCGAGTTTT	CAGACGGCCG
501	CCATTGGGTG	AAATGGGAAG	ACCCGTTTGC	CAAACCGAGT	TATCTGTTTG
551	CTTTGGTCGC	GGGCGATTTG	GCGGTAACGG	AAGACCGTTT	CACCACCATG
601	AGCGGCAGAA	ACGTCAAAAT	CGAGTTTTAC	ACCACCGAAG	CGGACAAACC
651	CAAGGTCGGC	TTTGCCGTGG	AATCGTTGAA	AAACGCGATG	AAGTGGGACG
701	AAACGCGCTT	CGGGTTGGAA	TATGACTTGG	ATATTTTCAT	GGTCGTCGCC
751	GTAGGCGATT	TCAATATGGG	CGCGATGGAA		TGAACATTTT
801	TAACACCAAG	TTCGTCCTCG	CCGACAGCCG	CACCGCCACC	GATACCGATT
851	TCGAAGGCAT	TGAATCCGTG	GTCGGACACG		CAACTGGACG
901	GGCAACCGCG	TAACCTGCCG	CGACTGGTTC	CAGCTTTCGC	TGAAGGAAGG
951	GCTGACCGTG	TTCCGCGACC	AAGAGTTTTC		GCCGGCCGCG
1001	CCGTGCGCCG	CATCGAGAAC	ATCCGCCTGC		CCAGTTCCCC
1051	GAAGACGCAG	GCCCGACCGC	CCATCCGGTG		GCTATGAGGA
1101	GATGAACAAT	TTCTACACCA	TGACCGTTTA		GCGGAAGTGG
1151	TGCGGATGTA	TCATACCCTG	CTCGGCGAAG		AAAAGGCATG
1201	AAGCTATATT	TCCAACGCCA	CGACGGACAG		GCGACGATTT
1251	CCGCGCGGCG	ATGGCGGATG	CGAACGGCAT		CAGTTCGCCT
1301	TGTGGTACAG	CCAGGCGGGC	ACGCCCGTTT		AGGCCGTCTG
1351	AAAAACAATG	TTTTCGAGTT	AACCATTAAA		CGCCCACGCC
1401	CGATATGGCG	GACAAACAGC	CGATGATGAT	TCCCGTCAAA	GTCGGGCTTC
1451	TGAACCGCAA	CGGCGAAGCG	GTGGCATTCG	ATTATCAGGG	
1501	ACCGAAGCCG	TGTTGCTGAT	GACCGAAGCC	GAACAGGCCT	
1551	AGGTGTAACC	GAAGCCGTCG	TTCCCTCGCT	GCTGCGCGGG	
1601	CAGTGTATCT	GAACTATCCG	TACAGCGACG		
1651	GCCCACGACA	GCGACGCTTT	CACGTGCTGG		
1701	CCGTCGCGCC	GTCGCCGCCA	ACCTTGCCGC	GCTTTCAGAC	GGCATCGGGT

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1063
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1751 TGCCGAAACA CGAAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
     GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTTGGGCG TGCCGTCCGA
     AGCCGAACTG TGGGACGGCA CGGAAAACAT CGACCCGCTG CGCTACCATC
     AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCGCTT CCTGCCGAAA
     TGGCACGAAT TGGACCGTCA GGCGGCGAAG CAGGAAAACC AAAGTTACGA
     ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
     CCTTCGTCCT GCGCGCCGAC CCCGCGCACA TCGAAACTGT TGCCGAAAAA
     TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCGCCCTT
     ATCGGCTCAA GCCGCCGCAG CGACACCCTG CAACAGGTTC AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG AATTGCAGTG CATTCGGGCG
     CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AGATTTTGGG
```

#### This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>: g665-1.pep

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1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPQRAGEPLV
   LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSERFTVEV ETEILPAENK
    SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
101
    LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDIFMVVA
    VGDFNMGAME NKGLNIFNTK FVLADSRTAT DTDFEGIESV VGHEYFHNWT
    GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR AGRAVRRIEN IRLLRQNQFP
    EDAGPTAHPV RPVSYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
    KLYFORHDGO AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
    KNNVFELTIK QTVPPTPDMA DKQPMMIPVK VGLLNRNGEA VAFDYQGKRA
451
    TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
    DLLDNAFKAL LLGVPSEAEL WDGTENIDPL RYHQAREALL DTLAVRFLPK
    WHELDRQAAK QENQSYEYSP ETADWRTLRN VCRAFVLRAD PAHIETVAEK
    YGEMAONMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
    QEGLSKDVGE IVGKILG*
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2167>: m665-1.seq

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1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
     TATTCTCAAA ACCGATTTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
 51
     TGAAGTCGCG TTTGACGGTT GAGCCGCAGA GGGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
     AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
     TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTTGTTTA CCCAGTGCGA
301
     GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
     TGTCCAAGTT CACCACCACC ATCGTCGCCG ACAAAAAACG CTATCCCGTT
401
     TTGCTTTCCA ACGGCAACAA AATCGACGGC GGCGAGTTTT CAGACGGCCG
451
     CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
501
     CTTTGGTCGC GGGCGATTTG GCGGTAACGG AAGACTATTT CACCACCATG
     AGCGGCAGAA ACGTCAAAAT CGAGTTTTAC ACCACCGAAG CGGACAAGCC
     CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATCTT
     TAACACCAAG TTCGTCCTTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
     CCGTGCGCCG CATCGAAAAC ATCCGCCTGC TGCGCCAGCA CCAGTTCCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCCGCCA GCTATGAGGA
     GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTAG
     TGCGGATGTA TCACACCCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1151
     AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATTT
1201
     CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
     TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGGAAGCGGA AGGTCGTCTG
     AAAAACAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCCACGCC
1351
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCG ACTATCAGGG CAAACGCGCG
```

q665-1

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ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
     AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
      CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
     GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1651
     CCGCCGCGC GTCGCCGCCA ACCTTGCCAC GCTTTCAGAC GGCGTTGAGC
1701
      TGCCGAAACA CGAAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1751
     GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTTGGGCG TGCCATCCGA
1801
      AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
      AGGCGCGCGA AGCCTTGTTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1901
      TGGCACGAAT TGAACCGTCA GGCGGCGAAG CAGGAAAACC AAAGCTACGA
1951
      ATACAGCCCC GAAGCCGCCG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2001
      CCTTTGTCCT GCGCGCCGAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
2051
      TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2101
      CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2151
      CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTTGCCCTC
2201
      GTCGGCTCAA GCCGCCGCAG CGACACCCTG CAACAGGTTC GAACCGCCTT
2251
      GCAGCATCCG AAATTCAGCC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2301
      TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2351
      GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2401
      GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2451
      AGCCGCACCG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTCGGGCG
2501
      CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGGA
2551
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This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pe	p			0m: !!!!! 0 T M!!	PROPUGERTU
1	MSKTVHYLKD	YQTPAYHILK	TDLHFDINEP	QTVVKSRLTV	EPQRVGEPLV
51	LDGSAKLLSV	KINGAAADYV	LEGETLTIAG	VPSERFTVEV	ETEILPAENK
101	SLMGLYASGG	NLFTQCEPEG	FRKITFYIDR	PDVMSKFTTT	IVADKKRYPV
151	LLSNGNKIDG	GEFSDGRHWV	KWEDPFSKPS	YLFALVAGDL	AVTEDYFTTM
201	SGRNVKIEFY	TTEADKPKVG	FAVESLKNAM	KWDETRFGLE	YDLDIFMVVA
251	VGDFNMGAME	NKGLNIFNTK	FVLADSRTAT	DTDFEGIESV	VGHEYFHNWT
301	GNRVTCRDWF	OLSLKEGLTV	FRDQEFSGDR	ASRAVRRIEN	IRLLRQHQFP
351	EDAGPTAHPV	RPASYEEMNN	FYTMTVYEKG	AEVVRMYHTL	LGEEGFQKGM
401	KLYFQRHDGQ		MADANGINLD	QFALWYSQAG	TPVLEAEGRL
	KNNIFELTVK		DKOPMMIPVK	VGLLNRNGEA	VAFDYQGKRA
451			EAVVPSLLRG	FSAPVHLNYP	YSDDDLLLLL
501	TEAVLLLTEA	EAAOTLYRRA	VAANLATLSD	GVELPKHEKL	
551	AHDSDAFTRW		WDGAENIDPL		DTLAVHFLPK
601	DLLDNAFKAL		EAAGWRTLRN	VCRAFVLRAD	PAHIETVAEK
651	WHELNRQAAK				
701	YGEMAQNMTH		NESDTRNRLL	_	
751	VGSSRRSDTL		KFSLENPNKA		
801	GYRFIADKVI	EIDRFNPQVA	ARLVQAFNLC	NKLEPHRKNL	VKQALQRIRA
851	OEGLSKDVGE	IVGKILD*			

m665-1/g665-1 96.1% identity in 866 aa overlap 30 10 20 MSKTVHYLKDYQTPAYHILKTDLHFDINEPQTVVKSRLTVEPQRVGEPLVLDGSAKLLSV m665-1.pep MSKTVRYLKDYQTPAYRILETELHFDIAEPQTVVKSRLTVEPQRAGEPLVLDGSAKLLSV q665-1 40 50 30 20 10 90 100 80 70 KINGAAADYVLEGETLTIAGVPSERFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG m665-1.pep KINGAAADYVLEGETLTIADVPSERFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG q665-1 100 80 90 170 180 160 150 140 FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFSDGRHWVKWEDPFSKPS m665-1.pep FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFSDGRHWVKWEDPFAKPS q665-1 170 180 160 150 130 140 210 200 YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGFAVESLKNAMKWDETRFGLE m665-1.pep YLFALVAGDLAVTEDRFTTMSGRNVKIEFYTTEADKPKVGFAVESLKNAMKWDETRFGLE q665-1 210 230 190 200 260 270 280 290 250 YDLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDTDFEGIESVVGHEYFHNWT m665-1.pep 

YDLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDTDFEGIESVVGHEYFHNWT

						200	300
		250	260	270	280	290	
	CNDUMCE	310 RDWFQLSLKEG	320	330 SGDRASRAVRI	340 RIENIRLLROE	350 HOFPEDAGPT	360 AHPV
m665-1.pep	1111111				111111111:	:	1111
g665-1	GNRVTCF	RDWFQLSLKEO	SLTVFRDQEFS 320	GDRAGRAVRI 330	RIENIRLLROI 340	NQFPEDAGPTA	360
				390	400	410	420
m665-1.pep	RPASYE	370 EMNNFYTMTV)	380 (EKGAEVVRM)	YHTLLGEEGF	OKGMKLYFQR	HDGQAVTCDD	FRAA
	(1.111)				[1111111111	[	1111
g665-1	RPVSYE	370	380	390	400	410	420
		430	440	450	460	470	480
m665-1.pep	MADANG	INLDOFALWY	SOAGTPVLEA	EGRLKNNIFE	LTVKQTVPPT:	PDMTDKQPMM	IPVK
g665-1	MADANG:		SQAGTPVLEA	EGRLKNNVFE	LTIKQTVPPT:	PDMADKQPMM	IPVK
9003 1		430	440	450	460	470	480
		490	500	510	520	530	540
m665-1.pep	111111	NGEAVAFDYQ	111111111	:11111:1	11111111	111111111:	1111
g665-1	VGLLNRI	NGEAVAFDYQ	GKRATEAVLL	MTEAEQAFPL 510	EGVTEAVVPS 520	LLRGFSAPVY 530	LNYP 540
		490	500	310			
	ACDDDI.	550 LLLLAHDSDA	560 ETRWEAAOTI.	570 YRRAVAANLA	580 TLSDGVELPK	590 HEKLLAAVEK	600 VISD
m665-1.pep	111111	1111111111	11 1111111	11111111111	:1111: 111	111111111	! ! ! !
g665-1	YSDDDL	LLLLAHDSDA 550	FTCWEAAQTL 560	YRRAVAANLA 570	ALSDGIGLPK 580	590	600
		610	620	630	640	650	660
m665-1.pep	DLLDNA	FKALLLGVPS	EAELWDGAEN	IDPLRYHQAR	EALLDTLAVH	FLPKWHELNE	QAAK
-	111111		:       EARLWDGTEN		:         EALLDTLAVR		IIII QAAK
g665-1	אאסקונט	610	620	630	640	650	660
		670	680	690	700	710	720
m665-1.pep	QENQSY	EYSPEAAGWR	TLRNVCRAFV	LRADPAHIET	VAEKYGEMAQ	NMTHEWGILS	SAVNG
g665-1	QENQSY	EYSPETADWR	TLRNVCRAFV	LRADPAHIET	VAEKYGEMAC	NMTHEWG1LS	SAVNG
<b>3</b> ·		670	680	690	700	710	720
		730	740	750	760	770	780
m665-1.pep	111111	NRLLAQFADK	1111111111	11111:1111			
g665-1	NESDTE	RNCLLAQFADE	FSDDALVMD	KYFALIGSSRI	RSDTLQQVQT <i>I</i> 760	ALQHPKFSLEI	NPNKA 780
		730					0.40
m665-1.pep	PST.TG9	790 SFSRNVPHFH	800 AEDGSGYRFI	810 ADKVIEIDRFI	820 NPQVAARLVQ1	830 AFNLCNKLEPI	840 HRKNL
• •	111111		1:11111111		1111111111	1	11111
g665-1	RSLIGS	FSRNVPHFHA	800 AODGSGYRF17	810	820	830	840
		850	860				
m665-1.pep	VKQAL(	ORIRAQEGLS	KDVGEIVGKI:	LDX			
a 6 6 5 1	VKOET	 QCIRAQEGLS	 KDVGEIVGKI	l LGX			
g665-1	4.1/Z+11/	850	860				
The follow	ina nar	tial DNA	sequence v	was identi	fied in N.	meningitio	dis <s< th=""></s<>

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2169>: a665-1.seq

-1.sec	I				
1	ATGAGCAAAA	CCGTGCATTA	TCTCAAAGAC	TATCAAACGC	CCGCCTACCA
51	TATTCTCAAA	ACCGATTTAC	ATTTTGATAT	TAACGAACCG	CAAACCATTG
101	TGAAGTCGCG	TTTGACGGTC	GAGCCGAAGA	GGGTGGGAGA	GCCGCTGGTG
151	TTGGACGGTT	CGGCGAAACT	CTTGTCCGTC	AAAATCAACG	GCGTGGCGGC
201	GGATTATGTG	TTGGAAGGCG	AGACGCTGAC	GATTGCGGAC	GTGCCGTCCG
251	AACGCTTCAC	CGTCGAAGTG	GAAACCGAAA	TCCTGCCGGC	GGAAAACAAA
301	TCGCTGATGG	GGCTGTATGC	GTCCGCCGGT	AACCTGTTTA	CCCAGTGCGA
351	GCCGGAGGGC	TTCCGCAAAA	TCACGTTCTA	TATCGACCGT	CCGGATGTCA
401	TGTCCAAGTT	CACGACCACC	ATCGTCGCGG	ACAAAAAACG	CTATCCCGTT
451	TTGCTCTCCA	ACGGCAACAA	AATCGACGGC	GGCGAGTATT	CAGACGGCCG

501	CCATTGGGTG	1 11 11 1 0 0 0 1 1 1 1	ACCCGTTTGC	CAAACCGAGT	TATCTGTTTG
551	CTTTGGTCGC	GGGCGATTTG	GCGGTCACGG	1110110111111	CACCACCATG
601	AGCGGCAGAA	ACGTCAAAAT	CGAGTTTTAC	1100110001110	CGGACAAGCC
651	CAAGGTCGGC	TTTGCCGTGG	AATCGCTGAA	AAACGCAATG	AAGTGGGACG
701	AAACGCGCTT	CGGTTTGGAA	TACGACTTGG	ATATTTTCAT	GGTCGTCGCC
751	GTGGGCGATT	TCAATATGGG	TGCGATGGAA	AACAAGGGTT	TGAACATCTT
801	TAACACCAAG	TTCGTCCTTG	CCGACAGCCG	TACCGCCACC	GATACCGATT
851	TTGAAGGCAT	CGAATCCGTG	GTCGGACACG	AATATTTCCA	CAACTGGACG
901	GGCAACCGCG	TGACCTGCCG	CGACTGGTTC	CAGCTTTCGC	TGAAGGAAGG
951	GTTGACCGTG	TTCCGCGACC	AAGAATTTTC	CGGCGACCGC	GCCAGCCGCG
1001	CCGTGCGCCG	TATCGAAAAC	ATCCGCCTGC	TGCGCCAGCA	CCAGTTCCCC
1051	GAAGACGCAG	GTCCGACCGC	ACATCCGGTG	CGCCCCGCCC	GATATGAGGA
1101	GATGAACAAT	TTCTACACCA	TGACCGTTTA	TGAAAAAGGC	GCGGAAGTGG
1151	TGCGGATGTA	TCACACCTTG	CTCGGCGAAG	AGGGCTTCCA	AAAAGGTATG
1201	AAGCTCTATT	TCCAACGCCA	CGACGGACAG	GCTGTTACCT	GCGACGATTT
1251	CCGCGCGGCG	ATGGTGGACG	CGAACGGCAT	CAACCTCGAC	CAATTCGCCT
1301	TGTGGTACAG	CCAAGCAGGT	ACGCCGGTTT	TAGATGCTCA	AGGGCGTCTG
1351	AAAAACAATG	TGTTCGAGTT	AACCATCAAA	CAAACCGTGC	CGCCCACGCC
1401	CGATATGGCG	GACAAACAGC	CGATGATGAT	TCCCGTCAAA	ATCGGGCTGC
1451	TGAACTGCAA	CGGCGAAGCG	GTGGCATTTG	ATTATCAGGG	CAAACGCGCG
1501	ACCGAAGCCG	TGTTGCTGCT	GACCGAAGCC	GAACAGACCT	TCCAGTTCGA
1551	AAGCGTAACC	GAAGCCGTCG	TTCCCTCGCT	GCTGCGCGGG	TTCAGCGCGC
1601	CGGTGCATCT	GAACTATCCG	TACAGCGACG	ACGACCTGCT	GCTTCTGCTC
1651	GCCCATGACA	GCGACGCCTT	CACGCGCTGG	GAAGCCGCAC	AAACGCTCTA
1701	CCGCCGTGCC	GTCGCCGCCA	ACCTTGCCGC	GCTTTCAGAC	GGCGTCGAGT
1751	TGCCGAAACA	CGAAAAACTG	CTTGCCGCCG	TCGAAAAAGT	CATTTCAGAC
1801	GACCTCTTAG	ACAACGCTTT	CAAAGCCCTG	CTTTTGGGTG	TGCCGTCTGA
	AGCCGAGCTG	TGGGACGGCG	CGGAAAACAT	CGACCCGCTG	CGCTACCATC
1851	AGGCGCGCGA			CCGTCCGCTT	TCTGCCGAAA
1901	TGGCACGAAT	TGAACCGTCA		CAGGAAAACC	AAAGCTACGA
1951	GTACAGCCCC			GCTGCGCAAT	GTCTGCCGCG
2001 2051	CCTTCGTCCT		CCCGCGCACA	TCGAAACCGT	TGCCGAGAAA
2101	TACGCCGAAA			GAATGGGGCA	TCCTGTCCGC
	CGTCAACGGC			CCGCCTGCTG	
2151	CCGACAAGTT			TGGACAAATA	TTTCGCCCTC
2201	GTCGGCTCAA			CAACAGGTTC	AAACCGCCTT
2251	GCAGCATCCG			CAACAAAGCC	CGCTCGCTCA
2301	TCGGCAGCTT			TCCACGCAGA	AGACGGCAGC
2351	GGCTACCGCT				GCTTTAACCC
2401	GCAGGTCGCC	·			AACAAGCTCG
2451	AGCCGCACCG				CATTCGGGCG
2501	CAGGAAGGAT				
2551		IGICGNANGA			
2601	TTGA				

## This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

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a665-1.pep
       1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
      51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSERFTVEV ETEILPAENK
     101 SLMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
     201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGLE YDLDIFMVVA
     251 VGDFNMGAME NKGLNIFNTK FVLADSRTAT DTDFEGIESV VGHEYFHNWT
          GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQFP
     351 EDAGPTAHPV RPARYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
     401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
     451 KNNVFELTIK QTVPPTPDMA DKQPMMIPVK IGLLNCNGEA VAFDYQGKRA
501 TEAVLLITEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
     551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVELPKHEKL LAAVEKVISD
      601 DLLDNAFKAL LLGVPSEAEL WDGAENIDPL RYHQAREALL DILAVRFLPK
          WHELNRQAAK QENQSYEYSP EAAGWRTLRN VCRAFVLRAD PAHIETVAEK
      651
      701 YAEMAQNMTH EWGILSAVNG NESDTRNRLL AQFADKFSDD ALVMDKYFAL
           VGSSRRSDTL QQVQTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
      751
      801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQRIRA
      851 QEGLSKDVGE IVGKILD*
```

#### a665-1/m665-1 97.2% identity in 867 aa overlap

2005 1/ 2005		=				
	10	20	30	40	50	60
	MSKTVHYLKDYQTPA	AVHTT.KTDT.H	FDINEPOTIV	KSRLTVEPKF	VGEPLVLDGS	AKLLSV
a665-1.pep			11111111:1		1111111111	11111
665 1	MSKTVHYLKDYQTP	AYHILKTDLH	FDINEPQTVV	/KSRLTVEPQF	RVGEPLVLDGS	AKLLSV
m665-1	10	20	30	40	50	60
	70	80	90	100	110	120

a665-1.pep	KINGVAADYVLEGETLTIADVPSERFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
a665-1.pep	130 140 150 160 170 180 FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYSDGRHWVKWEDPFAKPS
a665-1.pep	190 200 210 220 230 240 YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGFAVESLKNAMKWDETRFGLE
a665-1.pep	250 260 270 280 290 300 YDLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRTATDTDFEGIESVVGHEYFHNWT
asss-1.psp m665-1	310 320 330 346 350 360 360 GRANTERINGENTALIZATION CONTROL OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STAT
a665-1.pep	370 380 390 400 410 420  RPARYEEMNNFYTMTVYEKGAEVVRNYHTLLGEEGFOKGMKLYFORHDGQAVTCDDFRAA
a665-1.pep	430 449 450 460 470 480 MVDANGINLDQFALWYSQAGTPVLDAQGRLKNNVFELTIKQTVPPTPDMADKQPMMIPVK  :
a665-1.pep	490 500 510 520 530 540  IGLINCHGEAVAFDYOGKRATEAVLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP :
e665-1.pep	550 560 570 580 590 600 YSDDDILLI LAHDSDAFTRWEAAQTLYRRAVAANLAALSDGVELPKHEKLLAAVEKYTSD 
a665-1.pep	610 520 630 640 650 660 DLLDNAFKALLLGVPSEAELWDGAENIDPLRYHQAREALLOILAVRFLPKWHELNRQAAK HILLITTHITTHITTHITHITHITHITHITHITHITHITHITHI
a665-1.pep m665-1	670 680 690 700 710 720  QENQSYEYSPEAAGWRTLRNVCRAFVLRADPAHLETVAŁKYAEMAQNMTHEWGILSAVNC
a665-1.pep m665-1	730 740 750 760 770 780  NESOTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQCVQTALQHPKFSLENPNKA
a665-1.pep m665-1	790 800 810 820 830 840 RSEIGSFSRNVPRFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

1068

820

830

810

```
850
                           860
           VKQALQRIRAQEGLSKDVGEIVGKILDX
a665-1.pep
           1511111111111111111111111111111111
           VKQALQRIRAQEGLSKDVGEIVGKILDX
m665-1
                  850
                           860
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2171>:
     q666.seq
               ATGCTTTGTA TGAATTATCA ATCAAACTCA GGCGAAGGAG TGCTTGTAGC
               TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
           51
              GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
               ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
               ACAAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
               TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
              GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
              GTCAGGCTTG GGCGGTGGTG CATTTGTGTT GTATTGGGAC AATACCGCCA
          401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
               CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
              GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA
This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:
     g666.pep
               MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTNSAV
               IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATOAGY DILKOGGSAA
               DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
              PELFLDKDGX PLKFMEAVVA RXVRLLSLN*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2173>:
     m666.sea
               ATGCCTTGTA TGAATCATCA ATCAAACTCA GGCGAAGGAG TGCTTGTGGC
               TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
           51
               GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
               ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
               ACAAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
               TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
               GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
               GTCAGGCTTG GGCGGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA
          401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
               CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
              GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA
This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:
     m666.pep
              MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
               ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGGSAA
           51
               DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
               PELFLDKDGO PLKFMEAVVV VARWVRLLSL N*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
     m666/q666 93.9% identity in 181 aa overlap
                                                        40
                  MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE
     m666.pep
                  MLCMNYQSNSGEGVLVAKTYLLTALIMSMVISGCQVIHANQGKVNTNSAVIAGADAHTPE
     q666
                                    20
                                              30
                                                        40
                                                                  50
                          70
                                    80
                                              90
                                                       100
                                                                 110
                  HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL
     m666.pep
```

g666 m666.pep g666	:
m666.pep g666	NX    NX 180
a666.seq 1 51 101 151 201 251 301 351 401 451 501	Partial DNA sequence was identified in N. meningitidis <seq 2175="" id="">:  ATGCCTTGTA TGAATCATCA ATCAAACTCA GGCGAAGGAG TGCTTGTGGC TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA ACAAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC GTCAGGCTTG GGCGGTGGTG CATTTGTGTT GTATTGGGAT AATACCGCCA AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC GGTGGTCGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA  ds to the amino acid sequence <seq 2176;="" 666.a="" id="" orf="">:  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGGSAA DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT PELFLDKDGQ PLKFMEAVVV VARWVRLLSL N*</seq></seq>
m666.pep a666  m666.pep a666  m666.pep a666	100.0% identity in 181 aa overlap  10
m666.pep a666	NX ! I NX

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2177>:
     q667.seq
               atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
           1
               tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
           51
               cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAttgcg
          151 GAttteette agegtgeeeg egtgGAacge tteecacact ttgetgeegt
          201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTcgcCat atcgtccagC
          251 GGCACATTcg ccctcggctG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
          301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
          351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GGCGTTGATG
          401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
          451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAAACT
          501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
               TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
              ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
               GCTGCGCGAA CAGCACCACT TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
               TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
               CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ACtTGCGCCT
          801 ATTGTGtcaT TAA
This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:
     g667.pep
              MRFVFCLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
              DFLORARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
           51
               VALVITADVV VPLEIAAVAE IAVARIPIAR GVDAVYQGAV MQYGQVETAA
               VPADQLRRMF FNQFEKLGNH DFFAIVHLAD GADMNLVLPP AHTAGNRHNL
          201 MEVVLHKIAA GLCAAFLLRE QHHFVIRQGR RQVIQRTDTL HIGYGFNIES
          251 QNRIHGSTLH SKTDLRLLCH *
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2179>:
     m667.seq (PARTIAL)
            1 ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
           51 TTTCCATTTC GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
          101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
               GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
               CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
              GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
          251
              GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
          301
               TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGCGTTGATG
          351
          401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
          451 GTTCCAACTG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
          501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
          551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
          601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
          651 GCTGGGCAAT CAGCACCACT TG...
This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:
     m667.pep
               MRLFPGLCGQ VIPHPFDFHF VFVRIQPAAD QTETQVHQIS VCRVGFAIIA
           51 DFLQPARMEC LPNLAAVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
               VALVITADVV VPLEIAAVAE IAVAHIPIAR GVDAVYQGAV MQYGQIETAA
               VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHNL
               MKMMLHKIAA RLSTAFVLGN QHHL...
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
     m667/g667 75.0% identity in 224 aa overlap
                                              30
                                                        40
                          10
                                    20
                  MRLFPGLCGQVIPHPFDFHFVFVRIQPAADQTETQVHQISVCRVGFAIIADFLQPARMEC
     m667.pep
```

g667	MRFVFCLGGEIVSDPCDFHLVFVRVESAADQTETQIHQIRIHGIGFAIIADFLQRARVER 10 20 30 40 50 60
m667.pep g667	70 80 90 100 110 120 LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVVPLEIAAVAE :  ::
m667.pep g667	130 140 150 160 170 180 IAVAHIPIARGVDAVYQGAVMQYGQIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD     :
m667.pep g667	190 200 210 220  GADMYFILPPTHAARNRHNLMKMMLHKIAARLSTAFVLGNQHHL      ::  : :          ::
g667	HIGYGFNIESQNRIHGSTLHSKTDLRLLCHX 250 260 270
The following p  a667.seq  1 51 101 151 201 251 301 351 401 451 501	ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA TTTCCATTTC GTATTCGTCT GCGTCGAATC TGCCGCTGAC CGCAGATACA TCAGATAGGT ATTTACCGCA TCGGTTTCGC AATAATTGCG GATTTCCTTC AGCCTGCCG CGTGGAACG CTCCCACACC TTGCTGCCGT CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC GGCACATTCG CCCTCGGCTG GTAAAGCGC AGCAAATCCA TCAAATCGCA ATGACGTTGG TGGTAGCGC TGATGTAGTT GTTCCACTTG AAATCGCGC TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCCG GGCGTTGATG CCGTGTAGCA GCGAACGGTA ATGCAGAACC GGCAGGTCGA AACCGCCGCC GTTCCAACTG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT TGTACCGACA
551 601 651 701 751 801	TGGACTTTAT CCTGCCCCA ACGCATGCAG CACGAAATCG CCACAATCTG ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT GCTGGGCAAA CAGCACCACT TCATCGTCGG GCAGCGAGGA CGGCAAGTCA TACAGCGTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC CAAAATCGTG GTCATGACAG CACCTTGTAT TTAAAA.CAG ACTTGCGCCT ATTGTGTCAT TAA
This correspond a667.pep 1 51 101 151 201 251	MRFVFCLGGE IVSDPLDFHF VFVCVESAAD QTETQIHQIG IYRIGFAIIA DFLQPARVER LPHLAAVHTQ LARKTAQFRH IVQRHIRPRL VKREQIHQIA MTLVVAADVV VPLEIAAVAE IAVAHIPIAR GVDAV*QRTV MQNRQVETAA VPTDQLRRMF FNQLEKFGDN HFLAVIHLAD CTDMDFILPP THAARNRHNL MKMMLHKIPT RLSTAFLLGK QHHFIVGQRG RQVIQRTDTL HIGYGFNIES QNRGHDSTLY LKXDLRLLCH *
m667/a667	79.0% identity in 224 aa overlap
m667.pep a667	10 20 30 40 50 60  MRLFPGLCGQVIPHPFDFHFVFVRIQPAADQTETQVHQISVCRVGFAIIADFLQPARMEC    :    :::  :       ::         :  ::  :
m667.pep a667	70 80 90 100 110 120 LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVVPLEIAAVAE   :

WO 99/57280 PCT/US99/09346

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	70	80	90	100	110	120
	130	140	150	160	170	180
m667.pep	IAVAHIPIARGVDA	VYQGAVMQYG	QIETAAVPT	OQLRRMFFNQF	EKFSNDHFL <i>I</i>	AVIHLAD
		1 1 : 111	1:1111111	111111111111111111111111111111111111111	111:::111	
a667	IAVAHIPIARGVDA	VXQRTVMQNR	QVETAAVPTI	OQLRRMFFNQL	EKFGDNHFL/	AVIHLAD
	130	140	150	160	170	180
	190 GADMYFILPPTHAA	200	210	220 PAFVI.GNOHHI		
m667.pep	:11 111111111	11111111111		:     :       :		
a667	CTDMDFILPPTHAR	RNRHNLMKMM				IQRTDTL
	190	200	210	220	230	240
a667	HIGYGFNIESQNRG	HDSTLYLKXD	LRLLCHX			
	250	260	270			
		•				

# The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2183>:

g669.seq

- ATGCGCCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
- 51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
- 101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
- 151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
- 201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG 251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
- 301 GACATCAAAC GGATACTGTA A

### This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

g669.pep

- 1 MRRIVKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
  - 51 EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
- 101 DIKRIL*

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2185>:

m669.seq

- 1 ATGCGCCGCA TCATTAAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
- 51 TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
- 101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
- 151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
- 201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
- 251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
- 301 GACATCAAAC GGATACTGTA A

#### This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

m669.pep

- 1 MRRIIKKHQP INAPHIVLEI RIMKLHRAFV FLGRKRPHHH DSSLRRQHGI
- 51 EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
- 101 DIKRIL*

# Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIIKKHQPINAP:	HIVLEIRIME	CLHRAFVFLGR	KRPHHHDSSL	RRQHGIEGMG	FDFKQI
	[[]]:[][]:[]	1111111111			111111111	
q669	MRRIVKKHQPVNAP:	HIVLEIRIM	(LHRAFVFLGR	KRPHHHDRSL	RRQHGIEGMG	FDFKQI
-	10	20	30	40	50	60
	70	80	90	100		

```
FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
    m669.pep
                 FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
    q669
                                           90
                        70
                                  80
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2187>:
    a669.seq
              ATGCGCCGCA TCATTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
              TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
          51
         101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
         151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
         201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
         251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
         301 GACATCAAAC GGATACTGTA A
This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:
     a669.pep
              MRRIIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
              EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
          51
         101 DIKRIL*
              98.1% identity in 106 aa overlap
m669/a669
                                            30
                 MRRIIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSSLRRQHGIEGMGFDFKQI
     m669.pep
                 MRRIIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGIEGMGFDFKQI
     a669
                                                     40
                         10
                                                    100
                         70
                                  80
                                            90
                 FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
     m669.pep
                 FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
     a669
                                  80
                                            90
                         70
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2189>:
     q670.seq
              ATGACTTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTTGGTGAA
            1
              AAACGCTTCC GGCGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
           51
              TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
          101
          151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
          201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
              CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
          301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTTGTGTG CCAGTCCGAC
          351 GCGTTCCAAA AGCTCCATTG CCTTTTTCTC CGCCTGTTCC GCATTTTGCC
          401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
              GGGTAG
          451
This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:
     q670.pep
              MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
            1
              IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCCW
           51
          101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2191>:
     m670.seq
               ATGACCTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTTGGTAAA
               AAACGCTTCG GGCGTTTCGT CTTCGAGGAT TTGCCCTTTA TCGACGAAAA
           51
               TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
          101
               ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
               GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCGTCA AACAACATTA
          201
```

a670

	10/4
251 301 351 401 451	CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTTGTGTG CCAGTCCGAC GCGTTCCAAA AGCTCCATTG CCTTTTTCTC CGCCTGTTCC GCATTTTGCC CCTTAACCTT CATCGGTGCG AGGGTAATGT TTTCCAACAC GGTCAGGTGC GGGTAG
This correspond	s to the amino acid sequence <seq 2192;="" 670="" id="" orf="">:</seq>
m670.pep	MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
1 51	IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
101	PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151	G*
Computer analy Homology with	sis of this amino acid sequence gave the following results: a predicted ORF from N. gonorrhoeae
GRO / GRO	98.0% identity in 151 aa overlap
m670/g670	
	10 20 30 40 50 60 MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS
m670.pep	
g670	MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS 10 20 30 40 50 60
	10 20 00 10 10
680	70 80 90 100 110 120 FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCCWPPESWEGKASFLCASPTRSK
m670.pep	111111111111111111111111111111111111111
g670	FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCCWPPESWEGKASFLCASPTRSK 70 80 90 100 110 120
	70 80 50 100 110 120
45 A	130 140 150 SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
m670.pep	
g670	SSIAFFSACSAFCPLTFIGARVMLSNTVRCGX 130 140 150
The following p	partial DNA sequence was identified in N. meningitidis <seq 2193="" id="">:</seq>
a670.seq	ATGACCTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTTGGTAAA
1 51	
101	TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
151	THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE P
201 251	TOWNS THE CONCERNATION OF THE PROCESS OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE CONCERNATION OF THE C
301	
351	GCGTTCCAAA AGTTCCATCG CTTTTTTCTC TGCCTGTTCC GCATTTTGAC
401	
451	
This correspond	ds to the amino acid sequence <seq 2194;="" 670.a="" id="" orf="">:</seq>
a670.pep	MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
1 51	IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
101	PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151	
m670/a670	98.0% identity in 151 aa overlap
•	10 20 30 40 50 60
m670.pep	MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATSRANPISWVTHIIVMPLSAKS

	70 80 90 100 110 120
m670.pep	70 80 90 100 110 120 FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCCWPPESWEGKASFLCASPTRSK
mo/o.pep	
a670	FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCCWPPESWEGKASFLCASPTRSK 70 80 90 100 110 120
	70 80 90 100 110 120
	130 140 150
m670.pep	SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX
a670	SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX
<b>4.</b>	130 140 150
The following p	partial DNA sequence was identified in N. gonorrhoeae <seq 2195="" id="">:</seq>
g671.seq	· CONTRACTOR CANADOCCOM MECHANICA CONTRACTOR
1	ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC GCCCAAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
51 101	TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151	GAAATGAATG ACAGagccaa TGCAAACAgg cggggTTGGA ACGaggCAAA
201	GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251	CCACCCATGC CACCATCGAA CCTGCTTCCG CAATCACGCC GCGCATCGTG
301	GAAATGACGA TGCAGGCGGC GATGACGGCQ QAGGCGAGGA GGTCGGCAAT
351	GGGGAGGCTA TTCATTCGTT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401	TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTTATAGT TGCTTGA
This correspond	ds to the amino acid sequence <seq 2196;="" 671.ng="" id="" orf="">:</seq>
	15 to the annih dota bequence 152 (15 21) of out of 15-8
g671.pep 1	MISRVTIKTP FNAPNTPPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51	THE PROPERTY OF THE PARTY OF TH
101	TOTAL TOTAL TOTAL TOTAL UNACTION TO TROUBLE TO
The following t	partial DNA sequence was identified in N. meningitidis <seq 2197="" id="">:</seq>
m671.seq	
1	ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51	GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101	TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151	GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGAGGCAAA
201	GGCGAGGTCG GCGAAGGAGG CGGCAAAGAG TTTGGCGAAA AAGAAGGAAA
251	CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301	GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTCGGCAAT
351	GGGGAGGCTA TTCATTCGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401	TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTTATAGT TGCTTGA
This correspond	ds to the amino acid sequence <seq 2198;="" 671="" id="" orf="">:</seq>
m671.pep	
1	THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
51	EMNDRANANR RGWNEAKARS AKEAAKSLAK KKETTHAAIE PASAITPRIA
101	
	TOUR THE TENEDRE OF THE TENEDRE TOUR TOUR TOUR TOUR TOUR TOUR TOUR TOUR
~ . 1	DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*
Computer anal	DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*  ysis of this amino acid sequence gave the following results:
Computer analy Homology with	DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*
Homology with	pstmoaamta etrrsamgrl firyltgdtv yaofvolafg ipcvfiva* ysis of this amino acid sequence gave the following results: h a predicted ORF from N. gonorrhoeae
Homology with	DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*  ysis of this amino acid sequence gave the following results:
Homology with	ysis of this amino acid sequence gave the following results:  h a predicted ORF from N. gonorrhoeae  1 91.9% identity in 148 aa overlap
Homology with	pstmoaamta etrrsamgrl firyltgdtv yaofvolafg ipcvfiva*  ysis of this amino acid sequence gave the following results:  h a predicted ORF from N. gonorrhoeae  1 91.9% identity in 148 aa overlap  10 20 30 40 50 60  mtsrvtiktpfnapntppkmrlakpkptaetalvssersifwiroamtnremndrananr
Homology with	pstmoaamta etrrsamgrl firyltgdtv yaofvolafg ipcvfiva*  ysis of this amino acid sequence gave the following results:  h a predicted ORF from N. gonorrhoeae  1 91.9% identity in 148 aa overlap  10 20 30 40 50 60  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
Homology with	pstmoaamta etrrsamgrl firyltgdtv yaofvoiafg ipcvfiva*  ysis of this amino acid sequence gave the following results:  h a predicted ORF from N. gonorrhoeae  1 91.9% identity in 148 aa overlap  10 20 30 40 50 60  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
Homology with m671/g67	pstmoaamta etrrsamgrl firyltgdtv yaofvoiafg ipcvfiva*  ysis of this amino acid sequence gave the following results:  h a predicted ORF from N. gonorrhoeae  1 91.9% identity in 148 aa overlap  10 20 30 40 50 60  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
Homology with m671/g67	ysis of this amino acid sequence gave the following results: h a predicted ORF from N. gonorrhoeae  1 91.9% identity in 148 aa overlap  10 20 30 40 50 60  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
Homology with m671/g67 m671.pep g671	ysis of this amino acid sequence gave the following results:  h a predicted ORF from N. gonorrhoeae  1 91.9% identity in 148 aa overlap  10 20 30 40 50 60  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
Homology with m671/g67	ysis of this amino acid sequence gave the following results:  h a predicted ORF from N. gonorrhoeae  1 91.9% identity in 148 aa overlap  10 20 30 40 50 60  MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR

551

601

```
RGWNEAKARSAKGAAKSLAKKKETTHATIEPASAITPRIVEMTMQAAMTAEARRSAMGRL
     q671
                                                   100
                                                             110
                                  80
                        70
                       130
                                 140
                                         149
                 FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
     m671.pep
                 11111:1:1:1:1:11111111111111111111111
                 FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
     q671
                                 140
                       130
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2199>:
     a671.seq
              ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
              GCCCAAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCCCCGG
              TCAGCAGCGA GCGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
         101
              GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGATGCAAA
         151
              GGCGATGTCG GCGAAGGGTG CGGCAAAGAG TTTGGCGAAA AAAAAGGCAA
         201
              CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
         251
              GATAGCACGA TGCAGGCGGC GATGATGGCG GAGACGAGGA GGTCGGCAAC
         301
              GGGGAGGTTA TTCATTCGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
          351
              TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTTATAGT TGCTTGA
This corresponds to the amino acid sequence <SEQ ID 2200; ORF 671.a>:
     a671.pep
              MTSRVIIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
              EMNDRANANR RGWNDAKAMS AKGAAKSLAK KKATTHAAIE PASAITPRIA
              DSTMQAAMMA ETRRSATGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*
          101
              93.9% identity in 148 aa overlap
m671/a671
                                                              50
                                  20
                                           30
                                                     40
                 MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR
     m671.pep
                 MTSRVIIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR
     a671
                                                              50
                                                     40
                                  20
                                           30
                         10
                                                    100
                                                             110
                                            90
                         70
                                  80
                  RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL
     m671.pep
                  RGWNDAKAMSAKGAAKSLAKKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL
     a671
                                                             110
                                  80
                                            90
                                                    100
                         70
                        130
                                  140
                  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
     m671.pep
                  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
      a671
                                  140
                        130
 The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2201>:
      q672.seq
               ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
               ACTGTATGCC GCCCACGCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
           51
               CCCAAAGCCC CCGCGCTATC GACATCATTA AAGCACAAAA AATCGCCGCC
               GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
               GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
               TCCACGGCGA CGAAGACGAT GCATTCTGCC GGCAGTTCGA CCGCCCCTAT
               ATTAAAGCCA TTCGTGTTCA GACGCCATCA GACATCCGAA ACGCCGCCAC
               GCGCTTCCCC AACGCTCAGG CACTGCTGTT CGATGCCTAT CACCCTTCGG
               AATACGGCGG CACCGGACAC CGCTTCGact GGacgctgtt ggcggAATAT
```

TCGGGCAAGC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG

CGAAGCCGTC CGCATCACCG GAGCGGAAGC GGTCGACGTA TCCGGCGGCG TGGAAGCGTC TAAAGGCAAA AAAGACCCCG CCAAAGTCGC CGCCTTTATC

GCAACCGCCA ACCGCCTATC CCGTTAA

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
9672.pep

1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAI DIIKAQK<u>IAA</u>
51 ALPPFVSVVA LFVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRFP NAQALLFDAY HPSEYGGTGH RFDWTLLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDPAKVAAFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2203>:

```
m672.seq1ATGAGGAAAATCCGCACCAAAATCTGCGGCATCACCACACCGGAAGACGC51AGCTGCCGCCGCAGCGGCAGGTGCGGATGCCGTCGGGCTGGTCTTTTTCC101AAGGCAGCAGCCGGGCCGTCGATATTGCCCGCGCCAAAAAAATCACCGCC151GCACTGCCGCCGTTTGTCAGCGTTGTCGCCCTTTTCGTCAACGAAAGCGC201GCAAAACATCCGCCGCATCCTTGCCGAAGTGCCGATTACACATCATCCAAT251TCCACGGCGACGAAGACGACGCATTCTGCCGCCAGTTCCACCGCCCCTAT301ATCAAAGCCATTCGTGTTCAGACGGCATCAGACATCCGAAACGCCGCCAC351GCGCTTCCCCGACGCTCAGGCACTGCTGTTCGATGCCTACCATCCTTCGG401AATACGGCGGCACCGGAAACCGCTTCGACTGGACGCTGCTGGCGGAATAT451TCGGGCAAACCGTGGGTGCTTGCCGGCGGGCTGACCCCTGAAAACGTCGG501CGAAGCCGTCCGCATCACCGGAGCGGAATCGGTCGATGTATCCGGCGGTG551TGGAAGCGTCTAAAGGCAAAAAAGATGCCGCCAAAGTCGCCGCCTTTATC601GCAACCGCCAACCGCCTATCCCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep

1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQGSSRAV DIARAKKITA
51 ALPPFVSVVA LFVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRFP DAQALLFDAY HPSEYGGTGN RFDWTLLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAAKVAAFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae* 

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICGITTI	PEDAAAAAAA				PEVSVVA
			:    :		:  :	
g672	MRKIRTKICGITT				AQKIAAALPI 50	
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNESAQNIRRI	LAEVPIHIIQ	FHGDEDDAFCR	QFHRPYIKAI	RVQTASDIR	NAATRFP
		111111111	111111111	11 111111		
g672	LFVNESAQNIRRI	LAEVPIHIIQ	FHGDEDDAFCR	QFDRPYIKAI	RVQTASDIR	NAATRFP
,	70	. 80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFDAYHPSI	EYGGTGNRFD	WTLLAEYSGKE	WVLAGGLTPE	CNVGEAVRITO	GAESVDV
	:::::::::::::::::::::::::::::::::::::::	1111111111		111111111		:
g672	NAQALLFDAYHPS	EYGGTGHRFD	WTLLAEYSGKE			
-	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASKGKKDA		NRLSRX			
m672.pep			NRLSRX			
m672.pep g672		AKVAAFIATA 	11111			
	SGGVEASKGKKDA	AKVAAFIATA 	11111			

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2205>: a672.seq

```
1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
             ACTGTATGCC GCCCACGCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
         51
            CCCAAAGCCC CCGCGCTGTC GACATCATTA AAGCACAAAA AATCACCGCC
         101
         151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
         201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
            TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
         301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
         351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
         401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GGCGGAATAT
             TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
             CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTCGATGTA TCCGGCGGCG
             TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
             GCAACCGCCA ACCGCCTATC CCGTTAA
This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:
             MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAV DIIKAQKITA
             ALPPFVSVVA LFVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
          51
             IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLLAEY
             SGKPWVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPAKVAAFI
             ATANRLSR*
         201
             91.8% identity in 208 aa overlap
m672/a672
                       1.0
                                20
                                         30
                                                  40
                MRKIRTKICGITTPEDAAAAAAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA
    m672.pep
                MRKIRTKICGITTPEDALYAAHAGADALGLVFYPQSPRAVDIIKAQKITAALPPFVSVVA
    a672
                                                                     60
                                 20
                                          30
                                                  40
                                                            50
                                         90
                                                  100
                                 RΛ
                LFVNESAQNIRRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRFP
    m672.pep
                LFVNESAQNIRRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRFP
     a672
                                                  100
                                                           110
                                                                    120
                        70
                                 80
                                                           170
                                                                    180
                                                  160
                       130
                                140
                                         150
                DAQALLFDAYHPSEYGGTGNRFDWTLLAEYSGKPWVLAGGLTPENVGEAVRITGAESVDV
    m672.pep
                DAQALLFDAYHPSEYGGTGHRFDWTLLAEYSGKPWVLAGGLTPENVDEAIRITGAEAVDV
     a672
                                                                    180
                                140
                                         150
                                                  160
                       130
                       190
                                200
                                        209
                SGGVEASKGKKDAAKVAAFIATANRLSRX
     m672.pep
                 SGGVEASKGKKDPAKVAAFIATANRLSRX
     a672
                       190
                                200
```

# The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2207>:

g673.seq					_
1	ATGGATATTG	AAACCTTCCT	TGCAGGGGAA	CGCGCCGCCG	GCGGATACCG
51	TTGCGGCTTC	GTGGCGATTG	TCGGTCGTCC	GAACGTGGGC	AAATCAACGC
101	TGATGAACCA	TCTCATCGGT	CAGAAAATCA	GTATTACCAG	CAAAAAGGCG
151	CAGACGACGC	GCAACCGCGT	AACGGGGATT	TATACCGACG	ATACCGCGCA
201	GTTCGTGTTT	GTCGATACGC	CGGGCTTTCA	AACCGACCAC	CGCAACGCGC
251	TCAACGACAG	GCTGAATCAA	AATGTTACCG	AGGCGCTCGG	CGGTGTGGAT
301	GTGGTGGTTT	TCGTCGTGGA	GGCGATGCGC	CTTACCGATG	CCGACCGCGT
351	CGTGTTGAAA	CAACTGCCCA	AGCACACGCC	GGTCATTTTA	GTGATCAACA
401	AAATCGACAA	GGACAAGGCG	AAAGACCGTT	ACGCGCTGGA	GGCGTTTGTT
451	GCCCAAGTGC	GCGCCGAATT	TGAATTTGCG	GCGGCGGAGG	CGGTCAGTGC
501	GAAACACGGT	TTGCGGATTG	CCAACCTGTT	GGAGCTGCTC	AAGCCGTATC
551	TGCCCGAAAG	CGTACCGATG	TATCCCGAAG	ACATGGTTAC	GGACAAATCG
601		TGGCGATGGA			
001	000001111	• • • • • • • • • • • • • • • • • • • •		•••	

```
651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg CCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG
```

### This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```
g673.pep
         MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
      51 OTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
    101 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
    151 AQVRAEFEFA AAEAVSAKHG LRIANLLELL KPYLPESVPM YPEDMVTDKS
    201 ARFLAMEIVR EKLFRYLGEE LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
    251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
    301 FLRELGL*
```

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2209>:

```
m673.seq
         ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
      51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
     101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
     151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
     201 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
     251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
     301 GTGGTGGTTT TCGTCGTGGA GGCGATGCGC TTTACCGATG CCGACCGCGT
         CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
     401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCGTTTGTT
     451 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
     501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
     551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
     601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
     651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
     701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
     751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
     801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
     851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
     901 TTCCTGCGCG AGCTGGGTTT GTAG
```

# This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```
m673.pep
         MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
     51 OTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
     101 VVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
     151 AQVRAEFEFA AAEAVSAKHG LRIANLLELI KPYLPESVPM YPEDMVTDKS
     201 ARFLAMEIVR EKLFRYLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
     251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
     301 FLRELGL*
```

### Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m673/g673 98.4% identity in 307 aa overlap

	10	20	30	40	50	60
m673.pep	MDIETFLAGERAAG	<b>GYRCGFVAI</b>	/GRPNVGKSTLN	MHLIGQKIS	ITSKKAQTTR	NRVTGI
	11111111111111	11111111111	111111111111		1111111111	111111
g673	MDIETFLAGERAAG	GYRCGFVAI	/GRPNVGKSTL	MHLIGQKIS	ITSKKAQTTR	NRVTGI
90.5	10	20	30	40	50	60
		• •		4.00	110	100
	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTF	GFQTDHRNAI	LNDRLNQNVTE	ALGGVDVVVF	VVEAMRFTDA	DRVVLK
	11111111111111111	111111111			111111:111	11111

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g673	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK 70 80 90 100 110 120
m673.pep	130 140 150 160 170 180  QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEFAAAEAVSAKHGLRIANLLELI
g673	QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEFAAAEAVSAKHGLRIANLLELL 130 140 150 160 170 180
m673.pep	190 200 210 220 230 240 KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFRYLGEELPYAMNVEVEQFEEEDGLNR
g673	
	250 260 270 280 290 300 IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVKSGWADDIR
m673.pep	
g673	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDNKVFLKVWVKVKSGWADDIR 250 260 270 280 290 300
m673.pep	FLRELGLX
g673	FLRELGLX
680	artial DNA sequence was identified in N. meningitidis <seq 2211="" id="">:</seq>
a673.seq 1	ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51	THECOCCOTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101	TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
151 201	CHERGETETT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
201 251	TODACCACCE TITGATICA AACGITACCG AGGCACTCGG CGGCGTGGAT
301	CECCECCETT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351	CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401	AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GGCGTTTGTT GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGCGC
451	GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGCGCGATT AAGCCGTATC GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
501 551	TCCCCGAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601	CCCCCTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651	CCCCACGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701	AGGAGAGGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751	AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAAT TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
801	TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTCAATTCGATTCG
851 901	The second common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common common commo
	s to the amino acid sequence <seq 2212;="" 673.a="" id="" orf="">:</seq>
a673.pep	MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
1	OTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
51 101	WATERWEARD FTDADRVVLK OLPKHTPVIL VVNKIDKOKA KORYALEAFV
151	DOUBLE FE TA ADEAUSAKHG IRIANLLELI KPYLPESVPM YPEDMVTDKS
201	ADELAMETUR EKLERYLGEE LPYAMNVEVE QFEEEDGLNR IYLAVLVUKE
251	SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301	FLRELGL*
m673/a673	99.7% identity in 307 aa overlap
•	10 20 30 40 50 60
m673.pep	MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
. a673	MDIETFLAGERAADGIRCGIVATVGRINGELEGATION 10 20 30 40 50 60

1082

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m674/a674	97.9% identity in 141 aa overlap
110/4/90/	sylvia radically in 111 an overlap
	10 20 30 40 50 60
m674.pep	MKTARRRSRELAVQAYYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE
•	
g 674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD
	10 20 30 40 50 60
	70 80 90 100 110 120
m674.pep	70 80 90 100 110 120 YIRQIRPLLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK
MO, II pop	
g674	YIQKIRPLLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK
	70 80 90 100 110 120
624	130 140
m674.pep	FVNGILDKLAAQIR
g674	FVNGILDKLAAQIRPDEPKRRX
9071	130 140
The following p	partial DNA sequence was identified in N. meningitidis <seq 2217="" id="">:</seq>
a674.seq	1
1	ATGAAAACAG CCCGCCGCCG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51	CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAGATTGCT AAAAACATCC
101	
151	TTCTTCGGCA CGCAAACCAA TGCGGCAGAG TACATCCGAC AAATCCGCCC
201 251	CCTGCTCGAC CGCGACGAA AAGACCTCAA CCCCATCGAA CGCGCCGTCC
301	TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC GTCATCATCA ACGAAGCCAT CGAAGTAACC AAAACCTTCG GCGGCACGGA
351	CGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401	GTCCCGACGA GCCCAAACGC CGTTGA
This correspond	s to the amino acid sequence <seq 2218;="" 674.a="" id="" orf="">:</seq>
a674.pep	
1	MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMPDFA KADEELFNKL
51	FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101	VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*
	00 28 identity in 141 2
m674/a674	99.3% identity in 141 aa overlap
	10 20 30 40 50 60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE
	10 20 30 40 50 60
	70 00 00 100
m674 non	70 80 90 100 110 120
m674.pep	YIRQIRPLLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK
a674	YIRQIRPLLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK
~~·*	70 80 90 100 110 120
	130 140
m674.pep	FVNGILDKLAAQIRPDEPKRRX
cn .	
a 674	FVNGILDKLAAQIRPDEPKRRX

140

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2219>:

9675.seq

1 ATGAACACCA TCGCCCCaa cctcgacgC AAACACCTCC GCATCGGCAT
51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAA Catcaccgtc
151 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC
201 CTCTTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

PCT/US99/09346 WO 99/57280

1084

q675.pep 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI

101 GRVALDYNIP IANAVLTTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL

151 EEQFEDEE*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2221>:

m675.seq 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT

51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC

151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC

201 CTCTTCCGAA AAGTTTGACG CACTGATTGC GATCGGCGTC GTCATCCGTG 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC

301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC

351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG

401 ATGCCGCCAA AGTCGCCGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC

451 GAAGAACAGT TTGAAGACGA AGAATAA

#### This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

- 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLOE LGVADENITV
- ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV 51
- SRVALDYNIP IANAVLTTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL 101
- EEQFEDEE*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

#### m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLR	IGIVQARFTN	EIGSEMLKV	CCRTLQELGVA	DENITVATVE	PGALEIP
		1111111111	1111:1111	11111111111	1111111111	
g675	MNTIAPNLDGKHLR	IGIVQARFTN	EIGSQMLKV	CCRTLQELGVA	DENITVATVE	PGALEIP
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDA	LIAIGVVIRG	ETYHFELVSI	NESGAGVSRVA	LDYNIPIANA	AVLTTEN
		11111111	11111111:	, , , , , , , , ,	111111111	
g675	IALMNFASSEKFDA	LIAIGVVIRG	<b>ETYHFELVA</b> 1	NESGAGIGRVA	LDYNIPIANA	AVLTTEN
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASD	AAKVAVECAN				
	1111111111111			111111		
g675	DAQAIERIGEKASD	AAKVAVECAN	LVNLLLEEOI	FEDEEX		
-	130	140	150			

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2223>:

a675.seq ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT

101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC

151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC 201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG

251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC

301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC

351 CACGGAAAAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG 401 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC

451 GAAGAACAGT TTGAAGACGA AGAATAA

#### This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>: a675.pep

- MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
- 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNESGAGV

```
101 SRVALDYNIP IANAVLTTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
          151
               EEQFEDEE*
     m675/a675
                  100.0% identity in 158 aa overlap
                                   20
                                            30
                                                                50
                  MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP
     m675.pep
                  MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP
     a675
                                            30
                                                      40
                         70
                                   80
                                            90∉
                                                     100
                                                               110
                                                                        120
                  IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTTEN
     m675.pep
                  IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTTEN
     a675
                         70
                                   80
                                            90
                                                     100
                                                              110
                        130
                                  140
                                           150
                  DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX
     m675.pep
                  DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX
     a 675
                        130
                                  140
                                           150
The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 2225>:
     g677.seq
              ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
            1
           51
              ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
              TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCCGGCGT
          101
          151
              GTTCAAAACC ACTTCGTCGC CTTCGCGCGC TTTAATCAGG CAACGCGCCA
          201
              ACGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGACG
          251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
              GGTCGCCCC AAAAATACTT GGTCGGTCGC TTCGCGCAAT TCGGGATCGA
          301
              CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTCG
          351
          401 ATTTCGCGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
          451 GTCGCCGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
          501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
          551 GGCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA
This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:
     q677.pep
              MPQILVRIFL IRYSFIWETV RLCRFRRHSR SVDFDVFDRK DFNFLTAFRR
              VQNHFVAFAR FNQATRQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQTD
          51
         101
              GRAEKYLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
              VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2227>:
     m677.seq
              ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
          51
              GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
         101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCCGGCGT
         151 GTTCAAAACC ACTTCGTCGC CTTCGCGCGC TTTAATCAGA CAACGAGCCA
         201 GCGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGATG
         251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC
         301 CGTCGCGCCG AAAAACACTT GGTCGGTCGC TTCGCGCAAT TCGGGATCGA
             CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTCG
         351
             ATTTCGCGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
              GTCGCCGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
         451
              CTTTGTTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
         501
              GGCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA
This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:
    m677.pep
              MPQILVRIFL IRYSFIWETA RFCRFRRHSR SVDFDVFDRK DFNFLTPFRR
```

PCT/US99/09346 1086

51	VQNHFVAFAR	FNQTTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVVAQQSD
101	RRAEKHLVGR	FAQFGIDDDG	SLQTFGQETD	AAVDFAHTAF	AVKIVAVFAA

151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m677/g677 94.9% identity in 198 aa overlap

m677.pep	10 MPQILVRIFLIRYS	20	30	40	50	60
mo//.pep	11111111111111	IIIII:I:II		LILLILLILI	LIPERRVQNI	HEVAFAR
g677	MPQILVRIFLIRYS		FRRUCRCVNE	-	ון וווון זוג <i>רו</i> ז ממס גייה זי	מאים אנצים ני וון און א
9077	10	20	30	40	50	O6
			30	40	30	00
	70	80.	90	100	110	120
m677.pep	FNQTTSQRRNPRNF	TVLRGIDFIDA	DDFDGLLAPV	VAQQSDRRAE	KHLVGRFAQI	FGIDDDG
					1:1111111	
g677	FNQATRQRRNPRNF	VLRGIDFIDA	DDFDGLLAPV	'AAQQTDGRAE	KYLVGRFAQI	FGIDDDG
	70	80	90	100	110	120
	100	1.0				
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVD	FAHTAFAVKI	VAVFAAVAVA	CRPVDDLDDF	GAFFVDQLIF	<pre><lvfqcl< pre=""></lvfqcl<></pre>
		3111111111		111111111	1111:1111	11111
g677	SLQTFGQETDAAVD		VAVFAAVAVA	CRPVDDLDDF	GAFFIDQLI	KLVFQCL
	130	140	150	160	170	180
	190	199			•	
m677.pep	PSGGRNVVFGFGTH	IVCGX				
mopop		11111				
q677	PSGGRNVVFGFGTH	TVCGX				
90.,	190					
	-50					

The following partial DNA sequence was identified in N. meningitidis <SEO ID 2229>:

```
a677.seq
      1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
     51 GGAAACGGCG CGTTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
    101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCCGGCGT
    151 GTTTAAAACC ACTTCGTCGC CTTCACGCGC TTTAATCAGA CAACGAGCCA
    201 GCGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGATG
    251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC
    301 GGTCGCGCCG AAAAACACTT GGTCGGTCGC TTCGCGCAAT TCGGGATCAA
    351 CGACGACGGC GGCTTCCAAA CGCTTGGTCA GGAAACGGAT GCGGCGGTCG
    401 ATTTCGCGCA TACGGCGTTT GCCGTAAAGG TAGTCGCCGT TTTCGCTGCG
    451 GTCGCCGTTG CCTGCCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
    501 CTTTATTAAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
         GGCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA
```

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep					
1	MPQILVRIFL	IRYSFIWETA	RLCRFRRHSR	SVDFDVFDRK	DFNFLTPFRR
	V*NHFVAFTR				
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	AVKVVAVFAA
151	VAVACRPVDD	LDDFGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*
m677/a677	93.4% ic	dentity in 3	198 aa over	lap	

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYS	FIWETARFCR	FRRHSRSVDF	DVFDRKDFNF	LTPFRRVQNH	IFVAFAR
	1111111111111			111111111	1111111111	1111:1
a677	MPQILVRIFLIRYS	FIWETARLCR	FRRHSRSVDF	DVFDRKDFNF	LTPFRRVXNE	IFVAFTR
	10	20	30	40	50	60
	70	80	90	100	110	120

```
FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
m677.pep
          FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTDGRAEKHLVGRFAQFGINDDG
a677
                        80
                                90
                                       100
                130
                       140
                               150
                                       160
                                               170
                                                       180
          SLQTFGQETDAAVDFAHTAFAVKIVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
m677.pep
          GFQTLGQETDAAVDFAHTAFAVKVVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
a677
               130
                       140
                               150
                                       160
                                               170
               190
                       199
m677.pep
          PSGGRNVVFGFGTHIVCGX
          11111111111111111
          PSGGRNVVFGFGTHIVCGX
a 677
               190
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2231>:

```
g678.seq
          ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
       1
          CTGCATCGTC ATTTCCACGA TGCGCGGCGT GATTGCGGAA GCAggttcGA
     101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
     151 ttcgccgACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
     201 tCTGTCATTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
     251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
     301 AACCGCATTT TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
     351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
     451 GTGTTAAACC atacggaCAA CGCacccgaa tCCCtcgacg acgactaa
```

#### This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>: g678.pep

- MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
- 51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
- 101 NRILGGVFGA LKGVLIVTLL IMLASKTDLP DTEEWQQSYT VPFFVSLSEA
- VLNHTDNAPE SLDDD*

### The following partial DNA sequence was identified in N. meningitidis <SEO ID 2233>:

```
m678.seq
       1 ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
     51 CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCAGGCTCAA
     101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACTCTT TGCCGCCTCC
         TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCGCCTGT TTGCATTGGC
         TCTGTCGTTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
         TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
    301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
    351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
    401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
    451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA
```

#### This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>: m678.pep

```
1 MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
```

- 51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTS AVSAVGLGFA
- NRILGGVFGA LKGVLIVTLL VMLASKTDLP DTEEWRQSYT LPFFVSLSEA
- VLNHSGGTAE TPEDD*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAV					
				:	1111 1111	
g678	MNSLPIADLLASAV 10	TAACIVISTM 20	RGVIAEAGSN 30	IVAWVVSFFFA 40		
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLE	VIACLIQKML	RSLLTSAVSA			
		1111111111	11111:1111	+111111111111111111111111111111111111	11111111	111111
g678	PRLFALALSFISLE					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEE				DΧ	
• •	:1111111111111					
g678	IMLASKTDLPDTEE				ΣX	
	130	140	150	160		
The fellowing n	ortical DNIA sequence	a waa idant	fied in M .		∠cro m	2225
	artial DNA sequenc	e was ideiii	inea in iv. i	neningiliais	<seq id<="" td=""><td>2235&gt;:</td></seq>	2235>:
a678.seq 1	ATGAATAACC TCCCCG	<b>ምም</b> ርር <b>ርር</b> እርር	שככשב כשכש	CCCCCA MCAI	1000000	
51	CTGCATCGTG CTATCC					
101	TGGCGGCATG GGTGGT					
151	TTCGCCGACA TCGCCT					
201	TCTGTCGTTC ATTTCC					
251	TCCGCTCGCT GCTGAC					
301 351	AACCGCATTT TGGGCG TACCCTGCTG GTCATG					
401	AATGGCGGCA ATCTTA	CICG CIICA CACA CTGCC	ААААС СБАС СТТТТ ТССТ	ATCCCT TTC	CCGAAG	
451	GTGTTGAACC ATAGCG					
This correspond	s to the amino acid s	sequence <s< td=""><td>SEQ ID 223</td><td>36; ORF 678</td><td>}.a&gt;:</td><td></td></s<>	SEQ ID 223	36; ORF 678	}.a>:	
a678.pep		•		,		
1	MNNLPVADLL VSAIIA	ACIV LSAMR	GVIAE AGSM	AAWVVA FFFA	AKLFAAP	
51	FADIAFASFQ PRLFAL					
101	NRILGGVFGA LKGILI	ITLL VMLAS	KTDLP DTEE	WRQSYT LPFI	VSLSEA	
151	VLNHSGGTAE TPEDD*					
m678/a678	93.9% identity	in 165 aa	overlap			
111070740.5	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		0.022.02			
	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAV	IAACIVLSAM	RGVIAEAGSM	AAWVVSFFFA	(LFAASFADL	AFASFQ
	:  :  :    :	11111111111		11111:1111		
a678	MNNLPVADLLVSAI					
	10	20	30	40	50	. 60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLF					
	11111111111111	11111111:1	11111:1111	1111111111		11:11
a678	PRLFALALSFISLF			VGLGFANRILO	GVFGALKGI	LIITLL
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEE		150 VSLSEAVLNH	160 SGGTAETPEDE	)X	
a678	VMLASKTDLPDTEE				•	
	130	140	150	160		

#### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2237>: g680.seq

- 1 ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
- 51 GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTTCGA
- 101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTGttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTTG TTTAAACTGA TGTTTTTCTG TTTCACATGG TCGAGCAGCC
551 GTCCGACGGT GGCGACGACT ATTTCGCAGC CGGCACGCAG GTCGGCGGTT
    TGTTTGTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag
```

#### This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```
q680.pep
      1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCIACADRL
      51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
    101 ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
    151 SINPISNMRS ASSRTTISAL FKLMFFCFTW SSSRPTVATT ISQPARRSAV
    201 CLSMLTPPKR TVCRSGRFLM *
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2239>:

```
m680.seq
         ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCG CGATGTCGGT
      1
         GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTTCGA
     101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
     151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA
         GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
     251 GGTTGCGCTT CTGAATGGTA TCGACGCGA TGATGTGCTG CTCGACGTTG
     301 GCGTTGGTGG TGTTTTGCGC GGCGACTTCG ACGGTTTCGG GCGCGTTCAT
     351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
     401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
     451 TCGATAAAAC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT
     501 TTCGACTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC
     551 GTCCGACGGT GGCGACGACG ATTTCGCAGC CGGCACGCAG GTCGGCGGTC
     601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
     651 GTTTTTGATG TAG
```

### This corresponds to the amino acid sequence <SEO ID 2240; ORF 680>:

```
m680.pep
      1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCIACADRL
      51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
    101 ALVVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
    151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
     201 CLSIFIPPNK TVWRSGRFLM *
```

### Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

m680/g680	90.9% identity in	1 220 aa c	verlap			
	10	20	30	40	50	60
m680.pep	MTKGSSAMSSPRAAM	ISVATRTRRI	PSLKALSVSS	RLCWERSPCI	ACADRLRRTS	SSRVTRS
		111111111	11111111111	11111111	111111111	
g680	MTKGSSAMSSPRAAI	SVATRTRRI	PSLKALSVSS	LLCWERSPCI	ACADRLRRTS	SSRVTRS
	10	20	30	40	50	60
	70	80	90	100	110	120
m680.pep	TLCLVLQNTMTWFIC	KSTISRSSR	LRFXMVSTAM	MCCSTLALVV	FCAATSTVS	GAFMKSC
		: ! ! ! ! ! ! ! ! !	111 11111	111111111	1 1111111	
g680	TLCLVLQKTITWFIC	RSTISRSSR	LRFWKVSTAM	MCCSTLALVV	'FWAATSTVS	SAFMKSC
	70	80	90	100	110	120
	130	140	150	160	170	180
m680.pep	ASLRIGAEKVAEKSP	VWRWRGSIC	MILRMSSIKP	ISSIRSASSK	TTISTLFKWN	MFFCFTW

PCT/US99/09346 WO 99/57280

1090 ASLRIGAEKVAEKSRVWRWRGSICMILRMSSINPISNMRSASSRTTISALFKLMFFCFTW q680 130 140 150 160 170 180 190 200 210 m680.pep SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX q680 SSSRPTVATTISQPARRSAVCLSMLTPPKRTVCRSGRFLMX 190 200 210 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2241>: a680.seq ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCCGCGCGG CGATATCGGT 1 51 GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTTCGA 101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTTGTT TGGTTTTGCA GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA GGTTGCGCTT CTGAATGGTA TCGACGCGA TGATGTGCTG CTCGACGTTG GCGTTGGTGG TGTCTTGCGC GGCGACTTCG ACGGTTTCGG GCGCGTTCAT GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG TCGATAAAAC CCATATCCAG CATACGGTCG GCTTCGTCCA AAACGACGAT TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTCACGTGG TCGAGCAGCC GTCCGACGGT GGCGACGACG ATTTCGCAGC CGGCACGCAG GTCGGCGGTC TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG 651 GTTTTTGATG TAG This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>: a680.pep 1 MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCIACADRL RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL 51 ALVVSCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISOPARRSAV CLSIFIPPNK TVWRSGRFLM * 201 98.6% identity in 220 aa overlap m680/a680 20 30 40 50 MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCIACADRLRRTSSRVTRS m680.pep a680 MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCIACADRLRRTSSRVTRS 10 20 40 50 70 80 90 100 110  $\verb|TLCLVLQ| \verb|NTMTWFICKSTISRSSRLRFXMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC| \\$ m680.pep TLCLVLQNTMTWFICKSTISRSSRLRFXMVSTAMMCCSTLALVVSCAATSTVSGAFMKSC a680 70 80 90 100 110 120

SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX m680.pep a680 SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX 190 200 210 220

130

130

190

m680.pep

a680

The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 2243>: g681.seg

140

140

200

150

150

210

ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW

160

160

220

170

170

- ATGACGACGC CGATGGCAAT CAGTGCGTCA AATTTTTCGG AAGAGGCAAA
- GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGcgacgg

```
101 tgatgtTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
     TTGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCcgt cgaggttgGG GGCGATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCGG GGTCGTCGGT
451 GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651 TTTTACCACG ATTCCCGCGT TGTCGGCAGA CGGCGGCGGT TTGGTGGTAC
701 AATGTGCGCC GTTTGCAGCC TTAAGGTGTT TCTGTATTTT TGGAGTATGG
751 AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>: g681.pep

- 1 MTTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
- 51 LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
- 101 RLPVGNGLEC AVFGKLPRAA FGLGKQCGGF RVGFGDVGEA DDAEVVGVVG VFVGFVAAEE TPAAVVFKNG GFAVKEADGP VLFGDGVGGD AAVECRGKCL
- CKCVHCGNTL GGGKLADFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
- 251 KRIRAVFCGR R*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2245>:

- 1 ATGACGACGC CGATGGCAAT CAGTGCGTCA AACTTTTCGG AAGAGGCAAA
- 51 GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG 101 TAATGTTTTC GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
- 151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
- 201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GGCGATGGTG TTCATTGGGT
- 251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG 301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
- 351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
- TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCGGT 401
- 451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
- 501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTTTG
- 551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
- 601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATTT
- 651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
- 701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTTGG AGTATGGAAA
- 751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>: m681.pep

- MTTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
- 51 LSISLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
- 101 RLPVGDGLEC AVFGKLPCAA FGLGEQCGGF RVGFGDVGEA DDAEVVRIVG
- 151 VFVGLVAAEE TPAAVVFKNG GFAVEEADGP VLFGDGVGGD TAVECRGKCL
- 201 CKCVHYGNTL GXKLTDFTTI RALSADGGGL VVQCAPFAAL RCFCIFGVWK
- 251 RIRAVFCGRR *

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. meningitidis menA with menB

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from N. gonorrhoeae: m681/g681

30 MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV m681.pep MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV q681 10 20 30 40 50

	70 80 90 100 110 120
mC01 non	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGDGLECAVFGKLPCAA
m681.pep	RACIMI MARCHI SALIGARIVE IGCE DVEGVSECKLAVSVEKLEVGDGLECAVEGALECAV
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGNGLECAVFGKLPRAA
	70 80 90 100 110 120
	130 140 150 160 170 180
601	
m681.pep	FGLGEQCGGFRVGFGDVGEADDAEVVRIVGVFVGLVAAEETPAAVVFKNGGFAVEEADGP
g681	FGLGKQCGGFRVGFGDVGEADDAEVVGVVGVFVGFVAAEETPAAVVFKNGGFAVKEADGP
•	130 140 150 160 170 180
	100
	100 000 000
	190 200 210 220 230 239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA
g681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA
9001	100 000 . 010
	190 200 210 220 230 240
2	40 250 260
m681.pep	LRCFCIFGVWKRIRAVFCGRRX
moor.pep	
g681	LRCFCIFGVWKRIRAVFCGRRX
	250 260
The following	g partial DNA sequence was identified in N. meningitidis <seq 2247="" id="">:</seq>
a681.se	q
	1 ATAACGACGC CGATGGCAAT CAGTGCGTCA AATTTTTCAG AAGAGGCAAA
5	1 GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
10	
15	THE COMMEN COCKERS OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF
20	
25.	1 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
30	
35.	1 ACCOCCUCAC PRODUCTURES CARACTER COCCUCATION ACCOUNTS
40	
45.	1 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
50	
55:	
	GCGACGGIGI IGGIGGCGAI GCAGCGGICG AGTGCCGAGG AAAGTGCTTG
60:	
65.	1 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
70:	
75:	
13.	CGCATTCGGG CIGITITIG CGGAAGACGG TAA
This correspon	nds to the amino acid sequence <seo 2248;="" 681.a="" id="" orf="">:</seo>
•	· · · · · · · · · · · · · · · · · · ·
a681.pe	
	1 ITTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
5.	1 LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
10:	
	THE CONTROL AND SHEET AND THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTRO
15:	
20:	1 CKCVHCGNTX GGKLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
253	
CD1 /- CI	01 00 00 4 3-44 1 000
m681/a68	90.8% identity in 260 aa overlap
	10 20 30 40 50 60
m681.pep	
moor.bet	- III III JOOGA JEEGA I JAMIEL JAAR I VALVAT SAL PRISKV KQQTLSISLPISLV
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
	10 20 30 40 50 60
	20 00 00
	70
	70 80 90 100 110 120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGDGLECAVFGKLPCAA
-	
a 681	KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVGDGLECAVFCQFPRAA
0001	70 00 00 100 117
	70 80 90 100 110 120

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAE	EVVRIVGVFVG	LVAAEETPAA	VVFKNGGFAV	/EEADGP
a681	FRLGEQCGGFRVGF			LVAAEETPAA	VVFKNGGFAV	EEADGL
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKC	HYGNTLGXKL	TDFTTIRALS	ADGGGLVVQC	CAPFAAL
		1111111111		:11111	1111111111	111111
a681	VLFGDGVGGDAAVE	CRGKCLCKCV	HCGNTXGGKL	ADFTTILALS	ADGGGLVVQC	CAPFAAL
	190	200	210	220	230	240
		0.50				
	250	260				
m681.pep	RCFCIFGVWKRIRA	VFCGRRX				
		111111				
a681	RCFCIFGVWKRIRA	VFCGRRX				
	250	260				

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2249>: g682.seq

- 1 ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
- 51 GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
- 101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
- 151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
- 201 CTATATTTGT GTGAATGATG AAATAAAAAT GCCGTCTGAA CCCGATTGGA
- 251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA 301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
- 351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
- 401 GA

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>: g682.pep

- 1 MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
- 51 ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
- 101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2251>: m682.seg

- 1 ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
- 51 GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
- 101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
- 151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
- 201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTC
- 251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
- 301 CCCATTCGGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
- 351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>: m682.pep

- 1 MRDFTVWVSY GKWRKNWDIR YCLLHLIHLS STRLRKCGRI LSGICEPFCL
- 51 ITPDLTMHYC PILILIDY.. .. EMAMPSEP DWIQTAFCMA YGFIRFPTDR
- 101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. meningitidis menA with menB

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from N. gonorrhoeae:

m682/g682

```
20
                                     30
                                              40
                                                       50
            MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSTRLRKCGRILSGICEPFCLITPDLTMHYC
m682.pep
            q682
            MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC
                            20
                                     30
                                              40
                        70
                                 80
                                          90
                                                 100
            PILILIDY----EMAMPSEPDWIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
m682.pep
                    PILILIDYICVNDEIKMPSEPDWIQTAFCMA-GFIRFPTDRPILTRQSGVVRISPRTGFR
g682
                            80
                                     90
                                              100
             120
                       130
            YPTRSLPKSKKAYGX
m682.pep
            111111111111111
            YPTRSLPKSKKAYGX
q682
                   130
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2253>:
             ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
             GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
          51
             TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
         101
         151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
         .....TATA TTCGGTTTCC AACTGACCGA
             CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTCGC CACGAACGGG
             TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
         401
This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:
             MRDFTVWVSY GKWRKNWDIR YCLLHLIHLS STRLRKCGRI LSGICEPFCL
            ITPDLTMHYC PILILIEY.. ..... .... .... .... .... .... YIRFPTDR
          51
         101 PILTRPTGVV RISPRTGFRY PTRSLPKSKK AYG*
    m682/a682
                80.6% identity in 129 aa overlap
                                20
                                                  40
                                                           50
                MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSTRLRKCGRILSGICEPFCLITPDLTMHYC
    m682.pep
                MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSTRLRKCGRILSGICEPFCLITPDLTMHYC
    a682
                       10
                                20
                                         30
                                                  40
                                                           50
                                80
                                         90
                                                 100
                PILILIDYEMAMPSEPDWIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS
    m682.pep
                                         YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS
    a682
                PILILIEY---
                                         70
                                                  80
                                                           90
                                                                   100
                      130
                LPKSKKAYGX
    m682.pep
                a 682
                LPKSKKAYGX
The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 2255>
q683.seq
       ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTACT
       CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
   101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
   151 GACAGTGTGA GAAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
   201 TGTTACCAAT CTGAAACAAG AACGTTTTGC CAACACCCCC GCATACAAGA
   251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
```

301 AGTTCGCTAC AGTTATTTGA TACAAAAAC ACGGAAATTT CCACACAAA 351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA WO 99/57280

1095

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >: g683.pep

- MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK 1 DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL 51 101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL*
- The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2257>: m683.seq.
  - 1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
  - 151 GACAGCGTGA GAAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
  - 201 TGTTACCAAT CTAAAACAAG AACGTTTTGC CAACACCCCC GCATACAAGA
  - 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA 301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
  - 351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA

  - 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>: m683.pep..

- MIKETLMRPI FLSFVLFPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK 1
- DSVRKNGNLM IFQDKKVVTN LKQERFANTP AYKTAIAEWE IHCNNKTYRL 51
- 101 SSLOLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKOYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from N. gonorrhoeae:

```
m683/g683
          99.3% identity in 146 aa overlap
                 10
                         20
                                 30
                                          40
                                                  50
          MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
m683.pep
          MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
g683
                         20
                                 30
                 10
                                         40
                                                  50
                         80
                                 90
                                        100
          IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
m683.pep
          IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
q683
                 70
                         80
                                 90
                                        100
                130
                        140
          SSLRPMSILSGTLTEKQYETVCGKKLX
m683.pep
          3111311111111111111111111111
          SSLRPMSILSGTLTEKQYETVCGKKLX
a683
                130
                        140
```

The following partial DNA sequence was identified in N. meningitidis <SEO ID 2259>

```
a683.seq
```

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA 151 GACAGCGTGA GAAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT 201 TGTTACCAAT CTAAAACAAG AACGTTTTGC CNACACCCCC GCATACAAGA 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA 351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>: a683.pep

- MIKETLMRPI FLSFVLFPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
- 51 DSVRKNGNLM IFXDKKVVTN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMSILS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. meningitidis

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from N. meningitidis:

```
m683/a683
          97.9% identity in 146 aa overlap
                 10
                         20
          MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
m683.pep
          MIKETLMRPIFLSFVLFPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM
a683
                                  30
                                          40
                         80
                                  90.
                                         100
                                                 110
          IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA
m683.pep
          IFXDKKVVTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA
a 683
                         80
                                 90
                                         100
                130
                        140
          SSLRPMSILSGTLTEKQYETVCGKKLX
m683.pep
          111111111111111111111111111111111
a 683
          SSLRPMSILSGTLTEKQYETVCGKKLX
                130
                        140
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2261> g684.seq

```
1 ATGCGCCTTT TCCCCATCGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51 TGTGCAAAGC ACACAATATT TCGTGTTGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACCGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCATCAACAC
201 CGCACAAAAC CATGTTTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAC CTTTGTTCCT
301 GCCTCACGCA GCGGCAGTAC CGACAAATGG ACGGTCTATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGGTCAA AACAGGCCGGC
501 GCAACAGATG GTCGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684 >: g684.pep

```
1 MRLFPIAAAL TLAACGTVQS TQYFVLPDSR YIRPATQGGE TAVEVRLAEP
51 LKRGGLVYQT DPYRINTAQN HVWADTLDDM LEAALSNAFN RLDSTRTFVP
101 ASRSGSTDKW TVYIDAFQGS YTGKTLISGY AVLPDGTNRP FHIETEQQGD
151 GYAAMTAALE QGLKQAAQOM VE*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2263>:

```
1 ATGCGCCTTT TCCCGATTGC CGCCGCCCTG TCGCTTGCCG CCTGCGGTAC
51 TGTGCAAAGC ACACAATATT TCGTGTTGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGTCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCACGCA GCGGCAGTAC CGAAAAATGG ACGGTCATA TCGACGCATT
351 CCAAGGCAGC TACACGGGCA AAACCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG ACACCGAACA GCAGGGTGAC
451 GGCTACGCCG CGATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCCGGC
501 GCAACAGATG GTCGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>: m684.pep

- 1 MRLFPIAAAL SLAACGTVQS TQYFVLPDSR YIRPATQGGE TAVEVRLAEP
- 51 LKRGGLVYQT DPYRLNTAQN HVWADTLDDM LEAALSNAFN RLDSTRIFVP
- 101 ASRSGSTEKW TVYIDAFQGS YTGKTLISGY AVLPDGTNRP FHIETEQQGD

#### 151 GYAAMTAALE QGLKQAAQQM VE*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from N. gonorrhoeae:

```
m684/g684
          97.7% identity in 172 aa overlap
                10
                        20
                                30
                                        40
m684.pep
          MRLFPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYOT
          MRLFPIAAALTLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT
q684
                        20
                                30
                                        40
                                               50
                                90
                                       100
                                               110
          DPYRLNTAQNHVWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTEKWTVYIDAFQGS
m684.pep
          DPYRINTAQNHVWADTLDDMLEAALSNAFNRLDSTRTFVPASRSGSTDKWTVYIDAFQGS
g684
                70
                        80
                                90
               130
                       140
                               150
                                       160
                                               170
          \verb|YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQmvex|
m684.pep
          q684
          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
               130
                       140
                               150
                                       160
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2265> a684.seq

```
1 ATGCGCCTCT TCCCGATTGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51 TGTGCAAAGC ACACAATATT TCGTGTTGCC CGACAGCCGC TACATCCGTC
101 CTGCAACGCA AGGCGGCGAA ACTGCCGTCG AAGTCCGTCT TGCCGAACCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCCTACC GCCTCAACAC
201 CGCACAAAAC CACGTCTGGG CAGACACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCACGCA GCGGCAGTAC CGAAAAATGG ACGGCTTATA TCGACCGATT
351 CCAAGGCAGC TACACGGGCA AAACCCCTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
401 GGCTACGCCG CCATGACCGC CGCACTCGAA CAGGGACTGA AACAGGCCGC
501 GCAACAGATG GTCGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>: a684.pep

- 1 MRLFPIAAAL TLAACGTVQS TQYFVLPDSR YIRPATQGGE TAVEVRLAEP
  - 51 LKRGGLVYQT DPYRLNTAQN HVWADTLDDM LEAALSNAFN RLDSTRIFVP
  - 101 ASRSGSTEKW TVYIDAFQGS YTGKTLISGY AVLPDGTNRP FHIETEQQGD
  - 151 GYAAMTAALE QGLKQAAQQM VE*

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from N. meningitidis

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from N. meningitidis

m684/a684	99.4% identity	' in 172 aa	overlap			
	10	20	30	40	50	60
m684.pep	MRLFPIAAALSLAA	CGTVQSTQYE	VLPDSRYIRE	PATQGGETAVI	EVRLAEPLKRO	GGLVYQT
	111111111111111111111111111111111111111	#	1111111111		111111111	
a 684	MRLFPIAAALTLAA	CGTVQSTQYF	VLPDSRYIRE	PATQGGETAVI	EVRLAEPLKRO	GGLVYQT
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHVWA	DTLDDMLEAA	LSNAFNRLDS	TRIFVPASRS	SGSTEKWTVY	IDAFQGS
		111111111	1111111111	1111111111	1111111111	ШШ
a 684	DPYRLNTAQNHVWA	DTLDDMLEAA	LSNAFNRLDS	TRIFVPASRS	SGSTEKWTVY	DAFQGS
	70	80	90	100	110	120
	130	140	150	160	170	

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```
YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQQMVEX
    130
           140
                  150
                         160
```

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2267>

```
TTGTTTTGCC GTATCGGGAA TTTTGCGTTT TGCGGCGTGG TTTCTGCAGG
     TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
 51
101 CCGTGAAACC GCGTTTTTAT TGGGCAGcct GCGCCGTCCT GCCGGCCGCC
     TGTTCGCCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
151
     CGCATCCACA CCTGTCGCCA CGCTGACCGT GCCGACCGCG CGGGGCGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgtcg ccgtgtAcga CtggGCGGCG
301 TtggaTACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTGC AGCCTGCATT TGACAAGGCG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCATTA CCGGCGGGCC GGGTGCGGAA GCGTATGAAC AGTTGGCGAA
501 AAACGCGACC ACCATAGATT TGACGGTGGA CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAAGCG
601 CGCGTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTCG CCCAAAAGCG
651 CGAAGCCGCC AAAGGCAAAG GACGCGGGCT GGTGCTGTCG GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTTGGCAAG TTGGATACAC
751 GGCGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGGCA
801 CGGGCAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAGG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGGCGGC GTTTGAAAAG
1051 GCAGAACCCG TTGCGGCGCA GTAG
```

#### This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685 >: g685.pep

```
LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
  1
 51 CSPEPAAEKT VSAASQAAST PVATLTVPTA RGDAVVPKNP ERVAVYDWAA
101 LDTLTEPGVN VGATTAPVRV DYLQPAFDKA ATVGTLFEPD CESLHRHNPQ
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNGN IRTSGEKOME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAFG TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFEYIKEKN PGWIFIIDRT AAIGQEGPAA
301 VEVLDNALVC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAAFEK
351 AEPVAAQ*
```

### The following partial DNA sequence was identified in N. meningitidis <SEO ID 2269>:

```
m685.seq
          TTGTTTTGCC GTATCGGGAA TTTTGCGTTT TGCGGCGTGG TTTCTGCAGG
      51 TTGTTTGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
     101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCCT GCTGACCGCC
     151 TGTTCGCCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
          TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
     251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
     301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
     351 TTATTTGCAG CCTGCATTTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
     401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCATTACC
     451 GGCGGGCCGG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
     501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCGAAAAGC
     551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
     651 AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
     701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGCACG GGCAGCCTGT
     801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
     851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
     901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAGCGCA AGCAAATCAT
          CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCGCG CGGCAGTTGA
    1001 TTCAGGCGGC GGAGCAGTTG AAGGCGGCGT TTAAAAAGGC AGAACCCGTT
    1051 GCGGCGGGGA AAAAGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>: m685.pep

```
1 LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAFGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSFE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKKAEPV
351 AAGKK*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from N. gonorrhoeae:

```
m685/q685
          94.4% identity in 356 aa overlap
                        20
                                30
                                                50
                                                        60
          LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
m685.pep
          LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT
g685
                10
                        20
                                30
                                        40
                    70
                            80
                                   90
                                          100
          VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
m685.pep
                    a685
          VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV
                70
                                90
                                       100
                                               110
           120
                   130
                          140
                                  150
                                          160
                                                  170
          DYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGN
m685.pep
          DYLQPAFDKAATVGTLFEPDCESLHRHNPQFVITGGPGAEAYEQLAKNATTIDLTVDNGN
q685
               130
                       140
                               150
                                       160
                                               170
                                                      180
                   190
                          200
                                  210
                                          220
          IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAFG
m685.pep
          g685
          {\tt IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGKGRGLVLSVTGNKVSAFG}
               190
                       200
                               210
                                       220
           240
                  250
                          260
                                  270
                                          280
                                                  290
          TQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFEYIKEKNPDWIFIIDRTAAIGQEGPAA
m685.pep
          TQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFEYIKEKNPGWIFIIDRTAAIGQEGPAA
q685
               250
                       260
                               270
                                       280
                                              290
           300
                  310
                          320
                                  330
                                          340
                                                  350
          VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX
m685.pep
          g685
          VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX
                       320
                                      340
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2271> a685.seq

1	TTGTTTTGCC	GTATCGGGAA	TTTTGCGTTT	TGCGGCGTGG	TTTCTGCAGG
51	TTGTTTGCTT	AATAATAAAC	ATTCTTATTC	GTATGCAAAG	GAACCGCACA
101	CCGTGAAACC	GCGTTTTTAT	TGGGCAGCCT	GCGCCGTCCT	GCTGACCGCC
151	TGTTCGCCCG	AACCTGCCGC	CGAAAAAACT	GTATCCGCCG	CATCCGCATC
201	TGCCGCCACA	CTGACCGTGC	CGACCGCGCG		GTTGTGCCGA
251	AGAATCCCGA	ACGCGTCGCC	GTGTACGACT	GGGCGGCGTT	GGATACGCTG
301	ACCGAATTGG	GTGTGAATGT	GGGCGCAACC	ACCGCGCCGG	TGCGCGTGGA
351	TTATTTGCAG	CCTGCATTTG	ACAAGGCGGC	AACGGTGGGG	ACGCTGTTCG
401	AGCCCGATTA		CACCGCTACA		
451	GGCGGGCCGG	GCGCGGAAGC	GTATGAACAG	TTGGCGAAAA	ACGCGACCAC
501	CATAGATCTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC	GGCGAAAAGC
551	AGATGGAGAC	CTTGGCGCGG	ATTTTCGGCA	AGGAAGCGCG	CGCGGCGGAA
601	TTGAAGGCGC	AGATTGACGC	GCTGTTCGCC	CAAACGCGCG	
651	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCGGT	TACGGGCAAC	
701	CCTTCGGCAC	GCAGTCGCGG	TTGGCAAGTT		
751	CTACCGCCTG	TAGACGAATC	TTTACGCAAC	GAGGGGCACG	GGCAGCCTGT
801		TACATCAAAG			

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```
851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
     GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAGCGCA AGCAAATCAT
 951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>: a685.pep

- LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL 101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT GGPGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE 201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAFGTQSR LASWIHGDIG 251 LPPVDESLRN EGHGQPVSFE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
- 301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFEKAEPV

351 AAGKE*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. meningitidis

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from N. meningitidis:

m685/a685	98.9% identity in 355 aa overlap
m685.pep a685	10 20 30 40 50 60  LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
m685.pep	70 80 90 100 110 120 VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
m685.pep	130 140 150 160 170 180 PAFDKAATVGTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS
m685.pep	190 200 210 220 230 240  GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAFGTQSR
m685.pep	250 260 270 280 290 300  LASWIHGDIGLPPVDESLRNEGHGQPVSFEYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
m685.pep	310 320 330 340 350  DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2273> g686.seq (partial)

1	AATTTCTCCT	GCCGCGCCGA	TGATGTTTTT	GACGATATCT	GCAGTGCCGT
51	TGAAGGCTTC	ggcgGCATTG	CCCGATCTGT	CCAGCTCGGG	GCTGTATCGG
101	GTGGCGCGTT	TGAATCCGTC	GCCTACTCCT	TGCGTCAGCA	TAGCGCCGGC
151	ATTGTGGAAA	CGGTCGGCAA	GCCGTTGTCC	GGTGCTGCGG	TTGTCGGTCA
201	GGTTGAGGCG	GATATTTTGG	GCAACGCCTT	TTATGTCGTA	GCTGTATATA
251	TCCCTCGCGC	CTTTGGGAGC	GGGATAGCCG	CCGCCCTGTG	GCCCGTCATA
301	GCCGTCGGCG	GGATGGTGTT	CGTATCCGTC	CCAATGGATG	CGGTAAAGGC
351	TGAATCCGTC AF	ACGGGACTA CO	CGGCTTCGT CA	AGAATCGGA AT	rg <b>t</b> ga

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```
This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:
         (partial)
```

- ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI 51
- AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2275>: m686.seq..

```
1
    ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTTGGC
    GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
 51
101
    TCTCCTGCAG CGCCGATGAT GTTTTTAACG ATATCTGCAG TGCCGTTGAA
    GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
151
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGCG TCAGCATACT ACCGGCATTG
251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTCGTA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTCAACG GGACTACCGG CTTCATCAGA ATCGGAATGT GA
```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>: m686.pep

```
MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
```

- GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGOV
- 101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
- SVNGTTGFIR IGM*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from N. gonorrhoeae

g686/m686 95.4% identity in 131 aa overlap

```
20
g686.pep
                                 NFSCRADDVFDDICSAVEGFGGIARSVQLG
                                 LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
m686
              10
                      20
                              30
                                     40
                                             50
                       50
                               60
                                       70
g686.pep
         AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
          m686
          AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                      80
                                     100
                       110
                              120
         GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFVRIGMX
g686.pep
          GIAAALWPVIAVGGMVFVSVPMDAVKAKSVNGTTGFIRIGMX
m686
             130
                     140
                             150
                                    160
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2277> (partial) a686.seq

```
.. AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
 1
      TGAAAGCTTC GGCGGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
51
      GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCGTCAGCA TACTACCGGT
101
      ATTGTGGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
151
       GGTTGAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
201
251
      TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
      GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
301
      TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>: a686.pep (partial)

```
1 ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLROHTTG
51 IVETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
```

101 AVGGMVFVSV PMDAVKAESV NGTTGFIRIG M*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from N meningitidis:

```
96.2% identity in 131 aa overlap
m686/a686
                       20
                                               50
          LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
m686.pep
                                  a686
                                  NFSCRADDVFDDICSAVESFGGIARSVQLG
                                        10
                                                20
                       80
                               90
                                      100
                                              110
                                                      120
          AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
m686.pep
          a 68 6
          AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                40
                                60
                                        70
              130
                      140
                              150
          GIAAALWPVIAVGGMVFVSVPMDAVKAKSVNGTTGFIRIGMX
m686.pep
          GIAAALWPVIAVGGMVFVSVPMDAVKAESVNGTTGFIRIGMX
a686
               100
                       110
                               120
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2279> g687.seq

```
ATGAAATCCA GACACCTCGC CCTCGCCCTC GGCGTTGCCG CCCTGTTCGC
  1
 51
    CCTTGCCGCG TGCGACAGCA AAGTCCAAAC CAGCGTCCCC GCCGACAGCG
    CGCCTGCCGC TTCGGCAGCC GCCGCCCCGG CAGGACTGGT CGAAGGGCAA
101
151 AACTACACCG TCCTTGCCAA CCCGATTCCC CAACAGCAGG CAGGCAAGGT
    TGAAGTGCTT GAGTTTTTCG GCTATTTTTG TCCGCACTGC GCCCGCCTcg
251
    AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAAGACGA TATGTACCTG
301
    CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCGC TGGCACGCct
    CGCCGCCGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
351
    GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
401
451
    GAAGTCCTCA AAAAATGGCT GGGCGAACAA ACCGCCTTTG ACGGCAAAAA
    AGTCCTTGCC GCCTACGAAT CCCCCGAAAG TCAGGCGCGC GCcggcAAAA
501
    TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
551
    GTCGGCGGCA AATATAAAGT CGAATTTGCC GACTGGGAGT CCGGTATGAA
    CACCATCGAC CTTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
651
701
    AGTAG
```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687 >: g687.pep

```
1 MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGQ
51 NYTVLANPIP QQQAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
```

- 101 RTEHVVWQKE MLPLARLAAA VDMAAAESKD VANSHIFDAM VNQKIKLQEP
- 151 EVLKKWLGEQ TAFDGKKVLA AYESPESQAR AGKMQELTET FQIDGTPTVI
- 201 VGGKYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2281>: m687.seq

```
1 ATGAAATCCA GACACCTTGC CCTCGGCGTT GCCGCCTGT TCGCCCTTGC
51 CGCGTGCAC AGCAAAGTCC AAACCAGCGT CCCCGCCGAC AGCGCGCCTG
101 CCGCTTCGC AGCCGCCGCC CCGGCAGGC TGGTCGAAGG GCAAAACTAT
151 ACCGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAAT GGCTGGCGA ACAACCGCC TTTGACGGCA AAAAAGTCCT
```

```
501 TGCCGCCTAC GAGTCCCCCG AAAGCCAGGC GCGCCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>: m687.pep

- 1 MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
- 51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
- 101 EHVVWQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNPEV
- 151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
- 201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

ORF 687shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from N. gonorrhoeae:

```
m687/g687
          97.0% identity in 234 aa overlap
                         20
                                 30
                                                50
          MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIP
m687.pep
          a687
          MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIP
                10
                        20
                               30
                                       40
                 70
                         80.
                                 90
                                        100
          QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVVWQKEMLTLARLAAA
m687.pep
          g687
          QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTEHVVWQKEMLPLARLAAA
                70
                        80
                                      100
                                              110
         120
                130
                        140
                                150
                                       160
          VDMAAADSKDVANSHIFDAMVNQKIKLQNPEVLKKWLGEQTAFDGKKVLAAYESPESQAR
m687.pep
          VDMAAAESKDVANSHIFDAMVNQKIKLQEPEVLKKWLGEQTAFDGKKVLAAYESPESQAR
g687
               130
                       140
                              150
                                      160
                                              170
                190
                        200
                                210
                                        220
                                               230
         ADKMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
m687.pep
          AGKMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
a687
                       200
                              210
                                      220
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2283> a687.seq

```
ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
    CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCCGCCGAC AGCGCGCCTG
 51
    CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAAACTAT
101
151 ACTGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201
    CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCCAC CTCGAACCTG
    TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
251
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
    CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
351
    TTTTCGATGC GATGGTCAAC CAAAAAATCA AGCTGCAAGA GCCGGAAGTC
    CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT
451
    TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCCCGAC AAAATGCAGG
    AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCCACGGT TATCGTCGGC
551
    GGCAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
    CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCACTAA
```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>: a687.pep

- 1 MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
- 51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
- 101 EHVVWQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQEPEV
- 151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
- 201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from N meningitidis:

```
m687/a687
          98.7% identity in 232 aa overlap
                        20
                                30
                                        40
                                                50
          {\tt MKSRHLALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIPQQ}
m687.pep
          MKSKHLALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIPQQ
a687
                        20
                                30
                70
                        RN
                                90
                                               110
                                                       120
          QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVVWQKEMLTLARLAAAVD
m687.pep
          QAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTEHVVWQKEMLTLARLAAAVD
a687
                70
                        80
                                90
                                       100
                                               110
                                                      120
               130
                       140
                               150
                                       160
                                                      180
          MAAADSKDVANSHIFDAMVNQKIKLQNPEVLKKWLGEQTAFDGKKVLAAYESPESQARAD
m687.pep
          MAAADSKDVANSHIFDAMVNQKIKLQEPEVLKKWLGEQTAFDGKKVLAAYESPESQARAD
a687
               130
                       140
                               150
                                       160
                                              170
               190
                       200
                               210
                                       220
                                              230
          KMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
m687.pep
          KMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX
a687
               190
                       200
                               210
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2285> g688.seq

1 GTGCTACACT AGACATCCCG ATTTGCACAG AAAGGTTCTC CCGTGAACAA
51 AACCCTCATC CTCGCCCTTT CCGCCCTGTT CAGCCTGACC GCGTGCAGCG
101 TCGAACGCGT CTCGCTGTTT CCCTCCTACA AACTCAAAAT CATCCAAGGC
151 AACGAACTCG AACCGCGCGC CGTTGCCGCC CTGCGCCCCG GCATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCTTTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGAACGCA GCAACCTGAC CGTCTATTTT GAAAACGGCG TACTCGTCCG
401 AAAACGCAGA CAAACAATAA

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >: g688.pep

- 1 VLH*TSRFAQ KGSPVNKTLI LALSALFSLT ACSVERVSLF PSYKLKIIQG
- 51 NELEPRAVAA LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
- 101 KERSNLTVYF ENGVLVRTEG DALQNAAEAL RAKQNADKQ*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2287>: m688.seq

1 GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGTG
101 CCGAACGCGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCC AACCGCGCGC CGTTGCCGCC CTCCGCCCCG GCATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
351 CACCGAAGGC GCAATCTGAC CGTCTATTTT GAAAACGGCG TACTCGTCCG
351 CACCGAAGGC GACGTCCTGC AAAACCGTCC CGAAGCCCTC AAAGACCGCC

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>: m688.pep

- 1 VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSAERVSLF PSYKLKIIQG
- 51 NELEPRAVAA LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII
- 101 KERSNLTVYF ENGVLVRTEG DVLQNAAEAL KDRQNTDKP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from N. gonorrhoeae:

```
m688/g688
           90.6% identity in 138 aa overlap
                 10
                          20
                                  30
                                          40
                                                   50
                                                           60
           VLHYPSRFAQKGISVNKTLILALSALLGLAACSAERVSLFPSYKLKIIQGNELEPRAVAA
m688.pep
              VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVERVSLFPSYKLKIIQGNELEPRAVAA
q688
                 10
                          20
                                  30
                                          40
                                                   50
                          80
                                  90
                                         100
                                                  110
m688.pep
          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTVYFENGVLVRTEG
          LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGIIKERSNLTVYFENGVLVRTEG
q688
                         80
                                  90
                                         100
                                                 110
                130
                         140
m688.pep
          DVLQNAAEALKDRQNTDKPX
          1:111111111: :11:11
          DALQNAAEALRAKQNADKQX
g688
                130
                         140
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2289>

- a688.seq GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA 1 AACCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG 51 TCGAACGCGT TTCACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC 101
  - 151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCCGCCCCG GTATGACCAA AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC 201
  - 251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
  - 301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAAACGGCG TGCTCGTCCG
  - 351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAAC 401 AAAACGCAGA CAAACAATAA

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>: a688.pep

- VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLKIIQG
- NELEPRAVAS LRPGMTKDQV LLLLGSPILR DAFHTDRWDY TFNTSRNGII 51
- KDRSNLTVYF ENGVLVRTEG NALQNAAEAL RVKQNADKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from N. meningitidis

m688/a688	93.5% identity:	in 138 a	a overlap			
	10	20	30	40	50	60
m688.pep	VLHYPSRFAQKGISVI	NKTLILALS	SALLGLAACSA	ERVSLFPSYR	LKIIOGNELE	PRAVAA
•	11111111111111					11111
a688	VLHYPSRFAQKGISV	NKTLILALS	SALLGLAACSVI	ERVSLFPSYK	LKIIOGNELE	PRAVAS
	10	20	30	40	50	60
	70	80	90	100	110	120
m688.pep	LRPGMTKDQVLLLLGS	SPILRDAF	TDRWDYTFNT:	SRNGIIKERS	NLTVYFENGV	LVRTEG
				1111111:11		111111
a688	LRPGMTKDQVLLLLGS	SPILRDAF	HTDRWDYTFNTS	RNGIIKDRS	NLTVYFENGV	LVRTEG
	70	80	90	100	110	120
	130	140				
m688.pep	DVLQNAAEALKDRQNT	DKPX				
· •	::11111111::11:	11				
a688	NALQNAAEALRVKQNA	DKQX				
	130	140				

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2291> g689.seq (partial)
```

```
..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
  51
        GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCTAC CTGCCCGCGA
       TTCCCGAAAT GGCGCAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
 101
       AGTCTGAGTT TGTTTATGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
 151
       CGCGGTGTCC GACATCAAAG GGCGCAAACC CGTCGCCCTG ACCGGTTTGA
 201
       TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTTGCTTC GAGTACCGAA
 251
       CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
 301
       AGTCATCGTc ggtgcgatgg tgcgcgatTA TTATTCCGGA CGCAAAGCCG
 351
 401
       CGCAGATGTT TGCCCTTATC GGCATCATTC TGATGGTTGT GCCGCTGGCC
       GCACCCATGG TCGGCGCATT GTTGCAGGGA TTGGGCGGAT GGCGGGCGAT
 451
       TTTCGTTTTC ttggcGgcgT ATTCGCCGGT GCTGCCCGGT TTGGTACAGT
 501
       ATTTCCTGCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTC
 551
       GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
 601
       GGGTtatCTG TTTTTCAGG CATTCAGCTT CGGTTCGATG TTCGCCTTTC
 651
       TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
 701
       CGGTACGCAT GGGTGTTTGC ACTCAACATC ATCACGATGA TGTTTTTCAG
 751
       CCGCGTTACC GCGTGGCGGC TTAAAACCGG CGCGCATCCG CAAAGCATCC
801
       TGCTGCGGGG GATTGTCGTC CAATTTGCCG CCAACCCGTC CCAACTCGCC
851
       901
951
       GATGTTTTCC GTCGGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
       GCTTTATGTC TTATTTCAAA GAAGAGGCG GCAGCGCGAA CGCCGTGTCG
1001
       GGTGTATTCC GGTCCTTAAT CGGCGCGGGC GTGGTCATGG CGGCAACCGT
1051
       GATGGCGGCA ACCATGACCG CGTCCGCCTC TTGCGGCATT GCGCTTTTGT
1101
       GGCTCTGCTC GCACAAGGCG TGGAAGGAAA ACGAAAAAA GCGAATACTT
```

# This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689 >:

```
g689.pep
           (partial)
           ..SPPLPPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
       1
             SLSLFMFGTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
      51
             QLLNLRAVQA FGAGMAVVIV GAMVRDYYSG RKAAQMFALI GIILMVVPLA
     101
             APMVGALLQG LGGWRAIFVF LAAYSPVLPG LVQYFLPNPA VGGKIGRDVF
GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLTESSFV YRQLYHVTPH
     151
     201
     251
             RYAWVFALNI ITMMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSOLA
     301
             AVLFFGLPPF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
             GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL
     351
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2293>: m689.seq

```
TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
      GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
 101 GTGTTTTCCG CCGCCGGCCG GTTTGTTTGC GAATCGGACG AGAATTTATG
 151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAACTGATGG CGGTTTTGAT
 201 GGCGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
      CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
 301 CAGAGTTTGA GTTTGTTTAT GTTCGGCACG GCGTTCGGAC AGGTGGTCGG
 351 CGGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
     TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTTGT TTCGAGTGCC
     GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCGGTG CGGGCATGAC
     TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
     CCGCCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
 551
     GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
     GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
     AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG ACGGGACGTG
 751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
     GATGGGTTAT CTGTTTTTC AGGCATTCAG CTTCGGTTCG ATGTTCGCCT
     TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCG TGTTACGCCT
 851
 901 CATCAATACG CTTGGGCGTT TGCACTCAAC ATCATCACGA TGATGTTTTT
 951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
     TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTCGGTGCA AACACGCAGG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGCAC GACGGTTCGG CAACCGTGAT GGCGGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCTGTGGC TCTGCTCGCA TCGTGCGTGG
```

#### 1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>: m689.pep

1	LLIHYIVPVR	PVLPGLLLPP	VCAGVLKFSV	SAYCVFRRRA	VCLRIGREFM
51	<b>PSAHYPEMSE</b>	KLMAVLMAML	VTLMPFSIDA	YLPAIPEMAQ	SLNADVHRIE
101	QSLSLFMFGT		SDIKGRKPVA	LTGLIVYCLA	VAAIVFVSSA
151	<b>EQLLNLRVVQ</b>	AFGAGMTVVI	VGAMVRDYYS	GRKAAQMFAL	IGIILMVVPL
201		GLGGWQAIFV		GLVQYFLPKP	
251	FGLVAGRFKR	VLKTRAAMGY	LFFQAFSFGS	MFAFLTESSF	VYQQLYRVTP
301	HQYAWAFALN	IITMMFFNRV	TAWRLKTGVH	PQSILLWGIV	VQFAANLSOL
351	AAVLFFGLPP	FWLLVACVMF	SVGTQGLVGA	NTQACFMSYF	KEEGGSANAV
401	LGVFQSLIGA	GVGMAATFLH			
451	KENGQSEYL*				

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from N. gonorrhoeae:

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2295> a689.seq

```
TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
      GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
  51
      GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
 101
      CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAACTGATGG CGGTTTTGAT
      GGCGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
 201
      CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
 251
      CAGAGCCTGA GTTTGTTTAT GTTCGGCACG GCGTTCGGAC AGGTGGTCGG
 301
      CGGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
 351
      TGGCCGTCTA CTGCCTTGCC GTTGCCGCCA TCGTATTTGC TTCGAGTGCC
 401
      GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCGGTG CGGGCATGAC
 451
      TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
      CCGCCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
 551
      GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
 601
      GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
 651
 701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
      TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCCGTGCCGC
 751
     GATGGGTTAT CTGTTTTTC AGGCATTCAG CTTCGGTTCG ATGTTCGCCT
 801
     TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
     CACCAGTACG CTTGGGCGTT TGCACTCAAC ATCATCACGA TGATGTTTTT
 901
      CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
 951
     TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1001
     GCCGCCGTGC TGTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1051
     CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTCGGTGCA AACACGCAGG
1101
     CGTGTTTTAT GTCCTATTTC AAAGAAGAG GCGGCAGCGC AAACGCCGTA
1151
     TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1201
     CTTCTTGCAC GACGGTTCGG CAACCGTGAT GGCGGCAACC ATGACCGCGT
1251
1301 CTACCTCTTG CGGCATTGCG CTTTTGTGGC TCTGCTCGCA TCGTGCGTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>: a689.pep

```
LLIHYIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
     PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
 51
     OSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
101
    EQLLNLRVVQ AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
151
    VAPMVGALLQ GLGGWQAIFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251
    FGLVAGRFKR VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYHVTP
    HQYAWAFALN IITMMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
301
    AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
351
401
    LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
    KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. meningitidis* 

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from N. meningitidis:

```
m689/a689
          99.1% identity in 459 aa overlap
                         20
                                         40
          LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
m689.pep
          LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
a 689
                 10
                         20
                                 30
                                         40
                                                 50
                         80
                                 90
                                        100
                                                110
          KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
m689.pep
          KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
a689
                 70
                         80
                                 90
                                        100
                                                110
                130
                        140
                                150
                                        160
                                                170
          SDIKGRKPVALTGLIVYCLAVAAIVFVSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYS
m689.pep
          a 689
          SDIKGRKPVALTGLAVYCLAVAAIVFASSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYS
                130
                        140
                                150
                                        160
                                                170
                                                        180
                190
                        200
                                210
                                                230
                                                        240
          \tt GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP
m689.pep
```

```
GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP
a689
               190
                       200
                              210
                                      220
               250
                       260
                              270
                                      280
          {\tt AVGGKIGRDVFGLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP}
m689.pep
          a689
          AVGGKIGRDVFGLVAGRFKRVLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVTP
                       260
                              270
                                      280
               310
                       320
                              330
                                      340
                                             350
                                                     360
          HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPP
m689.pep
          HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPP
a 689
               310
                       320
                              330
                                      340
                                                     360
                                             350
                      380
                              390
                                      400
                                             410
                                                     420
         {\tt FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLH}
m689.pep
          FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLH
a689
                      380
                              390
                                     400
               430
                      440
                              450
                                     460
         DGSATVMAATMTASTSCGIALLWLCSHRAWKENGQSEYLX
m689.pep
         a689
         DGSATVMAATMTASTSCGIALLWLCSHRAWKENGQSEYLX
               430
                      440
                              450
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2297> g690.seq (partial)

```
ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
     GGCCGCGCGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
     CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCCAAAC CGATTTGCAA
101
     CCGGCCGCAT CCGCCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
     GTGAAATTGC ACCGGCCTGC ACCCCGCCGC CGGCATTGGC GATCTCATAC
201
     AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTTCCCAT
251
    AACGAACTGG AAACCCGTTT CGGCTTACCC GGCGGCGGCT ATGACAACAT
301
    ACAGCGGCTG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
351
    AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
    AGCCGGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
451
    AGCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACCCGC GGaCAAGGCG
551
    AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCGGCAAC ATCtgCCtaT
    TTgaaccggC ACAAcaacGG ACTTggcgGC AATTTCCAAT ACATCGGCCA
601
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
    TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
701
    ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
751
    AAATATCTAT...
```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690 >: g690.pep (partial)

```
1 MKNKTSSLPL WLAAIMLAAR SPSKEDKTKE NGASAASSSA SSASSQTDLQ
51 PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQQIAEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQKIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEEPKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPFLD
251 IHFDENGKIT RIVVYEKNIY ...
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2299>: m690.seq..

```
ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
CCGCTGCTTC GTCCTCCGCG TCATCAGCTC CTTCCCAAAC CGATTTGCAA
CCGACCGCAT CCGCCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
GTCAAATTGC ACCAGCCTGC ACCCCGCCAC CGGCATTGAC GATCTCATGC
ACCAGAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTTCCCAT
CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACACACT
ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACCGAAA GCGCACGATC
AGCCGCCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
AGCCGCCGCT TTGCTGATAC AGGAACCCCC GGACAAGGCCG
TTGCTGATACAAACCCC GCCTCCCAGGA
AGCCGCCGCT TTGCTGATAC AGGACCCC GCCTCCCGACGA
AGCCGCCGCT TTGCTGATAC AGGACCCCC GGACAAGGCCG
```

WO 99/57280 PCT/US99/09346

1110

```
551 AGGAGCCGAA ACGCACGCGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
    TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCCAAT ACATCAGCCA
601
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTTAGAC
751 ATCCATTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
    AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA
```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>: m690.pep

- MKNKTSSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQIAEHI DSDCLFALSH 51 101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI SRQAQNALME QERRLREATL LLIQGSQETR GQGEEPKRTR YFEVSATPAY SSRHNNGLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPDKPFLD
- 201 SSRHNNGLGG NFQYISQLPG YLKIHGEML 251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from N. gonorrhoeae

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from N. gonorrhoeae:

```
m690/g690
           89.3% identity in 408 aa overlap
                         20
                                  30
          MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPSQTDLQPTASAPDNVK
m690.pep
           MKNKTSSLPLWLAAIMLAARSPSKEDKTKENGASAASSSASSASSQTDLQPAASAPDNVK
g690
                                  30
                                          40
                 70
                         80
                                  90
                                         100
                                                 110
          QAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
m690.pep
           QAESAPLXNCTGLHPAAGIGDLIQQIAEHIDSDCLFALSHNELETRFGLPGGGYDNIQRL
q690
                 70
                         80
                                  90
                                         100
                                                 110
                130
                         140
                                 150
                                                 170
                                         160
          {\tt LFPDIRPEDPDYHQKIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQETR}
m690.pep
           {\tt LFPDIRPEDPDYHQKIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR}
q690
                130
                        140
                                 150
                                         160
                                                 170
                                                         180
                190
                        200
                                 210
                                         220
                                                 230
          GOGEEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
m690.pep
          GQGEEPKRARYFEVSATSAYLNRHNNGLGGNFQYIGQLPGYLKMHGEMLENQSLFRLSNR
g690
                190
                        200
                                 210
                                         220
                250
                        260
                                 270
                                        279
m690.pep
          ERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
          11111111111111111111111111111111111111
g690
          ERNPDKPFLDIHFDENGKITRIVVYEKNIY
                        260
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2301> a690.seq

```
ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51 GACCGCGTGT TCCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCCTC GTCCACGGCA TCCGCCGCTT CGTCTTCCGC GCCCCAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCCTGAT AACGTCAAGC AGGCAGAAAG
    CGTGCCGCCG TCAAATTGCA CCGACCTGCA CCCCGCCACC GGCATTGACG
201
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
    CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
    TGACAACATA CAGCGGCTGC TGTTTCCCGA CATCCGCCCT GAAGATCCCG
351
401
    ACTACCATCA GAAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501
    CCTCCGAGAA GCGACGCTGT TGCTGATACA GGGCAGTCAA GAAACCCGCG
    GACAAGGCGA GGAGCCGAAA CGCACGCGTT ATTTTGAAGT TTCGGCAACC
551
601 CCTGCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAAT ACACGGAGAA ATGCTTGAAA
```

PCT/US99/09346 WO 99/57280

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG

751 TTTTTAGACA TCCATTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>: a690.pep

MKNKTSSLLL WLAAMMLTAC SPSKEDKTKE NGASAASSTA SAASSSAPOT

- DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA 51
- LSHHELETRF GLPGGGYDNI QRLLFPDIRP EDPDYHQKII LAIEDLRYGK 101
- 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEEPK RTRYFEVSAT
- 201 PAYSSRHNNG LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP
- FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from N. meningitidis:

m690/a690	93.9% identity in 280 aa overlap
m690.pep a690	10 20 30 40 50  MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSSASAPSQTDLQPTASAPD
m690.pep a690	60 70 80 90 100 110  NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI
m690.pep a690	120 130 140 150 160 170 QRLLFPDIRPEDPDYHQKIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ
m690.pep	180 190 200 210 220 230  ETRGQGEEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRL
m690.pep	240 250 260 270 279  SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2303> g691.seq

- GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT 1 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA TCCCCCCGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGGCTG 101 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT 201 GGCGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGCGGT 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
- 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >: g691.pep

- VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFQ PNCDIRRLGL
- 51 TQGQHNELRK IRAAFKMAGD RARLKVMHSE HSRRRSVVEI ISSDVFNRNE
- 101 ARDYVESRYH SSMDFAVDEL EIQHRFFHIL TPQQQQMWLS SCLK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2305>: m691.889

```
1 GTGCCACTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
51 AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCCGAA CGATTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GGCGGGCAC AGGGCGCTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTTG TCCGGTATGG ATTTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>: m691.pep

- 1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFQ PNCDIRRLGL
- 51 TQSQHNELRK IRTAFKMAGD RARLKVMHSE HSRRRSVVEI ISSDVFNRNE
- 101 ARDYVESRYL SGMDFAVDEL EIQHRFFHIL TPQQQQMWLS SCLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from N. gonorrhoeae:

```
m691/g691
          97.2% identity in 144 aa overlap
                         20
                                 30
          VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFQPNCDIRRLGLTQSQHNELRK
m691.pep
          VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFQPNCDIRRLGLTQGQHNELRK
g691
                                 30
                                         40
                 70
                         80
                                 90
                                        100
                                                110
          IRTAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNRNEARDYVESRYLSGMDFAVDEL
m691.pep
          q691
          IRAAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNRNEARDYVESRYHSSMDFAVDEL
                 70
                         80
                                 90
                                        100
                                                110
                130
                        140
m691.pep
          EIQHRFFHILTPQQQQMWLSSCLKX
          #11FF1314F1111111111111111
g691
          EIQHRFFHILTPQQQQMWLSSCLKX
                130
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2307> a691.seq

```
GTGCCACTGC NTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
CCCCCTGAA CGATTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCGCCG CCTTCAAAAT
GGCGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
GTCGGACTG ATTTCCTCGG ATGTTTTTAA TCGGAACGAG
GCGCGCGATT ATGTCGAAAG CCGCTATTTG TCCGGTATGG ATTTTGCGGT
GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>: a691.pep

- 1 VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
- 51 TQGQHNELRK IRAAFKMAGD RARLKVMHSE HSRRRSVVEI ISSDVFNRNE
- 101 ARDYVESRYL SGMDFAVDEL EIQHRFFHIL TPQQQQMWLS SCLK*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from N. meningitidis

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from N. meningitidis:

```
m691/a691
          97.2% identity in 144 aa overlap
                10
                        20
                                30
                                        40
          VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFQPNCDIRRLGLTQSQHNELRK
m691.pep
          a691
          VPLXAPCRFAKPAASFLSMALLSCQLSHAATAYIPLNDFQPNCDIRRLGLTQGQHNELRK
                                30
                                        40
                                                50
                        80
                                90
                                       100
                                               110
          IRTAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNRNEARDYVESRYLSGMDFAVDEL
m691.pep
          {\tt IRAAFKMAGDRARLKVMHSEHSRRRSVVEIISSDVFNRNEARDYVESRYLSGMDFAVDEL}
a691
                70
                        80
                                       100
                                               110
               130
                       140
m691.pep
          EIQHRFFHILTPQQQQMWLSSCLKX
          a691
          EIQHRFFHILTPQQQQMWLSSCLKX
               130
                       140
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2309> g692.seq

```
GTATCGCACA CACGCTGTCG CTGTTCGGAA TCGAtaCGCC GGATTTGGCG
     GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATGCGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGT ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
     AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
201
251
     TGGCTGTCTT TGTCGGCGGT TTTgacGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGCTCT TGGAACAGGG CTTCGGTCAG CTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTGCGCGGC
401 AGTTGTGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTTTCCGC
451
     GATGTCGGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTTCAGC ATCACCAAGG CGCGTGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
     CAGTTTGCCC GGATACAGTC CCAAAGGCGC GGTCGGCACT TGGAAGGCTT
651 CGGTGATGTC CAGGTTGTGT TCTTTTTTGA AATCGTCAAG ATAGGGTTTG
701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCCGCCAATG CCAGATTCGG
751 GCGCACATAG TCggTAAATT cgaccaatTT gacgGTGTag cCTTTTTTCT
801 CCAGCTCGgc tTGGATTTGT TCTTTGACCA TATCgccgaa gtcgcccacg
851 gTCGTGCCGA agacgaTTTC TTTTTTCGCc GcgcCGTTAT CGGCAGAAGG
901 GGCGGCGgca gaggctgcGG GCGCGCTGTC TTTTtgaccG ccgCAGGCTG
951 CGAGGATGAG CGCGAGtgcg gcggcggaaa ggGTTTTGAA GAAGGTTTTC
1001 atATTTTCTc ctga
```

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692 >: g692.pep

```
1 VSHTRCRCSE SIRRIWRNGR EWRIKGQKCR LNTDAVQTAS FYTTALFGCA
51 FIPCGRVFVA LEAFVRVGFE RVGVIGLGYV FKPLAVFVGG FDGRPVDIGK
101 ARLLEQGFGQ LHAAAYGVVA VDDGKIHVGA AARQLCGFKL DDFDVFQVFR
151 DVGFGCGQRI DAVFEFDPTQ FVQHHQGACE VGRVVGRGYG AAVFDFFQRF
201 QFARIQSQRR GRHLEGFGDV QVVFFFEIVK IGFVLEDVDV QLALRQCQIR
251 AHIVGKFDQF DGVAFFLQLG LDLFFDHIAE VAHGRAEDDF FFRRAVIGRR
301 GGGRGCGRAV FLTAAGCEDE RECGGGKGFE EGFHIFS*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2311>: m692.seq

```
1 GTGTTGCACA CGCTTTGTCG CTGTTCGGAA TCGATACGCC GGATTCGGCG
51 GAATGGCAG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACAGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTCGGTCAG CTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
```

```
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCTCGGC
 451 GATGTCCGCT TTGGATGCGG TCAACGGATT GATGCCGTCT TTGAGTTTGA
 501 TCCAACCCAG TTCGTCGAGC ATCACCAAGA CGCGGGCGAA GTTGGACGGG
 551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATTT
 601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTCGGCACT TGGAAGACTT
 651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
 701 TGTTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
 801 CCAGCTCGGC TTGGATTTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTTCGCC GCGCCGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGCG CGCTGTCTTT TTGACCGCCG CAGGCGGCGA
 951 GGATGAGCGC GAGTGCGGCG GCGGAAAGGG TTTTGAAGAA GGTTTTCATA
1001 TTTTCTCCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>: m692.pep

- 1 VLHTLCRCSE SIRRIRRNGR EWRIKGQKCR LNTDTVQTAS FYTT<u>ALFGCA</u> 51 FIPCGRGFVA LEAFVRVGFE RVGVIGLGYV FKPLAVFVGG FDGRPVDIGK
- 101 ARFLEQGFGQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFQVLG
- DVRFGCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGRGYG AAVFDFFQRF QLARVQSQRR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
- 251 AYIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG
- 301 RSGCGGRAVF LTAAGGEDER ECGGGKGFEE GFHIFS*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from N. gonorrhoeae:

m692/g692	91.1% identit	y in 338 a	a overlap			
m692.pep	10 VLHTLCRCSESIRI	, , , , , , , , , , , , , , , , , , , ,	1 1 1 1 1 3 1 1 1 1 1	1:11111111	1117111111	111 111
	10	20	30	40	50	60
m692.pep	70 LEAFVRVGFERVGV			111111111		
g692	70	80 80	LAVFVGGFDGR 90	PVDIGKARLI 100	LEQGFGQLHAI 110	AAYGVVA 120
m692.pep	130 VDDGKIHVGAATRO	1 111111	11111111	111111111		
g692	VDDGKIHVGAAARÇ 130	LCGFKLDDFI 140	DVFQVFRDVGF 150	GCGORIDAVI 160	FEFDPTQFVQI 170	HQGACE 180
m692.pep	190 VGRVVGRGYGAAVF	200 DFFQRFQLAF	210 RVQSQRRGRHL	220 EDFGDVQIVE	230 FFEVVKIGFV	240 LEDVDV
g692	VGRVVGRGYGAAVF 190	DFFQRFQFAF 200	RIQSQRRGRHL 210	EGFGDVQVVF 220	FFEIVKIGFV 230	LEDVDV 240
m692.pep	250 QLALSQCQIRAYIV                   QLALRQCQIRAHIV 250		1111111111	1   1   1   1   1	111111111	:  AVIGRR
m692.pep g692	300 310 GGRSGCGGRAVFLT:                GGGRGCG-RAVFLT: 310	320 AAGGEDEREC	330 GGGKGFEEGFI	HIFSX	290	300

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2313> a692.seq

GTGTTGCACA CGCTTTGTCG CTGTTCGGAA TCGATACGCC GGATTCGGCG

51	GAATGGCAGG	GAATGGCGGA	TTAAAGGACA	3 3 3 3 mcccccm	GMG333G3
			-		CTGAACACGG
101	ATACGGTTCA		TTTTATACGA	CTGCCTTATT	TGGCTGCGCC
151	TTCATTCCAT	GCGGCAGGGG	ATTTGTAGCC	CTCGAAGCGT	TTGTGCGCGT
201	AGGCTTTGAA	CGCGTCGGAG	TTATAGGCCT	CGGTTACGTC	TTTAAGCCAT
251	TGGCTGTCTT	TGTCGGCGGT	TTTGACGGCA	GACCAGTTGA	CATAGGCAAA
301	GCTCGGTTCT	TGGAACAGGG	CTTCGGTCAG	CTTCATGCCG	CTGCTTATGG
351	CGTAGTTGCC	GTTGACGACG	GCAAAATCCA	CGTCGGCGCG	GCTACGCGGC
401	AGTTGCGCGG	CTTCAAGCTC	GACGATTTTG	ATGTTTTTCA	GGTTTTCGGC
451	AATGTCCGCT	TTGGATGCGG	TCAGCGGATT	GATGCCGTCT	TTGAGTTTGA
501	TCCAACCCAG	TTCGTCGAGC	ATCACCAAGA	CGCGGGCGAA	GTTGGACGGG
551	TCGTTGGGCG	CGGATACGGT	GCTGCCGTCT	TTGACTTCTT	CCAGCGATTT
601	CAGCTTGCCC	GGGTACAGTC	CCAAAGGCGC	GGTCGGCACT	TGGAAGACTT
651	CGGTGATGTC	CAGATTGTGT	TCTTTTTTGA	AGTCGTCAAG	ATAGGGTTTG
701	TGTTGGAAGA	CGTTGATGTC	CAACTCGCCC	TCAGCCAATG	CCAGATTCGG
751	GCGCACATAG	TCGGTAAACT	CGACCAGTTT	GACGGTGTAG	CCTTTTTTCT
801	CCAGCTCGGG	TTGGATTTGT	TCTTTGACCA	TATCGCCGAA	GTCGCCGACG
851	GTCGTGCCGA	AGACGATTTC	TTTTTTCGCC	GCGCCGTTGT	CGGCGGCGGC
901	AGAAGCGGAT	GCGGCGGCG	CGCTATCTTT	TTGACCGCCG	CAGGCGGCGA
951	GGATGAGCGC	GAGTGCGGCG	GCGGAAAGGG	TTTTGAAGAA	
1001	TTTTCTCCTG	A			

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

- 1 VLHTLCRCSE SIRRIRRNGR EWRIKGQKCR LNTDTVQTAS FYTTALFGCA
- 51 FIPCGRGFVA LEAFVRVGFE RVGVIGLGYV FKPLAVFVGG FDGRPVDIGK
  101 ARFLEQGFGQ LHAAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVFQVFG
  151 NVRFGCGQRI DAVFEFDPTQ FVEHHQDAGE VGRVVGRGYG AAVFDFFQRF

- 201 QLARVQSQRR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
- 251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG 301 RSGCGGRAIF LTAAGGEDER ECGGGKGFEE GFHIFS*

Computer analysis of this amino acid sequence gave the following results:

## Homology with a predicted ORF from N. meningitidis

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from N. meningitidis:

m692/a692	98.8% identity in 336 aa overlap
m692.pep	10 20 30 40 50 60  VLHTLCRCSESIRRIRRNGREWRIKGQKCRLNTDTVQTASFYTTALFGCAFIPCGRGFVA
a092	VLHTLCRCSESIRRIRRNGREWRIKGQKCRLNTDTVQTASFYTTALFGCAFIPCGRGFVA 10 20 30 40 50 60
m692.pep	70 80 90 100 110 120 LEAFVRVGFERVGVIGLGYVFKPLAVFVGGFDGRPVDIGKARFLEQGFGQLHAAAYGVVA
m692.pep a692	130 140 150 160 170 180 VDDGKIHVGAATRQLRGFKLDDFDVFQVLGDVRFGCGQRIDAVFEFDPTQFVEHHQDAGE
m692.pep a692	190 200 210 220 230 240 VGRVVGRGYGAAVFDFFQRFQLARVQSQRRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
m692.pep	250 260 270 280 290 300 QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDFFFRRAVVGGG
m692.pep a692	310 320 330 RSGCGGRAVFLTAAGGEDERECGGGKGFEEGFHIFSX

```
310 320 330
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2315>:

```
TCGGCATTTG TGTTGCCCAA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
       AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
   51
       GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
 101
 151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
 251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
 301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
 401 GTTTGCCGGT TGGTCGTCGC ATAGCAGATG TCTTCCTTGT GCGGATTGCG
 451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
      CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTC GGGGTTTCTG
 551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
 601 CGGTGCAAGC TGCCCCATCG TGCCTTCGAC CTCGGCGTGC CCCTTATGCC
 651 CGATCATGAT GATTTCACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTCG TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAAACCGCG
 751 CTCCGCCGCT TCCTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
 801 CCAGTGTCGC GCCCGGCGGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
 851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
 901 GCGCACATAA ACCGGCGCGC CGAATTCTTC CAAAGCACGT TCGACAATAC
 951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCATTC CGTGTTCAGA CGGCATTCAC
1051
      GTTTTTTTGC TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694 >: g694.pep (partial)

```
1 SAFVLPKHPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPFAHG
51 FMPPSAYGCQ YFPHQHFGRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHQR ASRIKYPETA
251 LRRFLLHRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQVV HDEFVVDDFV
301 AHINRRAEFF QSTFDNTDCP IHTGAEAARI GKDDGFSVHK FCIPCSDGIH
351 VFLLXLCDGR YCQAPPTPHR RR*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2317>:

```
TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
      GACGGCATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
 101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
 151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
 201 ATCCGCGTAT GGTTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
      GCGCCTGCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
 301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
 351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
     ATCACGATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCCGGTT
     GGTCGTCGCA TAGCAGATAT CTTCCTTGTG CGGATTGCGG ATATTGGGGA
 451
 501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
     GTGGTTTGGC TGACATAGGC GAGTTTGTCG GGGTTTCTGA CTTCGAGTTT
 551
     TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCGCAAGCT
 601
 651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG
 701 ATTTCACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
     CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
 751
801
     CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTCGCG
 851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
 901 CAGGTTGTCC ACGACGAATT TGTTGTGAAC GACTTCGTGG CGCACATAAA
     TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATT GCCCGA
     TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1001
     GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTTCTTCT
1051
     TGGGTTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>: m694.pep

- 1 LVSASGTROK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
- 51 HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
- 101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNHDVALF CQLFDGGLPV

```
151 GRRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF

201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR

251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT

301 QVVHDEFVVN DFVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL

351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from N. gonorrhoeae:

```
m694/g694
           86.8% identity in 372 aa overlap
                          20
                                             40
                                                     50
           LVSASGTRQKCRLKPVQTAFVLPKHS----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
m694.pep
                         :1111111
                                   {\tt SAFVLPKHPMPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR}
g694
                               10
                                       20
            60
                     70
                             80
                                     90
                                            100
                                                    110
           TLAFAYGFVPPSAYGCQYFPHQHFGRGRACRYADFVFALKPCALQVACIIHHIRIDSARC
m694.pep
             a694
           APPFAHGFMPPSAYGCQYFPHQHFGRGRACRYADFAFAFKPRALQVGRVVHHIRIDSARC
               50
                                       80
                                               90
           120
                    130
                            140
                                    150
                                            160
                                                    170
           RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRIADIFLVRIADIGETRVQRGDDV
m694.pep
           RHFAQAVAVGRIGRTDHNHDVALFRQLFDGGLPVGRRIADVFLVRIADIGETRVQRGDDV
g694
              110
                      120
                              130
                                      140
                                              150
                                                       160
           180
                   190
                            200
                                    210
                                            220
          FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFARRKLPHRSFDLDVPLMPDHDDFT
m694.pep
           FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFARCKLPHRAFDLGVPLMPDHDDFT
g694
              170
                      180
                              190
                                      200
           240
                   250
                            260
                                    270
                                            280
                                                    290
          VLGIQSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
m694.pep
          g694
          VLGIQSGDFLMHFRHQRASRIKYPETALRRFLLHRLRYAVCRINQCRARRHFRQVFDKHR
              230
                      240
                                      260
                                              270
                                                      280
           300
                   310
                            320
                                    330
                                            340
          TFFTQVVHDEFVVNDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
m694.pep
          q694
          AFFAQVVHDEFVVDDFVAHINRRAEFFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI
             290
                      300
                              310
                                      320
                                              330
                                                      340
           360
                   370
                            380
m694.pep
          SFSDGINIFLLGFYGGRCCPTPPTPHRRRX
            1111::11 : 11 | :11|11|11|
q694
          PCSDGIHVFLXXLCDGRYCQAPPTPHRRRX
             350
                      360
                              370
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2319>: a694.seq

```
TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
  1
     GACGGCATTT GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
 51
     AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
101
     CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
151
     ATCCGCGTAT GGTTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
     GCGCCTGCCG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
251
     CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
301
    CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
351
     ATCACGATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCCGGTT
401
    GGTCGTCGCA TAGCAGATAT CTTCCTTGTG CGGATTGCGG ATATTGGGGA
451
    AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
501
551 GTGGTTTGGC TGACATAGGC GAGTTTGTCG GGGTTTCTGA CTTCGAGTTT
    TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCGCAAGCT
601
    GCCCCATCGT TCCTTCGACC TCGACGTGCC CCTTATGCCC GATCATGATG
```

701	ATTTCACAGT	CTTGGGCATC	CAGTCGGGCG	ACTTCCTTAT	GCACTTTCGT
751	CACCAGCGGG	CAAGTCGCAT	CAAACACGCG	GAAACCGCGC	TCCGCCGCTT
801	CTTGCCGCAC	CGCCTTCGAT	ACGCCGTGTG	CCGAATAAAC	CAGTGTCGCG
851	CCCGGCGGCA	CTTCCGCCAA	GTCTTCAATA	AACACCGCAC	CTTTTTCACG
901	CAGGTTGTCC	ACGACGAATT	TGTTGTGAAC	GACTTCGTGG	CGCACATAAA
951	TCGGCGCGCC	GAACTCTTCC	AAAGCACGTT	CGACAATACT	GATTGCCCGA
1001	TCCACACCAG	CGCAGAAGCC	GCGCGGATTG	GCAAGGATGA	TGGTTTTCTC
1051	GTTCATAAGC	CCGGTATTTC	GTTTTCAGAC	GGCATCAATA	TTTTTCTTCT
1101	TGGGTTTTAC	GGTGGACGAT	GTTGTCCAAC	ACCGCCAACA	CCGCACCGAC
1151	GCAGATAA				

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>: a694.pep

- 1 LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
  51 HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
  101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNHDVALF CQLFDGGLPV
  151 GRRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
  201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
  251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
  301 QVVHDEFVVN DFVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
  351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*
- Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from N. meningitidis:

m694/a694	100.0% identit	y in 385 a	a overlap			
m694.pep a694	10 LVSASGTRQKCRLK             LVSASGTRQKCRLK  10	[				
m694.pep	70 AYGFVPPSAYGCQYI                   AYGFVPPSAYGCQYI 70		1111111111	1111111111		
m694.pep	130 QAVAVGRIGRTDHNE 		11111111	1111111111	1111111111	111111
m694.pep	190 DRERGLADIGEFVGV 		111111111	11111111111	111111111	141311
m694.pep	250 QSGDFLMHFRHQRAS                   QSGDFLMHFRHQRAS 250	11111111			LITTLE	11111
m694.pep	310 QVVHDEFVVNDFVAH              QVVHDEFVVNDFVAH 310				1111111111	111111
m694.pep a694	370 GINIFLLGFYGGRCC !!!!!!!!!!!!! GINIFLLGFYGGRCC. 370	111111111	1			

WO 99/57280 PCT/US99/09346

1119

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2321>:

```
TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
      TGTTGAACGG AAGGGTGATG CGCGAAGCGG CTTTTGATGC GCCGCCCAGT
 51
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTTAT CATTTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTTA CCCGTTCCGG AGGGCAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAATA
451 CACCCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAAACGGC
601 AGGTTTTCTG CCGCAGCCGC CTTGTTGAAG GGGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695 >:

```
1 LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCQNSQRF QSKPAERYAD
 51 CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSASCASVL PVPEGSRTEM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRTYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLLQ SRARMGNCES VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAAKRAAA
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2323>: m695.seg

```
TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
 51 TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTTAT CATTTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAGGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CCTGTTGAAA GGCGCGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>: m695.рер

```
1 LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAH
 51 RPHHPARRRR LDPASEKIMK IKLPLFIIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
    HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLY NQALKHYKSG
201 KFSAAASLLK GADGGDGGSI AQRSMYLLLQ SRARMGNCES VIEIGGRYAN
    RFKDSPTAPE AMFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAAKRAAA
301 AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from N. gonorrhoeae:

WO 99/57280 PCT/US99/09346

1120

```
m695/g695
          90.8% identity in 305 aa overlap
                         20
          {\tt LPQTRPSRRHHRHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR}
m695.pep
          LPQTRPARRHHRHRQYFVERKGDARSGFXCAAQCQNSQRFQSKPAERYADCPHHPARRRR
q695
                        20
                                        40
                                30
                                                50
                 70
                        80
                                90
                                       100
                                               110
                                                       120
          LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR
m695.pep
          FDPASEKIMKTKLPLFIIWLSVSASCASVLPVPEGSRTEMPTQENASDGIPYPVPTLQDR
q695
                70
                        80
                                90
                                       100
                                               110
                                                       120
                130
                        140
                                150
                                       160
                                               170
          LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDDRKLKEHYLNTEGGSASA
m695.pep
          LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDDRKLKEHYLNTEGGSASA
g695
                130
                        140
                               150
                                       160
                                               170
                190
                        200
                               210
                                       220
                                               230
                                                       240
          HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGSIAQRSMYLLLQSRARMGNCES
m695.pep
          HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGSIAQRSMYLLLQSRARMGNCES
g695
                190
                        200
                               210
                                       220
                                               230
                250
                        260
                               270
                                       280
                                               290
                                                       300
          VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQQKDIARATWRSLIQTYPGSPAAKRAAA
m695.pep
          VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQQKDIARATWRSLIQTYPGSPAAKRAAA
g695
                       260
                               270
                                       280
                                               290
          AVRKRX
m695.pep
          HHHH
q695
          AVRKRX
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2325>: a695.seq

```
TTGCCTCAAG CTTGTCCGGC AAGGCGGCAT CATTGCCATC GACAATATTT
     TGTTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
 51
101
     GTCGGCATCC TCAAAGATTT TAATCAAAAC CTGCCGAACG ATACGCGGAT
     TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCCTG CTTCTGAAAA
     AATAATGAAG ACCAAATTAC CGCTTTTTAT CATTTGGCTG TCCGTATCCG
201
251
     CCGCCTGTTC TTCCCCTGTT TCCCGCAATA TTCAGGATAT GCGGCTCGAA
     CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATTCCCTATC CCGTTCCCAC
301
351
     TCTGCAAGAC CGTTTGGATT ATCTGGAAGG CACACTCGTC CGCCTGTCGA
     ACGAAGTGGA AACCTTAAAC GGCAAAGTCA AAGCACTGGA GCATGCGAAA
401
     ACACACCCTT CCAGCAGGGC ATACGTCCAA AAACTCGACG ACCGCAAGTT
451
     GAAAGAGCAT TACCTCAATA CCGAAGGCGG CAGCGCATCC GCACATACCG
501
551
     TCGAAACCGC ACAAAACCTC TACAATCAGG CACTCAAACA CTATAAAAGC
     GGCAGGTTTT CTGCCGCTGC CTCCCTGTTG AAAGGCGCGG ACGGAGGCGA
601
651
     CGGCGGCAGC ATCGCGCAAC GCAGTATGTA CCTGTTGCTG CAAAGCAGGG
     CGCGTATGGG CAACTGCGAA TCCGTCATCG AAATCGGAGG GCGTTACGCC
701
    AACCGTTTCA AAGACAGCCC AACCGCGCCT GAAGCCATGT TCAAAATCGG
751
    CGAATGCCAA TACAGGCTTC AGCAAAAAGA CATTGCAAGG GCGACTTGGC
801
     GCAGCCTGAT ACAGACCTAT CCCGGCAGCC CGGCGGCAAA ACGCGCCGCC
851
    GCAGCCGTGC GCAAACGATA G
```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>: a695.pep

```
1 LPQACPARRH HCHRQYFVER KGDARSGFRC AAQRRHPQRF *SKPAERYAD
51 CPHHPARRR FDPASEKIMK TKLPLFIIWL SVSAACSSPV SRNIQDMRLE
101 PQAEAGSSDA IPYPVPTLQD RLDYLEGTLV RLSNEVETLN GKVKALEHAK
151 THPSSRAYVQ KLDDRKLKEH YLNTEGGSAS AHTVETAQNL YNQALKHYKS
201 GRFSAAASLL KGADGGDGGS IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251 NRFKDSPTAP EAMFKIGECQ YRLQQKDIAR ATWRSLIQTY PGSPAAKRAA
301 AAVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from N. meningitidis

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from N. meningitidis:

```
m695/a695
          88.3% identity in 308 aa overlap
                                 30
                                        40
                                                50
          LPQTRPSRRHHRHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR
m695.pep
          LPQACPARRHHCHRQYFVERKGDARSGFRCAAQRRHPQRFXSKPAERYADCPHHPARRRR
a695
                10
                         20
                                 30
                                                50
                         80
                                90
                                          100
                                                  110
          LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQT---EMSTRENASDGIPYPVPTL
m695.pep
          FDPASEKIMKTKLPLFIIWLSVSAACSS--PVSRNIQDMRLEPQAEAGSSDAIPYPVPTL
a695
                        80
                                  .90
                                         100
          120
                  130
                          140
                                  150
                                          160
                                                  170
          QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDDRKLKEHYLNTEGGS
m695.pep
          QDRLDYLEGTLVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLDDRKLKEHYLNTEGGS
a695
         120
                 130
                         140
                                 150
                                         160
                                                 170
          180
                  190
                          200
                                  210
                                          220
                                                  230
          ASAHTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGSIAQRSMYLLLQSRARMGN
m695.pep
          ASAHTVETAQNLYNQALKHYKSGRFSAAASLLKGADGGDGGSIAQRSMYLLLQSRARMGN
a695
         180
                 190
                         200
                                 210
                                         220
                                                 230
          240
                  250
                          260
                                  270
                                          280
                                                  290
          CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQQKDIARATWRSLIQTYPGSPAAKR
m695.pep
          CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQQKDIARATWRSLIQTYPGSPAAKR
a695
                 250
                         260
                                 270
                                         280
          300
m695.pep
          AAAAVRKRX
          111111111
a695
          AAAAVRKRX
```

The following partial DNA sequence was identified in N. gonorrhoeae g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>: g696.pep: not found

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2327>: m696.seq

```
1 TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51 ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGACTCAACG GCTTGAACCG CTTCCTTAAC
301 CTCCTGTTTG GCTTCTTGCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>: m696.pep

- 1 LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
- 51 SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
- 101 LLFGFLRTSC QGSRHHCGNQ *

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2329>: a696.seq

PCT/US99/09346 WO 99/57280

1122

```
1 TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
    ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCCTGAGT CGCGTCGGCA
    GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
101
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
    CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGACTCAACG GCTTGAACCG CTTCCTTAAC
301 CTCCTGTTTG GCTTCTTGCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>: a696.pep

- LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN 51
- LLFGFLRTSC OGSRHHCGNO *

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from N meningitidis

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from N. meningitidis:

```
m696/a696
          100.0% identity in 120 aa overlap
                 10
                         20
          {\tt LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC}
m696.pep
          a696
          LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
                 10
                         20
                                 30
                                         40
                 70
                         80
                                 90
                                        100
                                                110
                                                        120
          {\tt ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNGLNRFLNLLFGFLRTSCQGSRHHCGNQ}
m696.pep
          ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNGLNRFLNLLFGFLRTSCQGSRHHCGNQ
a696
                 70
                         80
                                 90
                                        100
m696.pep
          Х
a696
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2331>: g700.seq

```
ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
  1
    ATTTTTTATC CGTGTTCCCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
 51
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCG
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
    TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
    GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
    TGTGTCCGGC AAATTGATGT GCGATATTTG GATGCCGTCT GAAAACGCGG
    GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501
    GCTGTCGGTT TGGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
    CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
551
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
    GGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
    TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGGTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
    TGGTCAATAT CGCCGCCCCG TTTCTGATGG TGGTGTTTTC CACGCTGGGC
851
901
    TGA
```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>; g700.pep

- MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSLS
- 51 RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKGKGVS
- VGVSGSVRQL GCVLLGFVSG KLMCDIWMPS ENAGMYCLML LVFLIGVQLK SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

201	GFGWYSLSGL	VMTEAYGAVW	GSIMLLNDLA	RELFALAFIP	LLMKRFPDAA
251	VGVGGATSMD	FTLPVIQGAG	GLEVVPVAVS	FGVVVNTAAP	FLMVVFSTLG
201	*				T THIV V E ST TIG

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2333>: m700.seq

1		TGATGACGTT		TTGATACCGA	TGTTTGCCGG
51	ATTTTTTATC	CGTGTGCCCA	AGCCTTACCT	GCCCGCTTTG	GATAAGGTGC
101	TATCGGTCTT	GGTGTATGCT	GTGCTGCTGC	TGATCGGCGT	CTCGTTGTCG
151	CGCGTGGAGG	ATTTGGGTTC	GCGGTTGGAC	GATATGGCGT	TGACGGTTCT
201	GTGGCTGTTT	GTTTGTACGG	TCGGGGCGAA		TTGGCAGTGT
251	TGGGAAAGTT	ATTCCCGTGG	CGGATAAAGG	GGAAAGGGAA	
301	GTCGGCGTGT	CGGGCAGTGT	GGGGCAGCTC	GGATGCGTGC	TGCTCGGATT
351	TGCATTCGGC	AAACTGATGC	GCGATATTTG	GATGCCGTCT	GAAAGCGCGG
401	GCATGTATTG	TCTGATGCTG	CTGGTGTTCC	TCATCGGCGT	
451	AGCAGCGGCG	TATCGTTGCG	GCAGGTTTTG	GTCAACCGCA	
501	GTTGTCGGTC	TGGTTTATGC	TTTCATCTCT	TTCGGGCGGG	
551	CCGCATCGAC	AGACGGTGTG	TCGTGGACGA	AAGGTTTGGC	
601	GGCTTCGGTT	GGTATTCCCT	CTCGGGTTTG	GTCATGACCG	
651	CGCGGTATGG	GGCAGCATCA		CGATTTGGCA	
701	TTGCACTGGC	ATTTATCCCG	CTGCTGATGA		
751	GTGGGGGTTG	GCGGTGCGAC		TTTACATTGC	AGATGCGGCG
801	GGGTGCGGGC				
851	TGGTCAATAT			AGCGGTCAGC	
901	TGA		TITCIGATGG	TGGTGTTTTC	CGCTTTGGGT

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>: m700.pep

```
MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSLS
 51 RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLFPW RIKGKGKGVS
101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMPS ESAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASTDGV SWTKGLAMAS
201 GFGWYSLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMD FTLPVIQGAG GLEVVPVAVS FGVVVNIAAP FLMVVFSALG
```

301

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. gonorrhoeae with menB ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng)

from N. gonorrhoeae: m700/g700

m700.pep g700	10 MDSLMTLLSVLIPP  :    :  MSSLMTLFSVLVPP 10		11111 1111		11111111	LILILI
m700.pep g700	70 DMALTVLWLFVCTV            DMALTVLWLFVCTV 70	11111111	111 1111 1	1111111111	fit tilli	1111.
m700.pep g700	130 KLMRDIWMPSESAG	111111111		111111111	1111111111	
m700.pep g700	190 LLFAASTDGVSWTK         LLFAASADGVSWTK	3   1   1   1   1   1   1   1		111111111	1111111111	11111

	190	200	210	220	230	240
5.00	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGV	GGATSMDFTI	PVIQGAGGLE	VVPVAVSFGVV	יי אוד א א דידו כו א א דודו	IDOREO
	250	260	270	280	VNIAAPFLMV\ 290	
			•		230	300
	x					
	l X					
-						
The following	partial DNA se	quence wa	s identified	in <i>N. mening</i>	ritidis <seq< td=""><td>) ID 2335&gt;:</td></seq<>	) ID 2335>:
a700.seq 1						
51	ATGGACAGCC SATTTTTATC O	CGTGTGCCCA	AGCCTTCGGTZ	TTGATACCG	TGTTTGCCG	;G
101	THICGGICIT (	GIGIATECT	- GTGCTGCTGC	. TCDTCCCCC	CTCCTTCTT	
151	COCOLOGAGO A	71 1 1 G G G L L C	GCGGTTGGAC	GATATGGCCGT	TO A CCCOMM	m
201 251	GIGGCIGIII (	STITIGTACGG	TCGGGGCGAA	CCTCCTTCCT	mmcconomo	_
301	IGGGAAAGII A	TTCCCGTGG	CGGATAAAGG	GGAAAGGGAA	CCCCCMmma	•
351	GTCGGTGTGT C	APCTCATCC	GGGGCAGCTC	GGATGCGTGC	TGCTCGGAT	T
401	TGCATCCGGC A GTATGTATTG T	CTGATGCTG	CTGGTGCTCN	TCATCCCCTCT	GAAAACGCG	G
451	AGCAGCGGCG I	AICGITGCG	GCAGGTTTTC	GTCD DCCCCD	CCCCMAmmo	•
501	GIIGICGGIC 1	GGTTTATGC	TTTCATCTCT	TTCAGGCGGC	CTCCTCTTTTT	^
551	CCGCATCGGC A	CHCGGIGIG	TCGTGGGTGA	$\Delta \Delta CCTTTTCCC$	CAMCCCMMO	^
601 651	GGCIICGGIT G	GTATTCCCT	CTCGGGTTTG	GTGATGACCC	ACCOMMA CO.	<b>~</b> .
701	CGCGGIAIGG G	GCAGTATCG	CGCTTTTGAA	CGATTTGGCA	CCACACCMC	m.
751	TCGCGCTGGC A	CGGCGCGAC	CIGCIGATGA	AGCGTTTTCC	CGATGCGGC	P
801	GTGGGGGTCG G GGGTGCGGGC G	GCTTGGAAG	CAGTATGGAT	TTCACATTGC	CCGTGATTC	3
851	TGGTCAATAT C	GCCGCTCCG	TTTCTGATGG	TGGTGTTTTT	TTCGGCGTG	3
901	TGA			1001011110	CGCTTTGGGC	<i>:</i>
This correspond	s to the omina	ooid as an a	<000 0	2000		
This correspond	s to the anning	acid sequei	ice <seq ii<="" td=""><td>) 2336; ORF</td><td>7 700.a&gt;:</td><td></td></seq>	) 2336; ORF	7 700.a>:	
a700.pep 1	MDSLMTLLSV L	T PM FACEET	DUDYDYT DA T	B		
51	MDSLMTLLSV L	ALTVIWLE	VCTVCANITA	DKVLSVLVYA	VLLLIGVSLS	1
101	VGVSGSVGQL G	CVLLGFASG	KLMRDTWMPS	ENACMYCIMI	RIKGKGKGVS	
151	22GA2TKÕAT AI	AKKGIKTZA	WEMLSSISGG	LLEDAGADOU	CLIVILOT BACK	
201	GEGMISTORT AL	TTEAYGAVW	GSIALLNDI.A	RELEATARTD	LIMEDEDDAA	
251 301	VGVGGATSMD FT	LPVIRGAG	GLEAVPVAVS	FGVVVNIAAP	FLMVVFSALG	' I
201	Î					
m700/a700	97.0% ider	tity in 3	00 aa overl	an		
				~P		
m700.pep	10		30	40	50	60
m/ou.pep	MOSTWIFTS	LIPMFAGFF:	IRVPKPYLPAL	DKVLSVLVYAV	LLLIGVSLSR	
a700	1 1 1 1 1 1 1 1 1	11111111		1 1 1 1 1 1 1 1 1 1 1 1		
	10	20	) 30	DKVLSVLVYAV 40		
				40	50	60
700	70		90	100	110	120
m700.pep	DMALTVLWLF	VCTVGANLLA	LAVLGKLFPW	RIKGKGKGVSV	CUCCCUICAT A	
a700			1111111		1111111111	
4700	70	ACIAGMUPPE	THATIGKTEPW	RIKGKGKGVSV	GVSGSVGQLG(	CVLLGFASG
	70	80	90	100	110	120
	130	140	150	160	170	
m700.pep	KLMRDIWMPS	ESAGMYCLMI	LVFLTGVOLK	SSCUET BOTTE	170 JRRGTRI.SVWR	180
2700						
a700		21110111 0111	TATVIGAČTV:	SSGVSLRQVLVN	RRGIRLSVWE	MLSSLSGG
	130	140	150	160	170	180

m700.pep a700	190 LLFAASTDGVSWTK       :  LLFAASADGVSWVK 190			111111111	111111111	
m700.pep a700	250 LLMKRFPDAAVGVG             LLMKRFPDAAVGVG 250	111111111	11:411111:		1111111111	111111
m700.pep	x I X					,

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2337>: g701.seq

- ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACCG CTTCGATGGC ACAATCTACG CCGTCTTCGC CGACGATGGC GAAAACTTGT TTGGAGACGT CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCAACTC TTTCGCCGGT 151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA 201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA 251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG 301 TGGGCGGTCG GTAAAGCGTC GCTCAACAGC AGGGCGATTT CTTCGTTGAC 351 GTTGTCGTGC GGCGGCACGA GGCTGTTGTC GGCATAA
- This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>: g701.pep
  - 1 MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VWVAPNSFAG 51 FKRFSSISHT IMAAGLYSWA VNKADIBTOR 2007
  - FKRFSSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
  - 101 WAVGKASLNS RAISSLTLSC GGTRLLSA*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2339>: m701.seq

- 1 ATGTCTTGGC ACATATTCCA TGTAGCAGGG ATACCGACGG CTTCGATGGC 51 GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT 101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCCAATTC TTTCGCCAGT 151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA 201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG TGGGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGATTT CTTCGTTGAC 351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA
- This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>: m701.pep
  - 1 MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VWVAPNSFAS 51 FKRFSSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
  - 101 WAVGKASLNN RAISSLTLSG SGTRLLSA*

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. gonorrhoeae with menB

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*: m701/g701

204	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTA:	SMAQSTPSSP	TMAKTCLDTS	PEAGLMVWVA	PNSFASFKRFS	SSISOT
7.0.1	11111:11111	1111111	1111111:11		11111:1111	
g701	MSWHIFQVAGIPTAS	SMAQSTPSSP	TMAKTCLETS.	PEAGLMVWVA	PNSFAGFKRF9	SSISHT

				1120			
		10	20	30	40	50	60
		70	80	90	100	110	120
m701.pep	MMA	AGLYSWAVNRAD	IPTGPAPAN	INTVSPGLTSP	YCTPISWAVO	GKASLNNRATS	SLTLSG
g701	IMA		IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	 YCTPISWAVO	:      KASLNSRATS	  SLTLSC
-		70	80	90	100	110	120
		129					
m701.pep		RLLSAX					
g701		 RLLSAX					
_							
The follow	ving part	ial DNA seqı	uence was	identified i	n N. menin	gitidis <se< td=""><td>Q ID 2341&gt;:</td></se<>	Q ID 2341>:
a701	.seq						•
	1 A'	rgtcttggc ac Cagtccacg cc	GTCTTCCA	AGTTGCAGGG	ATACCGACG	G CTTCGATC	GC
	101 C	GCCGGAAGC AG	GGTTAATG	GTATGGGTTG	CGCCCAACT	C TTTCGCCA	GT.
	151 T	CAAACGGT TT	TCGTCCAT	<b>ATCGCAAACA</b>	ATGATGGCG	G CGGGGCTG	TA
	201 CA 251 TO	AGTTGGGCG GT	CGGCAAGG	CGGACATACC	GACAGGAGC	G GCACCTGC	GA
	301 TO	GAATACGGT GT GTGCGGTCG GC	AAAGCGTC	GCTCAACAAC	AGGGCGACT	AC GCCGATTT	CG
	351 G1	TTGTCGGGC AG	CGGCACGA	GGCTGTTGTC	GGCATAA	r crrcgrig	AC
This corre	enande te	the amino a	cid segue	nce <\$EO I	D 2242. OI	DE 701 ->	
	.pep	o the annio a	cia scquei	ince -SEQ I	D 2342, OI	Kr /01.a>:	
4,01	1 MS	WHIFQVAG IP	TASIAQST	PSSPTIAATC	LLTSPEAGL	M VWVAPNSF	AS
	51 FF	KRFSSISQT MM	AAGLYSWA	VGKADIPTGA	APAMNTVSP	G LTSPYCTP	ĪS
	101 CF	VGKASLNN RA	TSSLTLSG	SGTRLLSA*			
m701	/a701	92.2% iden	tity in 1	28 aa over	lap		
		10	2			0 5	0 60
m701	.pep	MSWHIFHVAG:	IPTASMAQS	TPSSPTMAKTO	CLDTSPEAGL	MVWVAPNSFA.	SEKRESSISOT
a701		MSWHTFOVAG	TPTASTAOS	:     TPSSPTTAAT/		MUMUA DNOED	
4,01		10	2	0 30			
		70	•	0 0.		_	
m701	.pep	70 MMAAGLYSWA	8 PTETGARINA			0 110	120
	· F - F		1::11111			1 11111111	111 111111
a701		MMAAGLYSWA	VGKADI PTG	AAPAMNTVSPO	GLTSPYCTPI:	SCAVGKASLNI	NRATSSLTLSG
		70	8	0 90	) 10	0 110	120
		129					
m701	.pep	SGTRLLSAX					
a701		 SGTRLLSAX					
Th. C. 11		-1 DNIA				_	
g702.seq	ing paru	al DNA sequ	ence was	identified in	ı N. gonorr	hoeae <se0< td=""><td>Q ID 2343&gt;:</td></se0<>	Q ID 2343>:
	ATGCCGT	GTt ccaAAGCC	AG TTGGAC	TTCG CCCGG	AGtaa caac	CCCCCC	
51	AATCAGG	GGA ATGCCGCT	GT TGCGGC	CCGCC TCTGG	CGAGG GATT	CGTGCA	
101	AACCCGG	GCT GATGGCGA	AA ACCGCG	SCCTG CGTCT	TCGAC GGCT	TTGAGC	
151	TGTTCGG	GAT TGGTTACC	GT ACCTGO	GCCG ATGAT	GGCGT TGGG	CATTTC	

```
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTCGAGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cGCCATCACA GGCACAACTG CGCCGGCGGT
351 CAGGATTTCG cggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>: g702.pep

PCT/US99/09346 WO 99/57280

1127

```
1 MPCSKASWTS PGVATPGIRG MPLLRPALAR DSCKPGLMAK TAPASSTALS
      51 CSGLVTVPAP MMALGISLAI RRMASSPTGV RKVISRVGMP PSTRARDKST
     101 AVLKSSIAIT GTTAPAVRIS RGVS*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2345>:
          ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
         AATCAGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
      51
         GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
     101
         TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
         TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
         TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
     301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACTG CGCCGGCGGT
     351 CAAAATTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAT
     401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG
This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:
m702.pep
         MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
      1
         CSGLVTVPAP TMALGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
      51
         AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*
ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng)
from N. gonorrhoeae:
m702/g702
                              20
                                       30
                                                 40
            MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVPAP
m702.pep
            MPCSKASWTSPGVATPGIRGMPLLRPALARDSCKPGLMAKTAPASSTALSCSGLVTVPAP
                    10
                                       30
                                                 40
                                                           50
                    70
                              80
                                       90
                                                100
            TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
m702.pep
             MMALGISLAIRRMASSPTGVRKVISRVGMPPSTRARDKSTAVLKSSIAITGTTAPAVRIS
                    70
                              80
                                       90
                                                100
                                                          110
                                                                   120
                   130
                             140
m702.pep
            RGVSLDISVLRVEWGILLRWDRLX
            1111
            RGVSX
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2347>:
     a702.seq
           1
              ATGCCGTGTT CCAAAGCCAG TTGGATTTCG CCCGGGGTGG CAACACCGGG
              AATCAGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
          51
              GCCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
         101
              TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
              TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
              TTTCGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
              GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAACTG CGCCGGCGGT
              CAAAATTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTCTC CGGGTGGAAT
              GGGGTATTTT ATTAAGATGG GACAGGTTGT AG
This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:
    a702.pep
              MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
          51
             CSGLVTVPAP TMALGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
             AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*
    m702/a702
                 100.0% identity in 143 aa overlap
```

10

20

30

40

50

60

q702

q702

q702

```
{\tt MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVPAP}
m702.pep
          MPCSKASWISPGVATPGIRGMPLLWPALARDSCSPGLMAKTAPASSTALSCSGLVTVPAP
a702
                         20
                                         40
                                                          60
                 70
                         80
                                 90
                                         100
                                                 110
                                                         120
          TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
m702.pep
          TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
a702
                         80
                                 90
                                        100
                                                 110
                130
                        140
          RGVSLDISVLRVEWGILLRWDRLX
m702.pep
          11111111111111111111111111111
a702
          RGVSLDISVLRVEWGILLRWDRLX
                130
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2349>: q703.seq

```
ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
 51 CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
   CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
    GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
    CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTTATAAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTTGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTTGACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTctgTGc gcTGTTgggt aaggCAAACA
851 TCAAACCTGC AAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>: g703.pep

```
MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
    EDTPOLROSL LENEVVNTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
 51
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
    DGYVPLKDLE QGVPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDSREV
251 KVPSFDEMKG QIAGNLQAER IDRAVCALLG KANIKPAK*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2351>: m703.seg

```
ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
    CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
    CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
    TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTTGGAA CAGGGTGTTC CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
```

701	AAAACGGCGA	TTTCTACGGC	GTTTATTATG	TCAACGACAG	CCGCGAGGTA
751	AAAGTGCCTT	CTTTTGATGA	AATGAAAGGA	CAGATTGCGG	GCAACCTTCA
801	GGCGGAACGG	ATTGACCGTG	CCGTCGGTGC	ACTGTTGGGC	AAGGCAAACA
	TCAAACCTGC				- I I I I I I I I I I I I I I I I I I I

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>: m703.pep

- 1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
- 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP 201 VGYVPLKDLE QGVPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNDSREV
- 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from N. gonorrhoeae: m703/g703

m703.pep	10 MKAKILTSVALLA            MKAKILTSVALLA 10	[	-		1111111111	111111
m703.pep	70	80	90	100	110	120
m/03.pep	LENEVVNTVVAQEV	VKTVTDK2VF	FKNALAKLRA	EAKKSGDDKI	<pre><psfktvwqa< pre=""></psfktvwqa<></pre>	VKYGLNG
g703		וווווווווווו	11:11:11			
9,05	LENEVVNTVVAQEV	80	FRUALAKURA			VKYGLNG
	70	80	90	100	110	120
	130	140	150	160	170	100
m703.pep	EAYALHIAKTQPVS	EOEVKAAYDN		VOLCETI TOE		180
• •	ППППППППППППППППППППППППППППППППППППППП	111111:11	111111111	TITITE TO L	HANNANA	DLKAKKG
q703	EAYALHIAKTOPVS	EOEVKAVYDN	TSGEYKGTOE	VOLCETI TO	ון ון ון ון ו	
,	130	140	150	160	LENAKKAVA 170	
			150	100	170	180
	190	200	210	220	230	240
m703.pep	FDAVLKQYSLNDRT	KQTGAPVGYV	PLKDLEQGVP	PLYQAIKDLK	KGEFTATPL	KNGDFYG
	_ 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1:		111111111	111111111	111111
g703	FDAVLKQYSLNDRT	KRTGAPDGYV	PLKDLEQGVP	PLYQAIKDLK	KGEFTATPL	KNGDFYG
	190	200	210	220	230	240
	250	260	270	280	289	
m703.pep	VYYVNDSREVKVPS	FDEMKGQIAG	NLQAERIDRA	VGALLGKANI	KPAKX	
			11111111	1 111111	11111	
g703	VYYVNDSREVKVPS	FDEMKGQIAG	NLQAERIDRA	VCALLGKANI	KPAKX	
	250	260	270	280		

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2353>:

```
a703.seq
        ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
      1
     51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
        CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
        GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
         CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
         AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
         GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
    301
         CTTGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
    351
    401
        CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTTACAAA
    451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
    501 TGCAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
    551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
    601 GTCGGATATG TGCCGCTGAA AGATTTGGAA CAGGGTGTTC CGCCGCTTTA
    651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
```

701 751 801 851	AAAGTGCCTT	TTTCTACGGC CTTTTGATGA ATTGACCGTG AAAATAA	AATGAAAGGA	CAGATTGCCC	CCAACCMMAA	
This correspond	s to the amin	o acid seque	nce <seq i<="" td=""><td>O 2354; ORI</td><td>F 703.a&gt;:</td><td></td></seq>	O 2354; ORI	F 703.a>:	
1 51 101 151 201 251	DDKKPSFKTV GTQEVQLGEI VGYVPLKDLE	LLACSGSLFA LENEVVNTVV WQAVKYGLNG LTDKEENAKK QGVPPLYQAI QIAGNLQAER	AQEVKRLKLD EAYALHIAKT AVADLKAKKG KDLKKGEFTA	RSAEFKNALA QPVSEQEVKA FDAVLKQYSL TPLKNGDEYG	KLRAEAKKSG AYDNISGFYK	
m703/a703	100.0% i	dentity in	288 aa over	lap		
m703.pep	111111111	VALLACSGSLF		IDSSVIDAQVA		
a703	MKAKILTS	10 2	AQTLATVNGQK 0 30	IDSSVIDAQVA	AFRAENSRAED 50	TPQLRQSL 60
m703.pep	LENEVVNT	VVAQEVKRLKL	0 90 DRSAEFKNALA	KIRAFAKKSCD	110 DKKPSFKTVWC	120 AVKYGLNG
a703	LENEVVNT		 DRSAEFKNALA	 KLRAEAKKSGD	11111111111	1111111
m703.pep	EAYALHIA	30 14 KTQPVSEQEVK	AAYDNISGFYK	160 GTQEVQLGEIL	170 FDKEENAKKAV	180 ADLKAKKG
a703	ENIALITA	KTQPVSEQEVK 30 14	AAYDNISGFYK	GTQEVQLGEIL	PDKEENAKKAV 170	ADLKAKKG 180
m703.pep	FDAVLKQY:	90 200 SLNDRTKQTGAI	PVGYVPLKDLE(			240 LKNGDFYG
a703	FDAVLKQI	SLNDRTKQTGAI 90 200	PAGAABTKDTE	QGVPPLYQAIKI 220	LKKGEFTATP	LKNGDFYG 240
m703.pep	VYYVNDSRI	50 260 EVKVPSFDEMKO	GOIAGNLOAERI	280 DRAVGALLGKA	289 NIKPAKX	
a703	VYYVNDSRI 25	SVKVPSFDEMKO	GQIAGNLQAER1	DRAVGALLGKA 280	NIKPAKX	

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2355>: a704.seq

J4.Seq					
1	ATGAAAAAA	CCTGTTTCCA	CTGCGGGCTG	GACGTTCCCG	AAAACCTGCA
51	TCTGACCGTC	CGTTACGAAA	ACGAAGACCG	CGAAACCTGC	TGCGCCGGTT
101	GTCAGGCAGT	CGCACAAAGC	ATTATTGACG	CGGGCTTGGG	CAGTTATTAC
151	AAACAACGCA	CCGCCGACGC	GCAAAAAACC	GAGCTGCCGC	CCCAAGAAAT
201	CCTCGACCAA	ATCCGCCTGT	ACGACCTGCC	CGAAGTCCAG	TCCGACTTTC
251	TGGAAACCCA	CGGCGGCACG	CGCGAGGCGG	TTTTAATGCT	CGGCGGCATC
301	ACCTGCGCCG	CCTGCGTCTG	GCTGATCGAA	CAGCAGCTTT	TGCGTACAGA
351	CGGCATCGTC	CGCATCGACC	TCAATTACAG	CACGCACCGC	TGCCGCGTCG
401	TCTGGGACGA	CGGCAAAATC	CGCCTTTCCG	ACATTCTGTT	GAAAATCAGG
451	CAGATAGGCT	ACACCGCCGC	ACCCTATGAC	GCGCAAAAA	TCGAAGCCGC
501	CAACCAAAAA	GAACGCAAAC	AATACATCGT	CCGCCTCGCC	GTTGCCGGGC
551	TGGGGATGAT	GCAGACGATG	ATGTTCGCGC	TGCCGACCTA	CCTTTACGGC
601	GGCGACATCG	AACCCGATTT	CCTGCAAATC		GCGGCTTTTT
651	AATGGTGCTG		TCTATTGCGC		TATCAAGGCG
701	CGCTGCGCGA	CTTGAAAAAC		GCATGGATAC	
751	GTCGCCATCA	TCATGACCTT	TATCGCCGGC		
					COCHOMM

			•		
801	TGCGGGGCAG			CGCGATGCTG	CTGTTTTTCC
851	TGCTGGGCGG		GAACACATTG	CCCGCCGTAA	
901	GCCGCCGAGA		GCTGATTCCT	GCGTTTTGCC	ATCATATGCC
951	CGATTACCCC			GGCAGCTGTC	GTCAAATTGA
1001	AGGCGGGCGA			GCGAAACCAT	
1051	GGCACGGTGC	TGGAAGGAAG		AACGAATCTA	TGCTGACCGG
1101	CGAGAGCCTG	CCCGTCGCCA			ACCGCCGGCA
1151	CACTCAACAC	GCAAAGCCCC			CACCGGCGGC
1201	GGCACGCGAC	TGTCGCACAT			CCTTAGCGCA
1251	AAAACCGCGC	ACTGCCGAGT	TGGCGGAACA		TCTTTCATAT
1301	TCGGCGAACT	CCTGCTTGCC		TCATCGGCTG	GACGCTGTAC
1351	GCCGACGCGC	ACACCGCATT		GTCGCCCTGC	TGGTCATTAC
1401	CTGCCCCTGC	GCCTTATCGC	TTGCCACGCC	GACCGCGCTG	GCAGCTTCTA
1451	CCGGTACGCT	GGCGCGCGAA	GGTATTTTAA	TCGGCGGAAA	GCAGGCAATC
1501	GAAACCCTCG	CCCAAACCAC	CGACATCATC	TTCGACAAAA	CCGGCACGCT
1551	GACCCAAGGC	AAACCCGCCG	TCCGCCGTAT	CTCATTGTTG	AGAGGCACAG
1601	ACGAAGCCTT	TGTTCTCGCG	GTGGCGCAGG	CTTTAGAACA	ACAGTCCGAA
1651	CATCCCCTTG	CCCGCGCCAT	CCTCAACTGC		ACGGCAGCGT
1701	CCCCGACATC	GCTATTAAAC	AACGCCTCAA	CCGCATCGGC	GAAGGCGTGG
1751	GCGCGCAACT	GACCGTCAAC	GGCGAAACAC	AGGTTTGGGC	ATTGGGCAGG
1801	GCATCCTATG	TCGCCGAAAT	TTCAGGTAAA	GAACCGCAAA	
1851	CGGCAGCGCG	GTTTACCTCG	GCAGTCAAAG	CGGTTTCCAA	
1901	ACCTGCAAGA	CCCGCTCAAA	GACAGCGCGG	CGGAGGCGGT	
1951	GCAGGCAAAA		GCACATTCTC	AGCGGCGACC	GTGAAACCGC
2001	CGTTGCCGAA	<del>-</del>	CCCTGGGTGT	CGCGCACTAC	CGCGCCCAAG
2051	CCATGCCCGA	GGACAAACTG	GAATACGTCA	AAGCCTTGCA	AAAAGAAGGG
2101	AAAAAAGTGC	TGATGATAGG	CGACGGCATC	AACGACGCGC	CCGTTTTGGC
2151	GCAGGCAGAC	GTATCCGCCG	CCGCAGCGGG	CGGGACGGAT	ATTGCGAGGG
2201	ACGGCGCGGA	CATTGTGTTA	TTGAACGAAG	ATTTGCGTAC	CGTCGCCCAC
2251	CTGCTCGATC	AGGCGCGGCG	CACCCGCCAT	ATTATCCGGC	AAAACCTGAT
2301	ATGGGCGGGC	GCGTACAATA	TCATTGCCGT		GTTTTGGGCT
2351	ATGTCCAACC	GTGGATAGCC	GCACTGGGTA		TTCGCTGGCG
2401	GTTTTGGGCA	ACGCCCTGCG	CCTTCACAAA	CGGGGGAAAA	
2451	AAAAATGCCG	TCCGAACAAT	GA		3

# This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

a704.pep			_	ŕ	
1	MKKTCFHCGL	DVPENLHLTV	RYENEDRETC	CAGCQAVAQS	IIDAGLGSYY
51	KQRTADAQKT	ELPPQEILDQ	IRLYDLPEVQ	SDFVETHGGT	REAVIMLEGT
101	TCAACVWLIE	QQLLRTDGIV	RIDLNYSTHR	CRVVWDDGKI	RLSDTLLKTR
151	QIGYTAAPYD	AQKIEAANQK	ERKQYIVRLA	VAGLGMMOTM	MEALPTYLYC
201	GDIEPDFLQI	LHWGGFLMVL	PVVFYCAVPF	YOGALRDLKN	RRVGMDTPTT
251	VAIIMTFIAG	VYSLATNAGQ	GMYFESIAML	LFFLLGGRFM	EHTARRKAGD
301	AAERLVKLIP	AFCHHMPDYP	DTQETCEAAV	VKLKAGDIVL	VKPGETTPVD
351	GTVLEGSSAV	NESMLTGESL	PVAKMPSEKV	TAGTLNTOSP	LITETORTGG
401	GTRLSHIVRL	LDRALAQKPR	TAELAEQYAS	SFIFGELLLA	VPVFTGWTT.Y
451	ADAHTALWIT	VALLVITCPC	ALSLATPTAL	AASTGTLARE	GTLIGGKOAT
501	ETLAQTTDII	FDKTGTLTQG	KPAVRRISLL	RGTDEAFVI.A	VACALECCE
551	HPLARAILNC	RISDGSVPDI	AIKQRLNRIG	EGVGAOLTVN	GETOVWALGE
601	ASYVAEISGK	EPQTEGGGSA	VYLGSOSGFO	AVFYLODPLK	DSAAEAVROL
651	AGKNLTLHIL	SGDRETAVAE	TARALGVAHY	RAOAMPEDKL	EYVKALOKEG
701	KKVLMIGDGI	NDAPVLAQAD	VSAAAAGGTD	IARDGADIVI.	LNEDLRTVAH
751	LLDQARRTRH	IIRQNLIWAG	AYNIIAVPLA	VLGYVQPWIA	ALGMSESSLA
801	VLGNALRLHK	RGKMQSEKMP	SEQ*		

# m704/a704 99.8% identity in 823 aa overlap

704	. 10	20	30	40	50	60
m704.pep	MKKTCFHCGLDVPE	HLHLTVRYEN	EDRETCCAGO	QAVAQSIIDA	GLGSYYKORT	'ADAOKT
- 70 4	11111111111111	:	1111111111	1111111111	1111111111	111111
a704	MKKTCFHCGLDVPE	NTHTLAKAEM	EDRETCCAGO	QAVAQSIIDA	GLGSYYKORT	'ADAOKT
	10	20	30	40	50	60
	70	80	90	100	110	120
m704.pep	ELPPQEILDQIRLY	DLPEVQSDFV	ETHGGTREAV	LMLGGITCAA	CVWLIEGOLL	RTDGTV
a704		111111111	111111111	BILLIAND	111111111	111(11

PCT/US99/09346

		70	80	90	100	110	120
m704.pep a704				150 LLKIRQIGYTA            LKIRQIGYTA   150		1111111111	1111
m704.pep			1111111111	210 DFLQILHWGGF          DFLQILHWGGF 210	1111111111	1111111111	1111
m704.pep a704	111111	11111111	1111111111	270 NAGQGMYFES           NAGQGMYFES 270	1111111111	1111111111	THIL
m704.pep	111111	111111111	11111111111	330 EAAVVKLKAG          EAAVVKLKAG 330	1111111111	11111111111	1111
m704.pep	111111		1111111111	390 TQSPLIIRTDI          TQSPLIIRTDI 390			HH
m704.pep	111111	111111111	1111111111	450 WTLYADAHTAI           WTLYADAHTAI 450		!	ELLI
m704.pep	AASTGTL	1111111		510 TDIIFDKTGTI           TDIIFDKTGTI   510	11111111111		1111
m704.pep	VAQALEQ         VAQALEQ	 QSEHPLARA:	[[[]]]	570 VPDIAIKQRLN           VPDIAIKQRLN 570	1111111111		111
m704.pep	ASYVAEI:        ASYVAEI:	1		630 SGFQAVFYLTE                                     	1111111111	11111111111	111
m704.pep	SGDRETA'			690 EDKLEYVKALÇ EDKLEYVKALÇ 690	KEGKKVLMIG	 DGINDAPVLA	111
m704.pep	VSAAAAGO			750 FVAHLLDQARR            FVAHLLDQARR 750	TRHIIRQNLI           TRHIIRQNLI	WAGAYNIIAV            WAGAYNIIAV	1.1.1
m704.pep	VLGYVQPV          VLGYVQPV		HIIIIIIII	RLHKRGKMQSE           RLHKRGKMQSE	HIHIT		

m705.pep

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2357>:
g705.seq
           GTGTTCAATA ATTTCCttgC CTCTCTGCCG TTTATGACGG AAACACGCGC
           TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTTAAAGCC GGCTTTACAG
       51
      101 TGTCTTtgcC TTTGGCGATC GCTTCTTTCG TTATCGGCAT GATTATTGCC
      151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTTCCAAAA
      201 ATGCTTGTTG AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
      251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC GTCCGTCGGC
     301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
      351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCGATTTTG TCCGTGCCGA
      401 AAGGGCAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
     451 TTCCGCCGCA TCGTCGCACC GCAGGCATTC CGCGTCGCCG TTCCGCCGTT
     501 GAGCAACGAG TTTATCGGCT TGTTCAAAAA CACCTCGCTT GCCGCCGTGG
     551 TAACGGTAAC GGAGCTTTTC CGTGTCGCAC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGGTTT ATTGGTGTTT
     651 CTGTAAAGTG CTGTTTTTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
     701 GTTATGTCGC CAAATAA
This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:
g705.pep
          VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
          VAVALVRIMP SGGIFQKCLL KLVEFYISVV RGTPLLVQLV IVFYGLPSVG
      51
     101 IYINPIPAAI IGFSLNVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMOT
     151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVY<u>IEA ALVYWCFCKV LFLIQ</u>ARLEK RFDRYVAK*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2359>:
m705.seq
       1
          GTGTTCAATA ATTTCCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
      51 CGATATGATT GTCAGCGCGT TTTTGCCTAT GGTCAAAGCC GGCTTCGCGG
     101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
     151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTGCGGAA
     201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
     251 CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
     351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
     401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
     451 TTCCGCCGCA TTGTCGCGCC GCAGGCATTC CGCGTTGCCG TGCCGCCTTT
     501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
     551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
     601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTT
651 TTGTAAAGTG CTGTTCCTGA TTCAGGCGCG TTTGGAAAAA CGTTTCGACC
          TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTT
     701 GCTACGTCGC CAAATAA
This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:
m705.pep
          VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
          VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVQLV IVFYGLPSVG
          IYIDPIPAAI IGFSLNVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
     151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
     201 YDFLPVYIEA ALVYWCFCKV LFLIQARLEK RFDRYVAK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from
N. gonorrhoeae:
m705/g705
             95.0% identity in 238 aa overlap
                                20
                                          30
                                                     40
             VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
m705.pep
             VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVAVALVRIMP
a705
                     10
                                20
                                80
```

90

AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY

100

110

g705	SGGIFQKCLLKLVE	FYISVVRGTP	LLVQLVIVFY	GLPSVGIYI1	NPIPAAIIGF	SLNVGAY
_	70	80	90	100	110	120
	130	140	150	160	170	180
m705.pep	ASETIRAAILSVPK	GQWEAGFSIG	MTYMQTFRRI	VAPQAFRVAV	PPLSNEFIG	LFKNTSL
		1111111111				
g705	ASETIRAAILSVPK	GQWEAGFSIG	MTYMQTFRRI	VAPQAFRVAV	PPLSNEFIG:	LFKNTSL
	130	140	150	160	170	180
	190	200	210	220	230	239
m705.pep	AAVVTVTELFRVAQ	ETANRTYDFL	PVYIEAALVY	WCFCKVLFLI	QARLEKRFD	RYVAKX
			1111111111	111111111	113111111	11111
g705	AAVVTVTELFRVAQ	ETANRTYDFL	PVYIEAALVY	WCFCKVLFLI	QARLEKRFDI	RYVAKX
	190	200	210	220	230	

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2361>: a705.seq

1	GTGTTCAATA	ATTTCCTTGC	TTCGCTGCCG	TTTATGACGG	AAACACGCGC
51	CGATATGATT	GTCAGCGCGT	TTTTGCCTAT	GGTCAAAGCC	GGCTTCGCGG
101	TCTCTCTGCC	TTTGGCGGCA	GCTTCTTTCG	TTATCGGTAT	GATGATTGCG
151	GTAGCCGTGG	CTTTGGTGCG	GATTATGCCC	GCCGGCGGCA	TCGTGCGGAA
201	AATCCTGCTG	AAATTGGTGG	AATTTTATAT	TTCCGTCATT	CGCGGTACGC
251	CGCTGTTGGT	TCAGCTTGTG	ATTGTGTTTT	ACGGGCTGCC	TTCCGTCGGC
301	ATCTATATCG	ACCCGATTCC	TGCCGCCATC	ATCGGCTTTT	CGCTCAATGT
351	CGGCGCATAT	GCTTCCGAAA	CCATACGCGC	GGCAATTTTG	TCCGTACCGA
401	AAGGCCAATG	GGAAGCAGGT	TTCTCCATCG	GCATGACCTA	TATGCAGACG
451	TTCCGCCGCA	TCGTCGCGCC	GCAGGCATTT	CGCGTTGCCG	TGCCGCCTTT
501	GAGCAACGAG	TTTATCGGTT	TGTTTAAAAA	CACCTCGCTC	GCGGCAGTCG
551	TGACGGTAAC	GGAATTATTC	CGCGTCGCGC	AGGAAACGGC	AAACCGCACT
601	TATGACTTTT	TGCCCGTCTA	TATCGAAGCC	GCTTTGGTTT	ACTGGTGTTT
651	TTGTAAAGTG	CTGTTCCTGA	TTCAGGCGCG	TTTGGAAAAA	CGTTTCGACC
701	GCTACGTCGC	САВАТАВ			

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>: a705.pep

- 1 VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
  51 VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVQLV IVFYGLPSVG
  101 IYIDPIPAAI IGFSLNVGAY ASETIRAAIL SVPKGQWEAG FSIGMTYMQT
  151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT

- 201 YDFLPVYIEA ALVYWCFCKV LFLIQARLEK RFDRYVAK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N meningitidis

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from N. meningitidis:

a705/m705	100.0% identity in 238 aa overlap	
		0
a705.pep	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIM	
m705	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIM	P
	10 20 30 40 50 6	0
	70	
	70 80 90 100 110 12	0
a705.pep	AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGA	Y
		1
m705	AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGA	Y
	70 80 90 100 110 12	0
	130 140 150 160 170 18	0
a705.pep	ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTS	L
		ł
m705	ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTS	Ĺ
	130 140 150 160 170 18	
	190 200 210 220 230 239	
a705.pep	AAVVTVTELFRVAQETANRTYDFLPVYIEAALVYWCFCKVLFLIQARLEKRFDRYVAKX	
m705	AAVVTVTELFRVAQETANRTYDFLPVYIEAALVYWCFCKVLFLIQARLEKRFDRYVAKX	
	190 200 210 220 230	

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2363>:
 g706.seq
           ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
           CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCggaa
       51
           ccgtCCTGTT CGCCACCGCA CTCGCCCGgc tACTCCACCT CCAacacggc
           GAATGGATAG GGALGACCGT CTTCGTCGTC CTCGGCATGC TCCAGTTCCA
      201 AGGCgcgatt tActccaacg cggtgGAacg taTGctcggt acggtcatcg
      251 ggctgGGCGC GGGTTTGGgc gTTTTATGGC TGAACCAGCA TTAtttccac
      301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGCG GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA
      401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
      451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC
      501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
      551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
      601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
      651 AATCAACGCA CGCATGGTCA AAAGCCGCAG CCACCTCGCC GCCACATCGG
      701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
      801 GCAATCTCCC AAACTCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
           TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC
      851
      901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
      951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
           GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
     1051 ACCCGCCGCA AATGGCTGGA TGCCCACGAA CGCCAACACC TGCGCCAAAG
     1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA
This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:
 g706.pep
          MNSSQRKRLS GRWLNSYERY RHRRLIHAVR LGGTVLFATA LARLLHLQHG
          EWIGMTVFVV LGMLQFQGAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH
       51
          GNLLFYLTIG TASALAGWAA VGKNGYVPML AGLTMCMLIG DNGSEWLDSG
      101
          LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
          RRMTRERLEQ NMVKMRQINA RMVKSRSHLA ATSGESRISP SMMEAMOHAH
      201
          RKIVNTTELL LTTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTAALING
     301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
         TRRKWLDAHE RQHLRQSLLE TREHG*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2365>:
          ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
          CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
      51
          CCGTCCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
     101
          GAGTGGATAG GGATGACCGT CTTCGTCGTC CTCGGCATGC TCCAGTTTCA
     151
          AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
          GGCTGGGCGC GGGTTTGGGC GTTTTATGGC TGAACCAGCA TTATTTCCAC
          GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG
          CTGGGCGGCG GTCGGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA
     351
     401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
     451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
     501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
          CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
     601 AGGCGCATGA CCCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
          AATCAACGCA CGCATGGTCA AAAGCCGCAG CCATCTCGCC GCCACATCGG
          GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCCAC
          CGTAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
          GCAATCTCCC AAACTCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
          TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
     901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
          AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
          GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
          ACCCGCCGCA AATGGCTGGA TGCCCACGAA CGCCAACACC TGCGCCAAAG
          CCTGCTTGAA ACACGGGAAC ACGGCTGA
This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:
m706.pep
          MNTSQRNRLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
       1
      51 EWIGHTVFVV LGMLQFQGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
     101 GNLLFYLTVG TASALAGWAA VGKNGYVPML AGLTMCMLIG DNGSEWLDSG
         LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
          RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
     201
         RKIVNTTELL LTTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING
```

201	DUADDYDTOM ATUDELE	373 000				
301 351	RHARRIRIDT AINPELE TRRKWLDAHE RQHLRQS	ALA EHLE LLE TREE	IYQWQGF LWL IG*	STNMRQE IS	ALVILLQR	
m706/q706	96.5% identity	in 375 a	a overlan			
m/00/g/00			•			
m706.pep	10 MNTSQRNRLVSRWLN	20 SYERYRYR	BLTHAURT CO	40	50	60
		111111:1	111111111	:111111		1111111
g706	MNSSQRKRLSGRWLN 10	SYERYRHR 20	RLIHAVRLGG 30	IVLFATALAR 40	LLHLQHGEWI	GMTVFVV
				40	50	60
m706.pep	70 LGMLQFQGAIYSKAV	80 ERMLGTVI	90 GLGAGLGVLWI	100	110	120
	111111111111	!		[	11111111	1111111
g706	LGMLQFQGAIYSNAVI 70	ERMLGTVI 80	GLGAGLGVLWI 90	LNQHYFHGNLI 100	FYLTIGTAS:	ALAGWAA
					110	120
m706.pep	130 VGKNGYVPMLAGLTM	140 CMLIGDNG	150 SEWLDSGLMRZ	160 MNULTGAAT	170	180
206			[	1111111111	311111111	111111
g706	VGKNGYVPMLAGLTMO 130	MLIGDNG:	SEWLDSGLMRÆ 150	MNVLIGAAIA 160	IAAAKLLPLI 170	KSTLMWR 180
	100				170	180
m706.pep	190 FMLADNLADCSKMIAE	200 SISNGRRM	210 FRERLEENMAK	220 MROINARMUK	230 SRSH1.Amed	240
~706				1111111111	11111111111	
g706	FMLADNLADCSKMIAE 190	200	rrerleqnmvk 210	MRQINARMVK 220	SRSHLAATS( 230	GESRISP 240
	250	260	070			240
m706.pep	AMMEAMQHAHRKIVNT	260 TELLLTT <i>i</i>	270 VAKLQSPKLNG	280 SEIRLLDRHF	290 TLLOTDLOOT	300
g706	:	1111111		11111111111	1111111111	
g/06	SMMEAMQHAHRKIVNT 250	260	AKLQSPKLNG 270	SEIRLLDRHF 280	TLLQTDLQQT 290	AALING 300
	310	220	222		-••	300
m706.pep	RHARRIRIDTAINPEL	320 EALAEHLH	330 YQWQGFLWLS	340 TNMROEISAL	350 VII.I.ORTRRK	360 WILDAHE
g706	T	1111111				111111
9700	RHARRIRIDTAINPEL 310	320	330	TNMRQEISAL 340	VILLQRTRRK 350	WLDAHE 360
	370					500
m706.pep	RQHLRQSLLETREHGX					
q706						
9.00	370					

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2367>: a706.seq

a706.seq				_	`
1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGG
101	CCGTCCTGTT			TGCTCCACCT	
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GTTTTATGGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCAC
751		TCAACACCAC			CCGCCAAGCT
801		AAACTCAACG			GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACCCC
					CAACGGC

901 951 1001 1051 1101	AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC ACCCGCCGCA AATGGCTGGA TGCCCACGAA CGCCAACACC TGCGCCAAAG CCTGCTTGAA ACACGGGAAC ACAGTTGA
This correspond	ls to the amino acid sequence <seq 2368;="" 706.a="" id="" orf="">:</seq>
а700.рер 1	MNTSODNDI V. CDUI NOVEDV. DATA
51	MNTSQRNRLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
101	EWIGMTVFVV LGMLQFQGAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH
151	GNLLFYLTVG TASALAGWAA VGKNGYVPML AGLTMCMLIG DNGSEWFDSG
201	LMRAMNVLIG AAIAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
251	RRMTRERLEE NMAKMRQINA RMVKSRSHLA ATSGESRISP AMMEAMQHAH
301	
351	RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR TRRKWLDAHE RQHLRQSLLE TREHS*
a706/m706 99	2.5% identity in 374 aa overlap
	10 20 20 40
a706.pep	MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV
• •	
m706	MNTSQRNRLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLHLQHGEWIGMTVFVV
	10 20 20 40
	10 20 30 40 50 60
	70 80 90 100 110 120
a706.pep	LGMLQFQGAIYSKAVERMLGTVIGLGAGI.GVI.WI.NOHYFHCNII FVI TVCTD CDI DCND D
m706	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVGTASALAGWAA
	70 80 90 100 110 120
	120
	130 140 150 160 170 180
a706.pep	VGKNGYVPMLAGLTMCMLIGDNGSEWFDSGLMRAMNVI.TGAATATAAKII DI KETI MUR
m706	VGKNGYVPMLAGLTMCMLIGDNGSEWLDSGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR
	130 140 150 160 170 180
	200
-706	190 200 210 220 230 240
a706.pep	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP
70 <i>C</i>	
m706	FHEADNIADCSRITAEISNGRRMTRERLEENMAKMRQINARMVKSRSHLAATSGESRISP
	190 200 210 220 230 240
	250 260 270 200 200
a706.pep	
aroo.pep	AMMEAMQHAHRKIVNTTELLLTTAAKLQSPKLNGSEIRLLDRHFTLLQTDLQQTVALING
m706	
111700	ATMIEATIONAL VNITELLETTAAKLQSPKLNGSEIRLLDRHFTLLQTDLQQTVALING
	250 260 270 280 290 300
	310 320 330 340 350 360
a706.pep	
<b>.</b>	RHARRIRIDTAINPELEALAEHLHYQWQGFLWLSTNMRQEISALVILLQRTRRKWLDAHE
m706	RHARRIRIDTA INPELEAL ACHI HYOMOGELMI COMPANIA
	RHARRIRIDTAINPELEALAEHLHYQWQGFLWLSTNMRQEISALVILLQRTRRKWLDAHE 310 320 330 340 350
	310 320 330 340 350 360
	370
a706.pep	RQHLRQSLLETREHSX
- <del>-</del>	[[]]]
m706	RQHLRQSLLETREHGX
	370

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2369>:

```
m707.seq
         ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
      1
      51 GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
    101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
    151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTTCTTT
    201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAAACT GGGATGTGTT
    251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
    301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
    351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
    401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
         GCATTCAATA ACAAATTTCC CTTATATAGG AACAAAATTC TCAATCTTCG
    501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTTAAAA
    551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
    601 ATCAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
         TGCGGGCGGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
         TCGATAACCC TTTGGGCTTA AGCGATTTGT TTTATGTTTC ATATGGACGC
    751 GGTTTGGCGC ACAAAACGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
         AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAAT
    851 GGCTGTTTTC TTTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
    901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
    951 GGCCGCCGAG CGCATGCTTT GGCGTAACAG ACTTCATAAA ACTTCAGTCG
   1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
   1051 ATCGAAGTAC AACGCCGCCG CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
   1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
         GCGGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
   1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGA
   1251 CGCAGCCGCC CCATTTATTT TAGGCAAACA GCAGTTTTTC TACGCAACCG
   1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
   1351
         TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
   1401 TTTCGGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
   1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
   1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
         GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
   1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
   1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA
```

### This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

```
m707.pep
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```
MEIINDAELI RSMQRQQHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51 RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSQA IIQPQNMDSG ILKLRVSAGE IGDIRYEEKR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQIIP SEEEGKSDLQ
101 IKWQQNKPIR FSIGIDDAGG KTTGKYQGNV ALSFDNPLGL SDLFYVSYGR
102 GYSVNYDYNG KQYQSSLAAE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
103 GYSVNYDYNG KQYQSSLAAE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
104 DILPGTSRMK IITASLDAAA PFILGKQQFF YATAIQAQWN KTPLVAQDKL
105 SIGSRYTVRG FDGEQSLFGE RGFYWQNTLT WYFHPNHQFY LGADYGRVSG
106 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
107 STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM STORM
```

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2371>:

```
a707.seq
      1 NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
     51 GAGCAGGCTA CAAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
    101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTC GGGAATTCTG
    151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
         ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
         TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
         TTGGAAAACC TGCGTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
    301
         ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
    351
         ATAAACCCAT ACGGTTCAGT ATCGGTATAG ATGATGCGGG CGGCAAAACG
    401
    451
         ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
    501 NTTAAGCGAT TNGTTTTATG TTTCATATGG ACGCGGTTTG GTGCACAAAA
    551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
    601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
    651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
    701 ACGATTACAA CGGCAAACAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG
```

751	CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC				
801	ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC				
851	GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC				
901	CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG				
951	CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA				
1001	NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT				
1051	ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTC AAGCTCAATG				
1101	GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT				
1151	ACACCGTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT				
1201					
	TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT				
1251	CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG				
1301	TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT				
1351	AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA				
1401	TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA				
1451	ATTACAGTTT CTAA				
This correspond	Is to the amino acid sequence <seq 2372;="" 707.a="" id="" orf="">:</seq>				
a707.pep					
1	XKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAII QPQNMDSGIL				
51	KLRVSAGEIG DIRYEEKRDX KSAEGSISAF NNKXPLYRNK ILNLRDVEQG				
101	ADAY SAGETG DIALEERADA KSAEGSISAF NNAAFLIKNA ILNLKDYEQG				
	LENLRRLPSV KTDIQIIPSE EEGKSDLQIK WQQNKPIRFS IGIDDAGGKT				
151	TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSRS				
201	YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNGKQ YQSSLAAERM				
251	LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRRSAGWE AELRHRAYLX				
301	RWQLDGKLSY KRGTGMRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX				
351	MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG				
401	FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH				
451	KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*				
a707/m707 95	a707/m707 95.3% identity in 486 aa overlap				
	10 20 30				
a707.pep	XKETAFKTGMCLGSNNLSRLQKAAQQILIVR				
m707	EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTGMCLGSNNLSRLQKAAQQILIVR				
	50 60 70 80 90 100				
	40 50 60 70 80 90				
a707.pep	GYLTSQAIIQPQNMDSGILKLRVSAGEIGDIRYEEKRDXKSAEGSISAFNNKXPLYRNKI				
m707	GYLTSQAIIQPQNMDSGILKLRVSAGEIGDIRYEEKRDGKSAEGSISAFNNKFPLYRNKI				
	110 120 130 140 150 160				
	100				
	100 110 120 130 140 150				
a707.pep	LNLRDVEQGLENLRRLPSVKTDIQIIPSEEEGKSDLQIKWQQNKPIRFSIGIDDAGGKTT				
атот.рер					
m707	LNLRDVEQGLENLRRLPSVKTDIQIIPSEEEGKSDLQIKWQQNKPIRFSIGIDDAGGKTT				
m / O /					
	170 180 190 200 210 220				
	160 170 100 100				
-707	160 170 180 190 200 210				
a707. <b>p</b> ep	GKYQGNVALSXDNPLGLSDXFYVSYGRGLVHKTDLTXATGTETESGSRSYSVHYSVXVKK				
m707	GKYQGNVALSFDNPLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRSYSVHYSVPVKK				
	230 240 250 260 270 280				
	220 230 240 250 260 270				
a707.pep	WLFSFNHNGHRYHEATEGYSVNYDYNGKQYQSSLAAERMLWXXXFXXTSVXMKLWTRQTY				
m707	WLFSFNHNGHRYHEATEGYSVNYDYNGKQYQSSLAAERMLWRNRLHKTSVGMKLWTRQTY				
	290 300 310 320 330 340				
	320 330 340				
	280 290 300 310 320 330				
a707.pep	KYIDDAEIEVQRRRSAGWEAELRHRAYLXRWQLDGKLSYKRGTGMRQSMPAPEENGGGTI				
pop					
m707	KYIDDAEIEVQRRRSAGWEAELRHRAYLNRWQLDGKLSYKRGTGMRQSMPAPEENGGDIL				
111707	250 260 250				
	350 360 370 380 390 400				

WO 99/57280

1140

```
350
                             360
                                     370
                                             380
          PXXSRMKIITAGLDAAAPXMLGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
a707.pep
          PGTSRMKIITASLDAAAPFILGKQQFFYATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDG
m707
                                    440
                    420
                            430
              400
                      410
                             420
                                     430
                                                    450
          EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK
a707.pep
          EQSLFGERGFYWQNTLTWYFHPNHQFYLGADYGRVSGESAQYVSGKQLMGAVVGFRGGHK
m707
                            490
                                   500
                    480
                                           510
              460
                      470
                             480
          VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
a707.pep
          VGGMFAYDLFAGKPLHKPKGFQTTNTVYGFNLNYSFX
m707
             530
                    540
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2373>: g708.seq

```
ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
 51 GGGCGCGTGC AGCACTTCCT ACCGCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
     GACTACCGTC AGGCAACGGC AAGTATTGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACTAC GGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTC
     CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCANAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTGC TGCTAGGCTG
GAAAATTGCC AAAGCCCTCG GCAACGTGCA GGCGGCATAC GAATATGAAG
CACAATTGCA GGCAAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 2374; ORF 708.ng>: g708.pep

```
MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
    DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLKVNDKAQ ESFRQALSIK
    PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKOGOFGLA EAYLKRSLAA QPQFPPAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2375>: m708.seq

```
ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
 51 GGGCGCGTGC AGCACTTCCT ACCGCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACTAC GGTTGGTTCC TATGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTC
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTGC TGCTAGGCTG
     CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
     GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
651
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ACCGGTCAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 2376; ORF 708>: m708.pep

```
MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
        DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLKVNDKAQ ESFRQALSIK
     51
        PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
    101
        SAKOGOFGLA EAYLKRSLAA QPQFPPAFKE LARTKMLAGO LGDADYYFKK
    151
    201
        YOSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
        TGO*
    251
m708/g708
           99.2% identity in 253 aa overlap
                          20
                                  30
                                           40
           MPFKPSKRISLLLVLALGACSTSYRPSRAEKANOVSNIKTOLAMEYMRGODYROATASIE
m708.pep
           MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
g708
                          20
                                  30
                                           40
                                                   50
                 70
                          80
                                  90
                                          100
                                                  110
                                                           120
           DALKSDPKNELAWLVRAEIYQYLKVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRLNR
m708.pep
           DALKSNPKNELAWLVRAEIYQYLKVNDKAQESFRQALSIKPDSAEINNNYGWFLCGRLNR
q708
                 70
                          80
                                  90
                                          100
                                                  110
                130
                         140
                                  150
                                          160
                                                  170
           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPPAFKE
m708.pep
           q708
           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSLAAQPQFPPAFKE
                         140
                130
                                  150
                                          160
                                                           180
                 190
                         200
                                  210
                                          220
           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF
m708.pep
           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNVQAAYEYEAQLQANF
g708
                190
                         200
                                 210
                                          220
                                                  230
                250
           PYSEELQTVLTGQX
m708.pep
           111111111111111
g708
           PYSEELQTVLTGQX
                250
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2377>:

```
a708.seq
         ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
         GGGCGCGTGC AGCACTTCCT ACCGCCCCTC GCGGGCAGAA AAAGCCAATC
      51
         AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
     101
         GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
    151
    201
         TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
         AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
     251
         CCCGACAGTG CCGAAATCAA CAACAACTAC NGCTGGTTCC TGTGCGGCAG
     301
     351
         GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
         ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
     401
         AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTC
     451
     501
         CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
         CCAAAATGCT GGCCGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
     551
         TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTGC TGCTAGGCTG
     601
     651
         GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
     701
         CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
         ATCGGTCAAT AA
```

### This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```
a708.pep

1 MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLKVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLNR PAESMAYFDK ALADPTYPXP YIANLNKGIC'
151 SAKQGQFGLA EAYLKRSLAA QPQFPPAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*
```

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVL	ALGACSTSY	RPSRAEKANQV	/SNIKTQLA	MEYMRGQDYR	ZXTASIE
			[]]		111111111	
m708	MPFKPSKRISLLLVL					QATASIE
	10	20	30	40	50	60
	70	80	90	100	110	120
a708 pep	DALKSDPKNELAWLV				AEINNNYXWF)	LCGRLNR
			,			
m708	DALKSDPKNELAWLV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADP	TYPXPYIANI				
m708	PAESMAYFDKALADP					PPAFKE
	130	140 [.]	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDAD	YYFKKYQSRI	/EVLQADDLLI	GWKIAKAL	GNAQAAYEYE <i>I</i>	AQLQANF
m708	LARTKMLAGQLGDAD					AQLQANF
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

# The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2379>:

1	ATGTTTGCTT	TCAAATCCTT	ACTCGATATG	CCGCGCGGTG	AGGCACTTGC
51	CGTCGTCGTC	GCTCTGATTG	CCGCAATGGG	CTATACCATC	ATTTCATTGG
101	AGTGGCTGCC	GCATATGTCC	ATTATTGCCG	CCATCGTCGT	GCTGATTTTG
151	TACGGCTTGG	CGCGCGGTTT	GAAATACAAC	GATATGCAGG	CAGGGATGAT
201	AGGCGCGTTG	AATCAGGGTA	TGGGCGCGGT	TTACCTGTTT	TTCTTCATCG
251	GGCTGATGGT	CAGCGCGCTG	ATGATGAGCG	GCGCGATTCC	GACGCTGATG
301	TATTACGGTT	TCGGGCTGAT	TTCCCCGACT	TATTTTTATT	TTTCCGCCTT
351	CGCGCTGTGT	TCCGTCATCG	GCGTGTCCAT	CGGCAGCAGC	CTGACCGCCT
401	GCGCCACTGT	CGGCGTTGCC	TTTATGGGGA	TGGCGGCGGC	GTTTCAGGCC
451	GATATGGCGA	TGACGgcggg		tccggTGTGT	
501	TAAAATGTCC	CCGCTTTCCG	ACACCACGGG	CATTTCCGCG	TCCATCGTCG
551	GTATCGACCT	GTTTGAACAC	ATCAAAAACA	TGATGTACAC	CACCATCCCT
601	GCGTGGCTTA	TCAGCGCGGC	ACTGATGCTT	TGGCTTCTTC	CCAGCGTCGC
651	CGCGCAGGAT	TTGAACAGCG	TCGAATCCTT	CCGCAGCCAG	CTTGAAGCCA
701	CGGGATTGGT	GCACGGCTAT	TCGCTGATTC	CGTTTGCACT	GTTGGTCGTT
751	TTGGCATTGA	TGCGCGTCAA	TGCCGTGGTC	GCCATGCTCT	TTACCGTCAT
801	TGCCGCCGTT	GCCGTAACGT	ATCTGCACAG	CACGCCCGAT	CTGCGTCAGC
851	TCGGCGCGTG	GTTTTATGGC	GGCTACAAAC	TCGAAGGCGA	AGCGTTTAAA
901	GACATTGCCA	AACTGATTTC	GCGCGGCGGC		TGTTCTTTAC
951	GCAGACCATC	GTTATCCTCG	GTATGAGTTT	GGGCGGGCTG	CTGTTTGCGC
1001	TCGGTGTGAT	TCCTTCCTTG	CTGGAGGCCG	TCCGTACCTT	CTTGACGAAT
1051		CGACGTTCAG			
1101	CCTGATTGGA	GAGCAATATT	TGAGCATCCT		GAAACGTTCA
1151	AACCCGTTTA	CGACAAACTC	GGCCTGCATT	CGTGCAACCT	GTCGCGGACT
1201	CTGGAAGATG		GATTAACCCG		GGAGCGTGTG
1251	CGGCGTATTT	ATCAGCCACG	CCCTTGGCGT	ACCCGTTTGG	GAATATCTGC
1301	CTTATGCCTT	TTTCTGCTAT	TTGAGTTTGG	CTTTAACCCT	GTTATTCGGC
1351	TGGACGGGGC	TGACTTTGAG	CAAAAAATAA		

### This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>: g709.pep

- MFAFKSLLDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL 51 YGLARGLKYN DMQAGMIGAL NQGMGAVYLF FFIGLMVSAL MMSGAIPTLM
- 101 YYGFGLISPT YFYFSAFALC SVIGVSIGSS LTACATVGVA FMGMAAAFQA 151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFEH IKNMMYTTIP
- 201 AWLISAALML WLLPSVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVV 251 LALMRVNAVV AMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
- 301 DIAKLISRGG LESMFFTQTI VILGMSLGGL LFALGVIPSL LEAVRTFLTN

```
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
451 WTGLTLSKK*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2381>:

```
ATGTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
      CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTCATTGG
  51
 101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
      TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
 201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
 301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTTATT TTTCCTCCTT
 351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT
 401 GCGCCACTGT CGGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
 451 GATATGCCGA TGACGGCGGG CGCGATTGTT TCGGGCGCAT TTTTTGGCGA
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTCGC
 651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCGCT GTTGGTCATT
 751 TTGGCATTGA TGCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
 801 GGTTGCCGTT GCTGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
 851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
 901 GATGTTGTCA AACTGATTTC GCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
 951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGCGC
1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
1051 GCCGGACGCG CGACGTTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCGGGT GAAACGTTCA
1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGC TGACTTTGAG CAAAAAATAA
```

#### This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>: m709.pep

MFAFKSLLDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM 101 YYGFGLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAAFQA 151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEH IKNMMYTTIP AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK DVVKLISRGG LESMFFTQTI VILGMSLGGL LFALGVIPSL LEAIRTFLTN 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLSRT LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG 451 WTGLTLSKK*

m709/a70996.9% identity in 459 aa overlap

		,	- · <b></b>			
	10	20	30	40	50	60
m709.pep	MFAFKSLLDMPRG	<b>EALAVVVALIA</b>	AMGYTIISLE	EWLPHMSIIAA	.IVVLILYGL	ARGLKYN
		11111111111	1111111111	1111111111	111111111	HIHH
g709	MFAFKSLLDMPRG	<b>EALAVVVALIA</b>	AMGYTIISL	EWLPHMSIIAA	IVVLILYGL	ARGLKYN
	10	20	30	40	50	60
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNQG	MGAIYLFFFIG	LMVSALMMS	GAIPTLMYYGF	GLISPTYFY	FSSFALC
	111 111111111	111:1111111	1111111111		111111111	H:111
g709	DMQAGMIGALNQG	MGAVYLFFFIG	LMVSALMMS	SAIPTLMYYGF	GLISPTYFY	FSAFALC
	70	80	90	100	110	120
	130	140	150	160	170	180
m709.pep	SVIGVSIGSSLTT	CATVGVAFMGM	AAAFQADMAN	<b>ITAGAIVSGAF</b>	FGDKMSPLSI	DTTGISA
	111111111111111111111111111111111111111			111111111111111111111111111111111111111		
g709	SVIGVSIGSSLTA	CATVGVAFMGM	AAAFQADMAN	<b>ITAGAIVSGVF</b>	FGDKMSPLSI	DTTGISA
_	130	140	150	160	170	180
	190	200	210	220	230	240
m709.pep	SIVGIDLFEHIKN	MMYTTIPAWLI	SAALMLWLLE	PNVAAQDLNSV	ESFRSQLEAT	rglvhgy
		11111111111		:::::::::::::::::::::::::::::::::::::::		
g709	SIVGIDLFEHIKN	MMYTTIPAWLI	SAALMLWLLE	SVAAQDLNSV	ESFRSQLEAT	rglvhgy
	190	200	210	220	230	240

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALM	RINAVVAML	FTVMVAVAVT	LHSTPDLRQI	GAWFYGGYK	LEGEAFK
	111111111111111	1:1111111	111::1111	11111111111	11111111	1111111
g709	SLIPFALLVVLALM	RVNAVVAML	FTVIAAVAVT	'LHSTPDLRQI	GAWFYGGYK	LEGEAFK
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESM	FFTQTIVIL	GMSLGGLLFAI	LGVIPSLLEAI	RTFLTNAGR	ATFSVAM
	1::		1111111111			
g709	DIAKLISRGGLESM		GMSLGGLLFAI	GVIPSLLEAV	RTFLTNAGR	ATFSVAM
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQYL	SILLSGETF	KPVYDKLGLHS	RNLSRTLEDA	GTVINPLVP	WSVCGVF
		1111111111			111111111	111111
g709	TSVGVNFLIGEQYL	SILLSGETFE	KPVYDKLGLHS	CNLSRTLEDA	GTVINPLVP	WSVCGVF
	370	380	390	400	410	420
			•			
	430	440	450	460		
m709.pep	ISHALGVPVWEYLP	YAFFCYLSL <i>i</i>	ALTLLFGWTGI	TLSKKX		
			:	11111		
g709	ISHALGVPVWEYLP	YAFFCYLSLA	ALTLLFGWTGI	TLSKKX		
	430	440	450	460		

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2383>: a709.seq

ATGTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC 1 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG 51 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG 101 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT 201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNTTT TTCTTCATCG GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTTATT TTTCCGCCTT CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT 401 GCGCCACTGT CGGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC 451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGGNCGCAT TNTTNGGCGN 501 CAAAATGTCN CCGCTTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCG GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC 551 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA 651 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGCGCT GTTGGTCGTT 701 751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC 801 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTNTANA 851 GACATTGCCA AACTCATTTC TCGCGGCGGT TTGGAAAGTA TGTTTTTCAC 901 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC 951 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT 1001 GCCGGGCGTN CCACATTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCNGGT GAAACGTTCA 1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG 1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG CGGCGTGTTC ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT TGGACGGGC TGACTTTGAG CAAAAATAA

### This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

a709.pep

1 MFAFXSLLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51 YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFGLISPT YFYFSAFALC SVIGVSIGSS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXSA SIVGIDLFEH IKNMMYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAVV AMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMFFTQTI VILGMSLGGL LFALGAIPSL LDAVRSFLTN
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLSRT

	401 451	LEDAGTVINE WTGLTLSKK*		EVF IXHALG	VPVW EYLPY	AFFCY LSLA	LTLLEG	
a709/m709	91	.1% identity		•				
a709.	pep	MFAFXSL	10 LDMPRGEAI	20 AVVVALIAA	30 MGYTIIXLEW	40 LPHMSIIAAI	50 VVLILYGLA	60 RGLKYN
m709		 MFAFKSL	 LDMPRGEAI	 AVVVALIAA	 MGYTIISLEW		VVLILYGLA	 RGLKYN
			10	20	30	40	50	60
a709.	pep	DMQQGMI	70 GALNQGMGA	80 LIYLFFFIGL	90 MVSALMMSGA	100 IPTLMYYGFG	110 LISPTYFYF	120 SAFALC
m709		 DMQQGMI	GALNQGMGA	IYLFFFIGL	 MVSALMMSGA	  IPTLMYYGFG	 LISPTYFYF	:      SSFALC
			70	80	90	100	110	120
a709.	pep	SVIGVSI				160 XXXIVXXAXX		•
m709		SVIGVSI		VGVAFMGMA		AGAIVSGAFF		TTGISA
			130	140	150	160	170	180
a709.	pep	SIVGIDL	190 FEHIKNMMY	200 TTIPAWLIS	210 XXLMLXLLPS	220 VAAQDLNSVE	230 SFRSQLEAT	240 GLVHCY
m709		SIVGIDL	FEHIKNMMY		AALMLWLLPN	VAAQDLNSVE	SFRSQLEAT	GLVHGY
			190	200	210	220	230	240
a709. _]	pep	SLIPFAL	250 LVVLALMRV	260 NAVVAMLETY	270 JIAAVAVTYL	280 HSTPDLRQLG	290 AWFYGGYKLI	300 EGEAXX
m709		SLIPFAL	:    : LVILALMRI 250		MVAVAVTYL	 HSTPDLRQLG	AWFYGGYKLI	EGEAFK
			310	320	270 330	280 340	290	300
a709.	pep	DIAKLIS	RGGLESMFF	TQTIVILGMS	SLGGLLFALG	340 AIPSLLDAVR: :     : :	350 SFLTNAGRXT	360 TFSVAM
m709		DVVKLIS	RGGLESMFF 310	TQTIVILGMS	SLGGLLFALG 330	VIPSLLEAIR	:	TFSVAM
			370	380	390	400	410	360 420
a709. ₁	pep	TSVGVNF	LIGEQYLSI	LLSGETFKPV	YDKLGLHSRI	NLSRTLEDAG:	TVINPLVPWS	SVCGVF
m709		TSVGVNF	LIGEQYLSI 370	LLSGETFKPV	YDKLGLHSRI 390	NLSRTLEDAG:	TVINPLVPWS 410	SVCGVF 420
			130	440	450	460	310	420
a709.	pep				LLFGWTGLT	LSKKX		
m709		ISHALGV			CLLFGWTGLT			
g710.s	seq	not found						
	-	not found						
The following m710.s		rtial DNA s	equence v	vas identifi	ed in N. me	eningitidis <	SEQ ID 2	:385>:
	1	ATGGAAACCC CCAGGAGGAT	ACGAAAAA ATGGCGGA	AT CCGCCTG	GAT GTCGG	ATTGA ATAAA	ATGGTC	
	L01	AAATCGAACG GCTCAGATTT	GGGCGAAA	CG CAGTTA	ATA TCCCG	CGTTT GGAGO	CAGTTG	
2	201	TGGGATGGTG TGTATGCGTC	TTTCAGAT'	TA ATGAAGG	TGA TAGTGO	STGGC GATAT	TGCGT	
						123707		

```
301 TTGAAACACT GCAAAGAAAT GTTGGAACAA AAAGACAAAG AAATCGAGCT
          351
              GCTCCGCAAG CTGACCGAAA CCGTTTAA
This corresponds to the amino acid sequence <SEQ ID 2386; ORF 710>:
     m710.pep
              METHEKIRLM REL'NKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
              AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
          101 LKHCKEMLEQ KDKEIELLRK LTETV*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2387>:
     a710.seq
              ATGGAAACCC ACGAAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC
           1
              CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA
          51
              AAATCGAACG AGGCGAAACG CAGTTGAATA TCCCGCGTTT GGAGCAGTTG
         101
              GCGCAGATTT TCAAAATTGA TATGTGGGAC TTGCTCAAAT CGGGCGGCGG
         151
              CGGGATGGTG TTGCAGATTA ACGATGTGGA TACCAACAGC GGGGAATTTG
         201
              CAATCTATAC CGCTCAGGAT GCATCNGGTA AAGCTGGATT TGTTAAAATG
         251
         301
              GAATTAAAAC ACTGTAAAGA AATGTTGGAA CACAAAGACA AAGAAATCGA
         351 GCTGCTCCGC AAGCTGACCG AAACCGTTTA A
This corresponds to the amino acid sequence <SEQ ID 2388; ORF 710.a>:
     a710.pep
              METHEKIRLM RELNKWSQED MAEKLAMSAG GYAKIERGET QLNIPRLEOL
           1
             AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
          51
         101 ELKHCKEMLE HKDKEIELLR KLTETV*
a710/m710 85.7% identity in 126 aa overlap
                                  20
                                           30
                                                     40
                                                              50
                 METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD
    a710.pep
                 METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD
    m710
                        10
                                  20
                                           30
                                                     40
                                                              50
                        70
                                  80
                                           90
                                                   100
                 LLKSGGGGMVLQINDVDTNSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKEIELLR
    a710.pep
                 LLKSGGGGMVFQINEGDSG-GDIALYASGDVSMKIEFLKMELKHCKEMLEQKDKEIELLR
    m710
                                   80
                                            90
                                                    100
    a710.pep
                KLTETVX
                 111111
                KLTETVX
    m710
```

```
q711.seq not found
     g711.pep not found
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2389>:
     m711.seq
               ATGCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
            1
           51
               AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
               TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
               TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
               TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
          251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
          301 CCAGCCACCG GCGAGGTATT CGGTTCGCCG CGGAGGTTGG AGACGATTTA
          351 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
          401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
          451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
          501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
          551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
          601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAAATCTA
          651 CAACAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
          701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
          751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
          801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTTAAACAGC
               TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
              CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
               TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
              TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
         1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
              GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
              TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAAATAT
         1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
         1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:
     m711.pep
            1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
               LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
          101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
          201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDYNAGRM
          251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
          301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
          351 DSREGQNFDD SYYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
          401 IKEVDEIYLO SYRISNDKEI AKFMAKKKVL K*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2391>:
     a711.seq
               ATGCCCGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
           51 AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
          101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
          151 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
          201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
          251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
          301 CCAGCCACCG GCGAGGTATT CGGTTCGCCG CGGAGGTTGG AGACGATTTA
          351 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
          401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
          451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
          501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
          551 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
          601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAAATCTA
```

651 CAACAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACCAGC TTTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG

901 951 1001 1051 1101 1151 1201 1251 This correspond a711.pep 1 51 101 151 201 251	TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA GACAGCCGTG AAGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAAATAT ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG  Is to the amino acid sequence <seq 2392;="" 711.a="" id="" orf="">:  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFDYNAGRM</seq>	
301	NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV	
351	DSREGONFDD SYYAFLPDML ONPEHVIRDN RELIFTARYK GSALWAVLKY	
401	IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*	
a711/m711 99	9.8% identity in 431 aa overlap	
	10 20 30 40 50	60
a711.pep	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTASEIAKVYTIARMTDLDMLNDIK	TS
m711		11 TS
	10 20 30 40 50	60
	70 80 90 100 110 1	20
a711.pep	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYR	TN
m711		11
IR/II	70 00 00 100	TN 20
	120 140 150 150	
a711.pep	130 140 150 160 170 1 MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPP	80 NG
		1.1
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPP 130 140 150 160 170	
	130 140 150 160 170 1	80
. 711	190 200 210 220 230 2	40
a711.pep	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSLYT	TD
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSLYT	TĐ
	190 200 210 220 230 2	40
	250 260 270 280 290 30	00
a711.pep	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEVKORLDID	GK
m711		
	250 260 270 200	00
	310 320 330 340 350 36	
a711.pep	310 320 330 340 350 36  PDKEQKIKIRNALSRQLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFI	00 DD
		1.1
m711	PDKEQKIKIRNALSRQLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFI 310 320 330 340 350 36	
	310 320 330 340 350 30	60
-711	370 380 390 400 410 42	20
a711.pep	SYYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKE	EI
m711	SYYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDK	ΞI
	270 200 200	20

WO 99/57280

1149

PCT/US99/09346

a711.pep

AKFMAKKKVLKX IIIIIIIIIIIIIIIIIAKFMAKKKVLKX 430

m711

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g712.seq not found yet g712.pep not found yet
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# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2393>: m712.seq

```
ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
     CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
  51
 101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
 151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
 201 TTTGTTCGGA CAAGGCTCGC TGGCGCATTT GATGGTGCGC CAAGCATTTG
 251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
 301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
 351 GCCGGGCGTG GTGGAAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
 401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
 451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
     TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
     CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
     GGCGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTCCA AAGTGGCGGG
     CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
 701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
 751 GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
 801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GGCGGTGTTG
 901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
     GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTTAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GGCGCGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GGCGCATTGA
1401 TTTGATTTTG TAA
```

# This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>: m712.pep

```
1 MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPQKVL MVAPMLTAGI
51 QPALEPVQLF SDAEAADLFG QGSLAHLMVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLIKLD QAEIIENAEA NKGKLVVARA QNDPNRVNAI
```

a712.seq not found yet

a712.pep not found yet

PCT/US99/09346 WO 99/57280

1151

```
g713.seq not found yet
g713.pep not found yet
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2395>: m713.seq

```
ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
  51 AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTTAATCC
 101 CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTTGGGACC GGAGGCGGCC
 151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
 201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
 251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
 301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
 351 CAAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
     CCGAAAACAA CCCCGCTTTG GGCAAAATCG ACATCGAGCC GGGCGAAACC
     GTATGGCAGG CATTAACCCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
     GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
     CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
 601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
 651 TTTTTTGGCG CAATCGCACG GCCGCAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTTCTGAT
951 GGGGCGGCG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA
```

#### This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>: m713.pep

```
MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
    IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
 51
   CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLKWVYKD PTMTLHRPKT
251 VVVSDADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVLWQPGLR
301 VHVIDDEHGI DAVFFLMGRR FMLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGKR KGVSHKGKKG GKKQAETAVF E*
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2397>: a713.seq

```
ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
   1
  51 AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTTAATCC
     CTGCCGACAG CTTCGATTTT GTCATCGGCA GGTTGGGGCC GGAGGCGGCC
 151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
      CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
     GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
 301 TGCTCCGCGC CGCAGCTCAA TGTAAAGGGC ATGACGGTAT TGGATGCAGC
 351 CAAAAAGCTG GCCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
 401 TCGAAAACAA CCCCGCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
 451 GTATGGCAGG CATTAACCCA TATTGCCAAC TCGGTCGGGC TGCATCCGTG
 501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
 551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
 601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
 651 TTTTTTGGCG CAATCGCACG GCCGCAGCGG CGACAGCGCC AAACACGATT
     TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
 751 GTGGTGGTGT CCGATGCCGA CAATTTGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCAGCGT
 901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTTCTGAT
 951
     GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCACGCAA ACCGAGCTGC
1001
     GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
```

1101 CAAAAAAGGC GGCAAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

1101	CAAAAAAGGC GGCAAAA	AAC AAGCA	GAAAC GGCG	GTGTTT GA	ATGA	
This correspond	Is to the amino acid se	equence <9	EO ID 330	08. ODE 71	2 0>1	•
a713.pep	is to the allino acid so	equence \b		70, OKI 71	3.4.	
a715.pep	MQNNSYGYAV SVRVGGK	EHR HWERYI	DIDSD FLIP	ADSFDF VIO	SRIGPEAA	
51	IPDLSGESCE VVIDGQI	VMT GIIGS	QRHGK SKGG	RELSLS GRI	DLAGFLVD	
101	CSAPQLNVKG MTVLDAA	KKL AAPWP(	DIKAV VLKV	ENNPAL DK	DIEPGET	
151	VWQALTHIAN SVGLHPW	LEP DGTLV	VGGVD YSSP	PVATLC WSF	RTDSRRNI	
201	ERMDIEWDTD NRFSEVT	FLA QSHGRS	SGDSA KHDL	KWVYKD PTN	1TLHRPKT	
251 301	VVVSDADNLA ALQKQAK VHVIDDEHGI DAVFFLM	KOL ADWRLE	SGFTL TITV	GGHKTR DGV	LWQPGQR	
351	EAARKRKGKR KGVSHKG	KKG GKKOAI	TAVF E*	TVEDGI MIF	PDAIPKKA	
		<b>-</b>				
a713/m713 98	3.4% identity in 381 a	a overlap				
	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVG	GKEHRHWERY	OIDSDFLIP	ADSFDFVIGR	RLGPEAAIPD	LSGESCE
		1111111111		1111111111	111111111	
m713	MQNNSYGYAVSVRVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGS			AGFLVDCSAF	OLNVKGMTVI	DAAKKI.
				111111111	11111111	111111
m713	VVIDGQIVMTGIIGS	QRHGKSKGSF	RELSLSGRDL	AGFLVDCSAP	QLNVKGMTVI	DAAKKL
	70	80	90	100	110	120
	130	140	150	160	170	100
a713.pep	AAPWPQIKAVVLKVE					180
	111111111111111111111111111111111111111				11111111111	111111
m713	AAPWPQIKAVVLKAE	NNPALGKIDI	EPGETVWQA	LTHIANSVGL	HPWLEPDGTI	VVGGAD
	130	140	150	160	170	180
	190	200	010	000		
a713.pep	YSSPPVATLCWSRTD:		210 EMDTONDESI	220 EVTET AGENC	230	240
u/13.pcp		11   111111	111111111	TITITION CONG	ROGUSAKHUI	PKMAIKD
m713	YSSPPVATLCWSRTD	SRCNIERMDI	EWDTDNRFSI	EVTFLAOSHG	RSGDSAKHDI	KWVYKD
	190	200	210	220.	230	240
	0.50	0.50				
a713.pep	250 PTMTLHRPKTVVVSDA	260 NDNI A 1 020	270	280	290	300
a/13.pep		HIIIIIIIIIIII	HIIIIIIIIIIII	LEGETLTTTV	GGHKTRDGVL	WQPGQR
m713	PTMTLHRPKTVVVSDA	ADNLAALOKO	AKKOLADWR	LEGFTLTITV	GGHKTRDGVI	WOPGI.R
	250	260	270	280	290	300
	24.0					
2712 non	310	320	330	340	350	360
a713.pep	VHVIDDEHGIDAVFFI	LMGKKEMLSK	MDGTQTELRI	LKEDGIWTPD.	AYPKKAEAAR	KRKGKR
m713	VHVIDDEHGIDAVFFI	LMGRRFMLSR	MDGTOTELRI	LKEDGTWTPD	ΙΙΙΙΙΙΙΙΙΙΙ ΑΥΡΚΚΆΓΔΔΩ	KBKCKB
	310	320	330	340	350	360
- 74 0	370	380				
a713.pep	KGVSHKGKKGGKKQAF					
m713						
20	370	380				

```
q714.seq not found yet
     g714.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2399>:
     m714.seq
              ATGAGCTATC AAGACATCTT GCGGGGCCTG TTGCCCCCCG TGTCGTATGC
            1
              CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
           51
              TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
          101
              CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
          151
          201 CGGTACGGCC AAAAACCGCC AGCACCGTGT GTTGGCCGTC ATGGCCAAGC
          251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
          301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
          351 TGTAAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
          401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
          451 GGTATCTCGG CGGCGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
              CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
          551 CCTACCGCTA A
This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:
     m714.pep
              MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
              RSAGQMLADW ERVLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
          51
              AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
              GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2401>:
     a714.seq
              ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCCG TGTCGTATGC
           1
              CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
          51
              TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
              AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
             CGGTACGGCC AAAAACCGCC AGCGCCGTGT GTTGGCCGTC ATGGCCAAGC
         201
         251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
         301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
         351 TGTAAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
         401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
              GGTATCTCGG CGGCGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
              CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
         501
         551 CCTACCGATA A
This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:
    a714.pep
              MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVADAVDP
           1
          51
              SSAGQMLADW ERVLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
              AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVRG GNNRITRFRA
         101
              GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
a714/m714 98.9% identity in 186 aa overlap
                        10
                                           30
                 MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPSSAGQMLADW
    a714.pep
                 MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVADAVDPRSAGQMLADW
    m714
                        10
                                  20
                                           30
                                                     40
                                                              50
                                                                        60
                        70
                                  80
                                           90
                                                    100
                                                             110
                 ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAGYQIQIDEPQPFRAGVNR
    a714.pep
                 ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAGYQIQIDEPQPFRAGVNR
    m714
                        70
                                  80
                                           90
                                                   100
                                                             110
                                                                       120
                       130
                                 140
                                          150
                                                   160
                                                             170
                AGDRLAPQEIMWVWHVNVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
    a714.pep
```

```
AGDRLAPQEIMWVWHVNVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
      m714
                                               150
                                                         160
                   IRFTYRX
      a714.pep
                   111111
      m714
                   IRFTYRX
      g715.seq not found yet
      g715.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2403>:
      m715.seq
               ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
               GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
               CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
               CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
           201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
           251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACTT CGGCGGTATG
           301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
           351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
           401 CGGGTCTGAT ACCGTGA
This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:
     m715.pep
             1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
            51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
           101 AGRNRKVRIP QREFLTLTDD DKQALMDDVO DYFSGLIP*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2405>:
     a715.seq
               ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
            1
            51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
           101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
          151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC
          201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
          251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACTT CGGCGGTATG
          301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
          351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
          451 CGGGTCTGAT ACCGTGA
This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>
     a715.pep
               MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
            1
               PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
          101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGLIP*
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2407>:
g716.seq
      1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
         GGCCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
    101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
    151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
    201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
         AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
    301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA
This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:
```

g716.pep

- MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
- 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

```
101 EGKCGEGKCG SK*
```

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2409>:
         ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
         GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
      51
         TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
     101
        TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
         CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
     251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
        TCTAAATAA
This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:
         MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAHG SCGASKSAEG
     51
         SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
    101
           86.6% identity in 112 aa overlap
m716/g716
                           20
                                    30
                                            40
           MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAHGSCGASKSAEGSCGA-----
m716.pep
           g716
           MNKNIAAALAGALSLSLAAGAVAAHKPASNATGVQKSAQGSCGASKSAEGSCGASKSAEG
                                   30
                                            40
                                                     50
                  60
                                   80
                                            90
            ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
m716.pep
               SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
a716
                  70
                           80
                                   90
                                                    110
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2411>:
     a716.seq
              ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
              GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
           51
          101
              TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
              TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
              CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
              AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
          251
          301 TCTAAATAA
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2412.a>:
     a716.pep
              MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAHG SCGASKSAEG
              SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
           51
         101
a716/m716 100.0% identity in 102 aa overlap
                                                      40
                                                                50
                                                                          60
                 MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAHGSCGASKSAEGSCGAAGSKAG
     a716.pep
                 m716
                 MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAHGSCGASKSAEGSCGAAGSKAG
                         10
                                   20
                                            30
                                                      40
                         70
                                   RΛ
                                            90
                 EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
     a716.pep
                 EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
    m716
                         70
                                   80
                                            90
                                                     100
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2413>: g717.seq

¹ ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

```
51 GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCcccqCCG
 101 ACGACATCGG GCGCATCGTG CTGATGCAGA CGGCGGCGGG ACTGACGGTG
      TCGGTATTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
 201 CGCCGCCGAC AAAGACACTT TGTTCAAAAC CCTGTTCCTG CCGCCGCTGC
 251 TGTTTTCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC GTCCCTGCCG
 301 TCTGAAATCC TGTTTTCGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
 351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
 401 GTATGGAAGG GCGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGCCCAAA
 451 CTCGCCATTC TGCTGCTGTT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
      GGCGAACACC TCCGTCCTGA CCGCCGTTTA CGCGCTGGCA AACCTTGCCG
 551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGTCTGAA GGCCGTCCGG
 601 CGCGCGCCGT TTTCGCCCGC CGTCCTGCAC CGGGGGCTGC GCTACGGCAT
 651 ACCGCTCGCA CTGAGCAGCC TTGCCTATTG GGGGCTGGCA TCCGCCGACC
 701 GTTTGTTCCT GAAAAAATAT GCGGGCCTGG AACAGCTCGG CGTTTATTCG
 751 ATGGGTATTT CGTTCGGCGG GGCGGCATTA TTGCTCCAAA GCATCTTTTC
 801 AACGGTCTGG ACACCGTATA TTTTCCGTGC AATCGAAGAA AACGCCACGC
 851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCCTCC
 901 GCCCTCTGCC TGACCGGAAT TTTCTCGCCC CTCGCCTCCC TCCTGCTGCC
 951 GGAAAACTAC GCCGCCGTCC GGTTTACCGT CGTATCGTGT ATGCTGCCGC
1001 cgctGTTTTA CACGCTGACC GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGCAAAACGC GTCCGATCGC GCTTGCCACC TTGGGCGCCC TGGCGGCAAA
1151 CGGTTGCCTG TGCCGCCTCA TTCTGGTTGT TTTTTGTTTT CAAGACAGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAAA CGCCTGCCGC TTTATATGCA
1251 CACATTGTTC TGCCTgGCCT CCTCGGCGGC CTACACCTGC TTCGGCACAC
1301 CGGCAAACTA CCCcctgttt gccggcgtAT GGGCGGCATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AAATTTGCAC AAACTGTTTC ATTATTTGAA
1401 AAAACAAGGT TTCCCATTAT GA
```

### This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```
1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51 SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLFSAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLFE LSFLPIRFLL LVLRMEGRAL AFSSAQLVPK
151 LAILLLPLT VGLLHFPANT SVLTAVYALA NLAAAAFLLF QNRCRLKAVR
152 RAPFSPAVLH RGLRYGIPLA LSSLAYWGLA SADRLFLKKY AGLEQLGVYS
153 MGISFGGAAL LLQSIFSTVW TPYIFRAIEE NATPARLSAT AESAAALLAS
154 ALCLTGIFSP LASLLPENY AAVRFTVVSC MLPPLFYTLT EISGIGLNVV
155 RKTRPIALAT LGALAANLLL LGLAVPSGGT RGAAVACAAS FWLFFVFKTE
165 GGPANYPLF AGVWAAYLAG
```

451 CILRHRKNLH KLFHYLKKQG FPL*

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2415>:

```
m717.seq
      1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
      51 GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCCGCCG
     101 ACGACATCGG GCGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
    151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
    201 CACCGCCGAC AAAGACACCT TGTTCAAAAC CCTGTTCCTG CCGCCGCTGC
    251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC GTCCCTGCCG
    301 TCTGAAATCC TGTTTTCACT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
    351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
         GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGCCCAAG
    451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
    501 AGCGAACACC GCCGTCCTGA CCGCCGTTTA CGCGCTGGCA AACCTTGCCG
    551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGTCTGAA GGCCGTCCGG
    601 CACGCACCGT TTTCGCCCGC CGTCCTGCAC CGGGGGCTGC GCTACGGCAT
    651 ACCGATCGCA CTGAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
    701 GTTTGTTCCT GAAAAAATAT GCCGGCCTGG AACAGCTCGG CGTTTATTCG
         ATGGGTATTT CGTTCGGCGG GGCGGCATTA TTGTTCCAAA GCATCTTTTC
    801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGAA AACGCCCCGC
    851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCCTCC
    901 GCCCTCTGCC TGACCGGCAT TTTCTCGCCC CTTGCCTCCC TCCTGCTGCC
         GGAAAACTAC GCCGCCGTCC GGTTTATCGT CGTATCGTGT ATGCTGCCGC
   1001 CGCTGTTTTG CACGCTGGCG GAAATCAGCG GCATCGGTTT GAACGTCGTC
   1051 CGCAAAACGC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
   1101 CCTGCTGCTG CTGGGGCTTG CCGTGCCGTC CGGCGGCGCG CGCGGCGCGG
         CGGTTGCCTG TGCCGCCTCA TTCTGGCTGT TTTTTGCCTT CAAGACCGAA
   1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAAA CGCCTGCCGC TTTATCTGCA
   1251 CACATTGTTC TGCCTGACCT CCTCGGCGGC CTACACCTGC TTCGGCACGC
   1301 CGGCAAACTA TCCCCTGTTT GCCGGCGTAT GGGCGGCATA TCTGGCAGGC
   1351 TGCATCCTGC GCCACCGGAA AGATTTGCAC AAACTGTTTC ATTATTTGAA
   1401 AAAACAAGGT TTCCCATTAT GA
```

```
This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:
m717.pep
           MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
           SVLCLGLDQA YVREYYATAD KDTLFKTLFL PPLLSAAAIA ALLLSRPSLP
       51
           SEILFSLDDA AAGIGLVLFE LSFLPIRFLL LVLRMEGRAL AFSSAOLVPK
      101
           LAILLLEPLT VGLLHFPANT AVLTAVYALA NLAAAAFLLF QNRCRLKAVR
      151
           HAPFSPAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
           MGISFGGAAL LFQSIFSTVW TPYIFRAIEE NAPPARLSAT AESAALLAS
           ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
      301
           RKTRPIALAT LGALAANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
      351
           SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAYLAG
      401
           CILRHRKDLH KLFHYLKKQG FPL*
m717/q717
              96.4% identity in 473 aa overlap
                       10
                                  20
                                             30
                                                        40
                                                                   50
                                                                              60
              MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
m717.pep
              MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
q717
                       10
                                  20
                                             30
                                                                   50
                       70
                                  80
                                             90
                                                       100
              YVREYYATADKDTLFKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLFE
m717.pep
              YVREYYAAADKDTLFKTLFLPPLLFSAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLFE
g717
                                  80
                                             90
                                                      100
                      130
                                 140
                                            150
                                                      160
                                                                  170
              LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLLLPLTVGLLHFPANTAVLTAVYALA
m717.pep
              LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLLLPLTVGLLHFPANTSVLTAVYALA
g717
                     130
                                 140
                                            150
                                                      160
                                                                 170
                                                                            180
                     190
                                 200
                                            210
                                                      220
                                                                 230
              NLAAAAFLLFQNRCRLKAVRHAPFSPAVLHRGLRYGIPIALSSIAYWGLASADRLFLKKY
m717.pep
              NLAAAAFLLFQNRCRLKAVRRAPFSPAVLHRGLRYGIPLALSSLAYWGLASADRLFLKKY
g717
                                 200
                     190
                                            210
                                                      220
                                                                 230
                     250
                                 260
                                           270
                                                      280
                                                                 290
              AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
m717.pep
              AGLEQLGVYSMGISFGGAALLLQSIFSTVWTPYIFRAIEENATPARLSATAESAAALLAS
q717
                     250
                                260
                                           270
                                                      280
                                                                 290
                     310
                                320
                                           330
                                                      340
                                                                 350
                                                                            360
              ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
m717.pep
              £{{\\\}}{\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}{\\\}}\\\\}
g717
              ALCLTGIFSPLASLLLPENYAAVRFTVVSCMLPPLFYTLTEISGIGLNVVRKTRPIALAT
                     310
                                320
                                           330
                                                      340
                     370
                                380
                                           390
                                                      400
m717.pep
             LGALAANLLLLGLAVPSGGARGAAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
              LGALAANLLLLGLAVPSGGTRGAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
q717
                                380
                                           390
                                                      400
                                                                 410
                     430
                                440
                                           450
                                                      460
             CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKLFHYLKKQGFPLX
m717.pep
              q717
             CLASSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKNLHKLFHYLKKQGFPLX
                     430
                                440
                                           450
                                                      460
                                                                 470
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2417>:

a717.seq

1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51 GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAAC CCTGTTCCTG CCGCCGCTGC

251	TGTCTGCCGC	CGCGATAGCC	GCCCTGCTGC	TTTCCCGCCC	ATCCCTGCCG
301	TCTGAAATCC	TGTTTTCGCT	CGACGATGCC	GCCGCCGGCA	TCGGGCTGGT
351	GCTGTTTGAA	CTGAGCTTCC	TGCCCATCCG	CTTTCTCTTA	CTGGTTTTGC
401	GTATGGAAGG	ACGCGCCCTT	GCCTTTTCGT	CCGCGCAACT	CGTGTCCAAG
451	CTCGCCATCC	TGCTGCTGCT	GCCGCTGACG	GTCGGGCTGC	TGCACTTTCC
501	GGCGAACACC	GCCGTCCTGA	CCGCCGTTTA	CGCGCTGGCA	AACCTTGCCG
551	CCGCCGCCTT	TTTGCTGTTT	CAAAACCGAT	GCCGTCTGAA	GGCCGTCCGG
601	CGCGCACCGT	TTTCATCCGC	CGTCCTGCAT	CGCGGCCTGC	GCTACGGCAT
651	ACCGATCGCA	CTAAGCAGCA	TCGCCTATTG	GGGGCTGGCA	TCCGCCGACC
701	GTTTGTTCCT	GAAAAAATAT	GCCGGCCTAG	AACAGCTCGG	CGTTTATTCG
751	ATGGGTATTT	CGTTCGGCGG	AGCGGCATTA	TTGTTCCAAA	GCATCTTTTC
801	AACGGTCTGG	ACACCGTATA	TTTTCCGCGC	AATCGAAGCA	AACGCCCCGC
851	CCGCCCGCCT	CTCGGCAACG	GCAGAATCCG	CCGCCGCCCT	GCTTGCCTCC
901	GCCCTCTGCC	TGACCGGCAT	TTTCTCGCCC	CTCGCCTCCC	TCCTGCTGCC
951	GGAAAACTAC	GCCGCCGTCC	GGTTTATCGT	CGTATCGTGT	ATGCTGCCTC
1001	CGCTGTTTTG	CACGCTGGTA	GAAATCAGCG	'GCATCGGTTT	GAACGTCGTC
1051	CGAAAAACAC	GCCCGATCGC	GCTCGCCACC	TTGGGCGCGC	TGGCGGCAAA
1101	CCTGCTGCTG	CTGGGGCTTG	CCGTACCGTC	CGGCGGCGCG	CGCGGCGCGG
1151	CGGTTGCCTG	TGCCGCCTCA	TTTTGGCTGT	TTTTTGTTTT	CAAGACCGAA
1201	AGCTCCTGCC	GCCTGTGGCA	GCCGCTCAAA	CGCCTGCCGC	TTTATATGCA
1251	CACATTGTTC	TGCCTGGCCT	CCTCGGCGGC	CTACACCTGC	TTCGGCACTC
1301	CGGCAAACTA	CCCCCTGTTT	GCCGGCGTAT	GGGCGGTATA	TCTGGCAGGC
1351	TGCATCCTGC	GCCACCGGAA	AGATTTGCAC	AAACTGTTTC	ATTATTTGAA
1401	AAAACAAGGT	TTCCCATTAT	GA		

# This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

a717.pep					
1	MDTKEILGYA	AGSIGSAVLA	VIILPLLSWY	FPADDIGRIV	LMOTAAGLTV
51	SVLCLGLDQA	YVREYYAAAD	KDTLFKTLFL	PPLLSAAAIA	ALLLSRPSLP
101	SEILFSLDDA	AAGIGLVLFE	LSFLPIRFLL	LVLRMEGRAL	AFSSAQLVSK
151	LAILLLPLT	VGLLHFPANT	AVLTAVYALA	NLAAAAFLLF	QNRCRLKAVR
201	RAPFSSAVLH	RGLRYGIPIA	LSSIAYWGLA	SADRLFLKKY	AGLEQLGVYS
251	MGISFGGAAL	LFQSIFSTVW	TPYIFRAIEA	NAPPARLSAT	AESAAALLAS
301	ALCLTGIFSP	<u>L</u> ASLLLPENY	AAVRFIVVSC	MLPPLFCTLV	EISGIGLNVV
351	RKTRPIALAT	LGALAANLLL	LGLAVPSGGA	RGAAVACAAS	FWLFFVFKTE
401	SSCRLWQPLK	RLPLYMHTLF	CLASSAAYTC	FGTPANYPLF	AGVWAVYLAG
451	CILRHRKDLH				

### a717/m717 97.9% identity in 473 aa overlap

//III/1/ 9/.97	o lucility in 4/3 as	a overlap				
	10	20	30	40	50	60
a717.pep	MDTKEILGYAAGSIG	SAVLAVIIL	PLLSWYFPADI	DIGRIVLMOT	'AAGLTVSVLO	LGLDOA
				111111111	111111111	111111
m717	MDTKEILGYAAGSIG	SAVLAVIILI	PLLSWYFPADI	DIGRIVLMOT	AAGLTVSVLO	LGLDOA
	10	20	30	40	50	60
	70	80	90	100	110	120
a717.pep	YVREYYAAADKDTLF	KTLFLPPLLS	SAAAIAALLLS	SRPSLPSEIL	FSLDDAAAGT	GLVLEE
	11111111:111111					
m717	YVREYYATADKDTLF	KTLFLPPLLS	BAAAIAALLLS	RPSLPSEIL	FSLDDAAAGT	GLVLEE
	70	80	90	100	110	120
						120
	130	140	150	160	170	180
a717.pep	LSFLPIRFLLLVLRM	EGRALAFSS <i>A</i>	OLVSKLAILI	LLPLTVGLL		
					11111111111	
m717	LSFLPIRFLLLVLRM	EGRALAFSSA	OLVPKLAILI	LLPLTVGLL	ΗΓΡΑΝΨΑ <b>ΥΙ.</b> Ψ	ΑΙΚΑΝΙΑ
	130	140	150	160	170	180
				200	170	00
	190	200	210	220	230	240
a717.pep	NLAAAAFLLFQNRCRI	LKAVRRAPFS	SAVLHRGLRY			עאאואו
		11111:1111			1111111111	
m717	NLAAAAFLLFQNRCRI	LKAVRHAPFS	PAVLHRGLRY	GTPTALSST	ΔΥΜ <u></u> ζΙ.Δ <u>ς δ η</u> ρ	יוווון דוועט
	190	200	210	220	230	240
				440	230	240
	250	260	270	280	290	300
a717.pep	AGLEQLGVYSMGISFO				ፈ ጋሀ አይ፤ ሮአጥአድሮች	טטכ
			- CIVILIII	TOTPUNELL	<b>HUTOWI WEON</b>	WWTTW2

```
AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
m717
               250
                       260
                              270
                                      280
                                             290
                                                     300
               310
                       320
                              330
                                      340
                                             350
                                                     360
          ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
a717.pep
          ALCLTGIFSPLASLLLPENYAAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
m717
               310
                       320
                              330
                                      340
                                             350
               370
                       380
                              390
                                      400
                                             410
                                                     420
          LGALAANLLLLGLAVPSGGARGAAVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF
a717.pep
          LGALAANLLLLGLAVPSGGARGAAVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF
m717
               370
                      380
                              390
                                      400
               430
                      440 .
                              450
                                      460
         CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKLFHYLKKQGFPLX
a717.pep
          CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKLFHYLKKQGFPLX
m717
               430
                      440
                              450
                                      460
g718.seq not found yet
q718.pep not found yet
```

#### The following partial DNA sequence was identified in N. meningitidis <SEO ID 2419>: m718.seq

J. 3E4					
1	TCAGACGGCC	TTTACGTACC	CCGAAACTTT	ATCCACCGCC	CGCAAAGCTG
51	GTTCAAATGG	GACAAAGACA	ACGGGCTGCT	GCTGCGTACC	CGCGAAAATC
101	CGGAAGGCGA	AGCGTTGTGG	CCGCTGGGCT	GGGTCGTTCA	TACCCAAAAA
151	TCGCGCAGCG	TCCAGCAGGC	GCGCAACGGG	CTTTTCCGCA	CGCTTTCCTG
201	GCTGTATATG	TTCAAACACT	ACGCCGTCCA	CGATTTTGCC	GAGTTTTTGG
251	AGCTGTACGG	CATGCCCATC	CGTATCGGCA	AATACGGCGC	GGGCGCAACC
301	AAAGAGGAAA	AAAACACCCT	GCTTCGAGCG	GTGGCGGAAA	TCGGTCACAA
351	CGCGGCAGGC	ATCATGCCAG	AAGGTATGGA	AATAGAGCTC	CACAACGCGG
401	CAAACGGTAC	GACGGCAACC	AGCAATCCGT	TTTTGCAGAT	GGCCGACTGG
451	TGCGAAAAAT	CGGCGGCGCG	GCTGATTTTG	GGGCAAACGC	TGACCAGCGG
501		AAATCCAGCA	90.2.00000	GGGCAATATC	CACAACGAGG
551	TACGCCGCGA	TTTGCTGGTG	TCGGACGCAA	AACAGGTGGC	GCAAACCATC
601	ACAAGCCAAA		GTTCCTGCAA	ATCAACTATC	CCCATGCCGA
651	CCCAAACCGC	GTGCCGAAAT	TTGAATTTGA	CACGCGCGAG	CCGAAAGACA
701	TCGCGGTCTT	TGCCGACGCT	ATCCCGAAAC	TGGTGGATGT	CGGCGTACAA
751	ATCCCCGAAA	GCTGGGTGCG	CGACAAACTG	GTCATTCCAG	ATGTGCAGGA
801	GGGTGAGGCT	GTGTTGGTGC	GGCAGGTACC	GGACAATCCG	GTAAACAGAA
851	CTGCATTGGC	GGCTTTATCC	GCCCACACCG	TACCATCTAA	GGCTACGGGC
901	AGGCATCAGG	AAATATTGGA	CGGCGCGTTG	GATGACGCGC	TGGTTGAGCC
951	CGATTTCAAT	TCTCAGCTCA	ACCCGATGGT	GCGTCAGGCG	GTTGCCGCAC
1001	TTAATGCTTG	CAACAGCTAC	GAGGAGGCAG	ATGCCGCACT	GAATGCGCTT
1051	TATCCGAATT	TGGACAACGC		ACCTATATGC	AGCAGGCCTT
1101	GTTTATCAGC	GATATTTTGG	GACAAGACCA	TGCCCGCGCC	TGA

#### This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>: m718.

. pep					
1		IHRPQSWFKW			
51	SRSVQQARNG	LFRTLSWLYM	FKHYAVHDFA	EFLELYGMPI	RIGKYGAGAT
101	KEEKNTLLRA	VAEIGHNAAG	IMPEGMEIEL	HNAANGTTAT	SNPFLQMADW
151	CEKSAARLIL	GQTLTSGADG	KSSTNALGNI	HNEVRRDLLV	SDAKOVAOTI
201	TSQIIGPFLQ	INYPHADPNR	VPKFEFDTRE	PKDIAVFADA	IPKLVDVGVO
251	IPESWVRDKL	VIPDVQEGEA	VLVRQVPDNP	VNRTALAALS	AHTVPSKATG
301	RHQEILDGAL	DDALVEPDFN	SQLNPMVRQA	VAALNACNSY	EEADAALNAL
351	YPNLDNAKLR	TYMQQALFIS	DILGQDHARA	*	

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2421>:

710	·
a718.seq	
1 51	
101	
. 151	
201	
251	
301	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
351	
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1001	
1051	
1101	
1151	
1201	
1251	
1301	
1351	
1401	
1451	
1501	
1551	TATTTTGGGA CAAGACCATG CCCGCGCCTG A
This correspond	ds to the amino acid sequence <seq 2422;="" 718.a="" id="" orf="">:</seq>
1	MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51	
	ATPEEEKLSD QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDGL
151	
201	QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251	NTLLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMADWCEKS
301	AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351	IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401	WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451	ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501	DNAKLRTYMQ QALFISDILG QDHARA*
<b>a718/m718</b> 98	8.4% identity in 380 aa overlap  120 130 140 150 160 170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFSDGLYLPRNFIHRPQSWFKWDKDNGLLLRT
a, rotheb	
m718	SDGLYVPRNFIHRPQSWFKWDKDNGLLLRT
111.120	10 20 30
	10 20 30
	180 190 200 210 220 230
a718.pep	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI
u/10.pup	
m718	
	RENPEGEALWPLGWVVHTOKSRSVOOARNGI.FRTI.SWI VMFVUVAVUDEAERI ET VONDT
	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI
	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI 40 50 60 70 80 90
	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI 40 50 60 70 80 90
	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI 40 50 60 70 80 90  240 250 260 270 280 290
a718.pep	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI 40 50 60 70 80 90  240 250 260 270 280 290 RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLOMADW
	RENPEGEALWPLGWVVHTQKSRSVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI 40 50 60 70 80 90  240 250 260 270 280 290

	100	110	120	130	140	150
	300	310 32	0 330	340	350	)
a718.pep	CEKSAARLILG	QTLTSGADGKSS	TNALGNIHNEIR	RDLLVSDAKQ	VAQTITSQI	IGPFLO
		11111111111				
m718	CEKSAARLILG	QTLTSGADGKSS	TNALGNIHNEVR	RDLLVSDAKQ	VAQTITSOI	IGPFLO
	160	170	180	190	200	210
	360	370 38	0 390	400	410	)
a718.pep	INYPHADPNRV	PKFEFDTREPKD	IAVFADAIPKLV	DVGVQIPESW	VRDKLVIPE	VOEGEA
•			11111111111		1111111	
m718	INYPHADPNRV	PKFEFDTREPKD:	IAVFADAIPKLV	DVGVQIPESW	VRDKLVIPD	VOEGEA
	220	230	240	250	260	270
	420	430 440	0 450	460	470	)
a718.pep	VLVRQVPDNPV	NRTALAALSAHT				
		111111111111				
m718	VLVRQVPDNPVI	NRTALAALSAHT	PSKATGRHOEI	LDGALDDALVI	EPDFNSOLN	PMVROA
	280	290	300	310	320	330
	480	490 500	510	520		
a718.pep	VAALNACNSYE	EADAALNALYPNI	LDNAKLRTYMQQ		DHARAX	
m718	VAALNACNSYEI	EADAALNALYPNI	LDNAKLRTYMQQ	ALFISDILGQ	DHARAX	
	340	350	360	3.70	380	

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2423>: m718-1.seq 1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC

1	ATGGAGCCGA	TAATGGCAAA	AAAGAACAAT	AAAACTAAAA	TCCAAAAGCC
51	CGAAGCTGCA	TTGCAGACGG	ACGTGGCTCA	AATTACGGCG	ACCGGTCGGG
101	TTATCGCCGA	GCATCCGTCC	AATTTTATTA	CGCCGCAAAA	GATGCGGGCC
151	CTCTTCGAGG	ACGCAGAAAG	CGGCGACATC	CGCGCCCAAC	ACGAGCTTTT
201	CGCGGACATT	GAGGAGCGCG	ACAGCGACAT	CGCGGCAAAT	ATGGGGACGC
251	GCAAACGCGC	GCTGCTGACG	CTCAACTGGC	GCGTCGCCCC	GCCGCGAAAT
301	GCGACGCCCG	AAGAAGAAAA	GCTGTCCGAC	CAAGCCTACG	AAATGATGGA
351	CAGCCTGCCT	ACCCTCGAAG			
401	GGCACGGATT	TTCTGCGTTG	GAGGTCGAGT	GGGTATTTTC	AGACGGCCTT
451	TACCTACCCC	GAAACTTTAT	CCACCGCCCG	CAAAGCTGGT	TCAAATGGGA
501	CAAAGACAAC	GGGCTGCTGC	TGCGTACCCG	CGAAAATCCG	GAAGGCGAAG
551	CGTTGTGGCC	GCTGGGCTGG	GTCGTTCATA	CCCAAAAATC	GCGCAGCGTC
601	CAGCAGGCGC			CTTTCCTGGC	
651	CAAACACTAC	GCCGTCCACG	ATTTTGCCGA	GTTTTTGGAG	CTGTACGGCA
701	TGCCCATCCG	TATCGGCAAA		GCGCAACCAA	
751	AACACCCTGC	TTCGAGCGGT		GGTCACAACG	
801		GGTATGGAAA		CAACGCGGCA	
851	CGGCAACCAG			CCGACTGGTG	
901	GCGGCGCGGC	TGATTTTGGG		ACCAGCGGTG	
951		AACGCGCTGG			
1001	TGCTGGTGTC		CAGGTGGCGC		
1051	ATCGGACCGT	TCCTGCAAAT		CATGCCGACC	
1101	GCCGAAATTT				
1151	CCGACGCTAT		GTGGATGTCG		CCCCGAAAGC
1201	TGGGTGCGCG		CATTCCAGAT		
1251		CAGGTACCGG			GCATTGGCGG
1301		CCACACCGTA			GCATCAGGAA
1351	ATATTGGACG	GCGCGTTGGA	TGACGCGCTG	GTTGAGCCCG	ATTTCAATTC
1401	TCAGCTCAAC	CCGATGGTGC	GTCAGGCGGT	TGCCGCACTT	AATGCTTGCA
1451		GGAGGCAGAT		ATGCGCTTTA	TCCGAATTTG
1501	GACAACGCGA	AACTGCGTAC	CTATATGCAG	CAGGCCTTGT	TTATCAGCGA
1551	TATTTTGGGA	CAAGACCATG	CCCGCGCCTG	A	•

### This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>: m718-1.pep.

- 1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA 51 LFEDAESGDI RAQHELFADI EERDSDIAAN MGTRKRALLT LNWRVAPPRN 101 ATPEEEKLSD QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDGL
- 151 YLPRNFIHRP QSWFKWDKDN GLLLRTRENP EGEALWPLGW VVHTQKSRSV 201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
- 251 NTLLRAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQMADWCEKS 301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

m718-1

```
351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
          WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
          ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNI.
          DNAKLRTYMO QALFISDILG ODHARA*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2425>:
a718.seq
          ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
          CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
      51
          TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
     101
     151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
     201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAT ATGGGGACGC
     251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
     301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
     351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
     401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
          TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
     451
     501 CAAAGACAAC GGGCTGCTGC TGCGTACCCG CGAAAATCCG GAAGGCGAAG
     551 CGTTGTGGCC GCTGGGCTGG GTCGTTCATA CCCAAAAATC GCGCAGCGTC
     601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
     651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTTGGAG CTGTACGGCA
          TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
     751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTCACAACG CGGCAGGCAT
          CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
     851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
     901 GCGGCGCGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
    951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACGAMAAA CAGGTGGCGC
          TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
    1051 ATCGGACCGT TCCTGCAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
    1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
         CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCGAAAGC
    1151
    1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
    1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
    1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
          ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
    1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
    1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
    1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A
This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:
a718.pep
         MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
      51 LFEDAESGDI RAQHELFADI EERDSDIAAN MGTRKRALLT LNWRVAPPRN
         ATPEEEKLSD QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDGL
     101
     151 YLPRNFIHRP QSWFKWDKDN GLLLRTRENP EGEALWPLGW VVHTQKSRSV
     201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
     251 NTLLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMADWCEKS
         AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
     301
     351 IGPFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
     401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHOE
    451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*
a718/m718-1 99.0% identity in 526 aa overlap
                              20
                                        30
            MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI
a718.pep
            MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI
m718-1
                    10
                              20
                                        30
                                                  40
                    70
                              80
                                        90
                                                100
            RAQHELFADIEERDSDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP
a718.pep
            m718-1
            RAQHELFADIEERDSDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP
                    70
                              80
                                        90
                                                100
                                                          110
                             140
                                       150
                                                160
            TLEDLIMDLMDAVGHGFSALEVEWVFSDGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENP
a718.pep
```

TLEDLIMDLMDAVGHGFSALEVEWVFSDGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENP

160

170

150

a718.pep	190 EGEALWPLGWVVHTQ					
m7181	EGEALWPLGWVVHTQ 190					
a718.pep m718-1	250 YGAGATKEEKNTLLR             YGAGATKEEKNTLLR			111111111111111111111111111111111111111	:::	111111
M713 1	250	260 320	270. 330	280	290 350	300
a718.pep	AARLILGQTLTSGAD	GKSSTNALGI	NIHNEIRRDL	LVSDAKQVAÇ 	TITSQIIGP	FLOINYP
m718-1	AARLILGQTLTSGAD 310	GKSSTNALGI 320	NIHNEVRRDLI 330	LVSDAKQVAQ 340	TITSQIIGPI 350	FLQINYP 360
a718.pep	370 HADPNRVPKFEFDTR	380 EPKDIAVFAI	390 DAIPKLVDVG	400 VQIPESWVRD	410 KLVIPDVQEO	420 GEAVLVR
m718-1						
a718.pep	430 QVPDNPVNRTALAAL:					
m718-1	QVPDNPVNRTALAAL:					
a718.pep	490 NACNSYEEADAALNAI			_		
m718-1						

g719.seq not found yet

g719.pep not found yet

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2427>: m719.seq

. seq					
1	ATGGCAAACG	GGAACATGAA	ACTGTCGTTG	GTGTTAACCG	CCCGAGATGA
51	CGGAGCGAGA	CGGCTACTGG	CTGATACTCA	ACGACAATTA	GATCGTACCG
101	CGAAATCGCG	GGCGCAACTT	GAACGGCAAA	GCCATACTTA	TGCGTTGACC
151	GGCATCCGCT	CAGAAAAACA	GATTCAACGC	GAAATCATGC	TGACACAGGC
201	TGCGTTTAAC	CGTTTGGCGC	GCAGCGGCAA	GGCATCACAA	AATGATTTGG
251	CACGGGCGGC	GGTCGCTACG	CGTAACCGAA	TTCGCGAGCT	GAACGCGGAA
301	CTGAAACAGG	GCACGGGATT	TGCGGACAAG	ATGGGAAAAA	TCGGAAGATT
351	CGGTGCAGCT	GCGGTGGCTG	GTGGCGCGGC	AGCGTATACG	GTGCTTAAGC
401	CTGCTATGGA	CAACAGAAAG	CAGCTTGATG	AGAACATCAA	CCGCGTGTCC
451	AGACAGGCAT	TTATTGAGGA	TAACAGTAAA	TCGGCAGCGT	GGATTGCAAC
501	TGAAGGTGCG	CAACAGATCA	AGGATTTGGC	ACTTGAACTT	GTCGAGAAAA
551	ATGGCGGGAC	CCACGATAAG	GCTTTGGATT	TAATCAGCGG	CATGATGACC
601	ACCGGTCTGA	ATTTTGCCCA	AACCAAGAAT	GAAGCGCAGG	CGGCATATGC
651	TTTTGCACTT	GCCTCAGAAG	GCAGTGGCGA	GGATACGGCA	AAACTGATTA
701	AAACCCTGAA	AGATGGCGGC	ATGAGCGGTA	AAGACCTGCA	ACTCGGGCTT
751	GAGCACGTCT	TGCAATCGGG	TTTAGACGGC	ACTTTCGAGG	TGCGGGATAT
801	GGTTCGGGAG	CTGCCGAGCC	TGCTCTCTGC	CGCGCAACAG	GCAGGGATGA
851	ATGGTGTCGG	CGGTTTGGAC	TACCTGCTCT	CACTCTTACA	ATCTGCGGCG
901	AATAAATCGG	GCAGTCCTGC	CGAAGCGGCG	ACTAATGTGC	AAAATCTTTT
951	GAGTAAAACT	CTGTCGCCTG	ACACGATAGG	TCGTCTGAAG	AAGATGGCAA
1001	ATCCGAATGA	CCCGAAGAAA	GGTGTCGATT	GGATAGGCTC	GGTTGTGCAA
1051	GGCAAGCAAA	ACGGCGAAAA	CGCAGTGCAG	GTGTTGTCCC	GTCTTGCCGA
1101	TGCCATGCTA	GTAAAGGATA	AGCAATACCA	AGATTATAAG	AAACGCGCGG
1151	CTGCAGGCGA	TAAGACGGCG	GCGGAGCAGG	CAAATATGCT	TAAGGGCGCG
1201	CTTTTGGCGC	AACTGCTGCC	TGATTTGCAG	GCAAAACAAG	GTTTGCTGGC
1251	TGCAACGGAT	ATGACGCAAA	TCCGTGAATA	TATGGCTTCG	TTGGCTGGCG

```
1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
     AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
     GTGACGGCAC ATTGCCAAAG GGTTTGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAAA CAACGGTATC CGATTTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GGCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
     GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151
     CGGCCGTGGA GCGGGTCAAT AA
```

#### This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>: m719.pep

```
1
    MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL EROSHTYALT
    GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
 51
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDGG MSGKDLQLGL
251 EHVLQSGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSGSPAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNGK IAKNNEARML
451 SAAAQQEQQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALOALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGGVPQYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
    DGRVIANEVS RYQVAMFGRG AGO*
```

a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2429>: m720.seq

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ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCGG
 51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GGCGGCGTGC
    TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTTT GAAAACGCCT
    TTTTGGTCGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TGCGGTGTTG GCGGTGGATG CGGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTTG GAGTGCGGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTTG TTTGATTTGG ACAAAATTGC CTTTCCCGAT
601 CGGGGCGGAT ACAGTGCAGC GGCGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGGTT GGTCGCCGCG ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCGGTTAA
```

PCT/US99/09346 WO 99/57280

1165

```
851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
          901 TCATCGCTGT TGTCGGTGGC AACGGCATTA ATCGAGGCGC ATGGCGAAGA
          951 GATGACCGCG CCCGATTTGA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
         1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
         1051 TCTGGTGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
         1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
         1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
         1201 ACGATACACC AAATCGCCCA CGAGTTTTAC GGCGATATAG CCCGCGCAGC
         1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA
This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:
     m720.pep
              MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
           51
             GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
              SYRHEADYVD YAGIDITFRE AAEAQEIFVF ENAFLVELEA LIANIDTYRE
          101
          151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
              RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRORF
              DGAAAVADRA AAIPDNLLTG RFSDGLQNRL NRLTAKQVQP VAQAVRLLST
             SSLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
              SGGLTANAVY TEAYQTAESL RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
         401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*
The following partial DNA sequence was identified in N. meningitidis <SEO ID 2431>:
     a720.seq
              (partial)
              GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCGGT
             AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
         101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTTGATT
         151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
             ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
              CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGCA
         301 GGCCGTCTGA ATGCGTTGGT TGCGGCGGTC ATCAACCAAA AGCCGCCGCT
             GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
         401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
             CATATCCACC ACCCCGCGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
         451
         501 TGCAAAATAA
This corresponds to the amino acid sequence <SEO ID 2432; ORF 720.a>:
     a720.pep
              (partial)
              GLONRLNRLT AKQVQPVAQA VRLLSTSSLL SVATALIEAH GEEMTAPDLI
          51 EVNRAMRRRM QAEIAALRAV QTAAAESGGL TANAVYTEAY QTAESLRAAA
         101 GRLNALVAAV INQKPPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
         151 HIHHPAFIKR GTLVNSYAK*
m720 / a720 100.0% identity in 169 aa overlap
                              260
                                       270
                                                          290
                 {\tt SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRLNRLTAKQVQPVAQAVRLLSTSSLL}
    m720.pep
                                              a720
                                              GLQNRLNRLTAKQVQPVAQAVRLLSTSSLL
                                                      10
                                                               20
                              320
                                       330
                                                 340
                                                          350
                 SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
    m720.pep
                 a720
                 SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
                         40
                                  50
                                            60
                                                      70
                    370
                              380
                                       390
                                                 400
                                                          410
                 QTAESLRAAAGRLNALVAAVINQKPPLIVRQAPIDGTIHQIAHEFYGDIARAAELVRLNP
    m720.pep
                 QTAESLRAAAGRLNALVAAVINQKPPLIVRQAPIDGTIHQIAHEFYGDIARAAELVRLNP
    a720
                                 110
                                           120
                                                   130
                                                              140
```

HIHHPAFIKRGTLVNSYAKX m720.pep

430

a720

g721.seq not found g721.pep not found

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2433>:

```
ATGTCCAAAA ATGCACAAAA AACCCTACTT GCCGTGTGCA GTTTCGAGGT
  1
  51
     GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTTCGCG
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
 151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
     TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA
351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT
     AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC
601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCGCGC AGCTGGCGGA
651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
     GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA
851 AAGGCGTATT GAAACAGCCG GGCGGCTTGG CATTTTTGAC CGGCTTTATT
901 GAAAACGCCC AGCCGGTCGC TGCACTGGCA GGCTCGCAAA CGGGCGGCAA
     AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG
1001 CAAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
1051 GAAGGTAAGT AA
```

# This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>: m721.pep

```
1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51 NGHDVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAAASA QILKPETEQN PMKELLQQLF DLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLKQP GGLAFLTGFI
301 ENAQPVAALA GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2435>:

a721.seg ATGTCCAAAA ATGCACAAAA AACCCTACTT GCCGTGTGCA GTTTCGAGGT 1 51 GCAGCCAAAA GACGGGCGAA TCCAACTGCT GCCATATGGC GAATTTCGCG 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA 151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT 201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG 251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTCGCGC AGCTGGCGGA 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT 701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG AAGGCGTATT GAAACAGCCG GGCGGCTTGG CATTTTTGAC CGGCTTTATT 901 GAAAACGCCC AGCCGGTCGC TGCACTGGCA GGCTCGCAAA CGGGCGGTAA 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG 1001 CAAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC

WO 99/57280

1167

```
GAAGGTAAGT AA
This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:
    a721.pep
             MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
          1
             NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
         51
             FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
         101
             MDEVLAAASA QILKPETEQN PMKELLQQLF GLPDAGEEEL KAALSALVEA
             KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
             AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
             ENAQPVAALA GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
         301
         351
             EGK*
          99.2% identity in 353 aa overlap
a721/m721
                       10
                                20
                                        30
                                                 40
                MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN
    a721.pep
                MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN
    m721
                       10
                                20
                                        30
                                                 40
                                                          50
                                                                   60
                       70
                               80
                                        90
                                                100
                                                         110
                                                                  120
    a721.pep
                SSRNQLVVDYEHXTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR
                SSRNQLVVDYEHQTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR
    m721
                       70
                               80
                                        90
                                                100
                      130
                               140
                                       150
                                                160
                                                         170
                                                                  180
                YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAAASAQILKPETEQNPMKELLQQLF
    a721.pep
                YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAAASAQILKPETEQNPMKELLQQLF
    m721
                      130
                               140
                                       150
                                                160
                                                                  180
                      190
                               200
                                       210
                                                220
               GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI
    a721.pep
                 DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI
    m721
                      190
                               200
                                       210
                                                220
                                                         230
                                                                  240
                      250
                               260
                                       270
                                                280
                SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGVLKQPGGLAFLTGFI
    a721.pep
                SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAKGVLKQPGGLAFLTGFI
    m721
                      250
                               260
                                       270
                                                280
                                                         290
                                                                  300
                               320
                                       330
                                                340
                                                         350
               ENAQPVAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKESEGKX
    a721.pep
                m721
               ENAQPVAALAGSQTGGKAPDERVAALTAEEAAAAKMLGMSGEEFVKIKESEGKX
                      310
                               320
                                       330
                                                340
    g722.seq not found yet
    q722.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2437>:
    m722.seq
             GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
          1
             TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
             ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
             CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
             TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GAGCCGCCGC AATCCTAĆCA
        201
             CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
```

GACGACCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG

CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

251

```
401 AGCCGGGCG GGCCGCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCCGCCG GTGTGGCCAC CGAATGCCG CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCAA TTAATGTAAC GGAGATGCCG
1051 TCATGA
```

### This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

```
m722.pep
```

```
1 VFETPTFEQI RERILRDTKS LWPDADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTVQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2439>:

```
a722.seq
```

```
GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
     TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
 51
     ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
     CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCGTTACG ACTATAAAAA CTGGGCGTTG
 601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTCGACA CCCTGATCCC CGGCGACGGC
     CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
     CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001
     ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
     TCATGA
1051
```

### This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

#### a722.pep

```
1 VFETPTFEQI RERILRDTKS LWPDADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTVQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*
```

```
q723.pep not found yet
```

g724.pep not found yet

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2441>:

```
m723.seq
         ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
      1
         AGTGATCACG CCCGAACACC TTATTTTTAC CGTTTACAAA CACAATACCG
     51
         TCTTCGCCCG CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
     101
     151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
     201 GGTTGCGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
     251 TAGCGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
     301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
     351 CCACCAGCGC GGTTTGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
     401 CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
     451 CTCAACCGTC GCGTATGCCA TTACTCGACC GCCTTGCGTT GCAGCATAGG
     501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
         CTTCGCGCCA GCCGCCGTCA AACAGCAGGC CGCCGCGCCA AAATTCTTTG
         CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
     651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
    701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTCAGCATT
    751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
    801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTTCGGCG GTTTCTGGTT
    851 TGTTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
    901 CGCATTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep

1 MRPKPRFRRS VIACSISVIT PEHLIFTVYK HNTVFARGHF FAAIIHAQLH
51 FAFGHSTQQV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RCVCCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGAAVSA VSGLLLVFAM MTPCFRRRRI
301 RI*

a723.seq not found yet

a723.pep not found yet
```

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
      ATGAGTTTGAGTAAATTGGCGAAAAAAACGGCACAAACTGCTAAAAATATCGGCGAAACC
     TACTCAAACTCATTTAACCGCTTTTTTTGCCGTGTTTGACGATTTTTATAGCCGCTTTGG
а
      M S L S K L A K K T A Q T A K N I G E T
      \tt CTGCGCGGGCCTTTCGGGGAAAAATCACGCTGGTGGTGTCGTCCGAGCCGATACAGCGC
    GACGCGCGCGGAAAGCCCCTTTTTAGTGCGACCACCACAGCAGGCTCGGCTATGTCGCG
      L R A A F R G K I T L V V S S E P I Q R
а
      \tt GTGCAGTTGAGCGGCTTGGCCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
   121 ------ 180
      {\tt CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAACTTGTAAACGTCCTTATG}
      V Q L S G L.A D E T L Q D L E H L Q E Y
а
      GGCTTTGCCAGCCATCCGCCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
   181 ------ 240
      \tt CCGAAACGGTCGGTAGGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCCGTTA
      G F A S H P P D G S E A V V I P L G G N
```

	0.41	ACTTCGCACGGTGTGATTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
a	241	TGAAGCGTGCCACACTAACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTTGGAATTC T S H G V I V C S Q H G S Y R I K N L K -
		CCCGGCGAGACGCGATTTTTAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
a	301	GGGCCGCTCTGCCGCTAAAAATTAGTACTCCCACGTTTTTAGCACTAATTCGTTCCGTTT  P G E T A I F N H E G A K I V I K O G K -
۵		ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAAACAATACGAGGTTAATGCG
	361	TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTTATGCTCCAATTACGC
a		I I E A D C D V Y R V N C K Q Y E V N A -
	421	GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCAGTGTTGACGGCGCAA+++ 480 CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACTGCCGCGTT
a		ATDAKFNAPLVETSAVLTAQ
	481	GGCCAAATCAACGGCAACGGCGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
a		CCGGTTTAGTTGCCGCCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAAATCG G Q I N G N G G M A V E G G D G A T F S -
	541	GGCGATGTTAACCAAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
a		CCGCTACAATTGGTTTGCCCGCCGTCGAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA G D V N Q T G G S F N T D G D V V A G N -
	601	ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
a	901	TATAGCAACGCGGTCGTGGGCGTATGGCTGTCGTAGCCGCCGTTTTGGAATGGCCGCCCTT  I S L R Q H P H T D S I G G K T L P A E -
		CCGGCATAG
2	661	GGCCGTATC  P A * -
a Enz	vmes t	hat do cut: NONE
Enz	ymes t	hat do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI SphI XbaI XhoI
This corr	espond	Is to the amino acid sequence <seq 2444;="" 724="" id="" orf="">:</seq>
m72	1 1	MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
	101	LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK PGETAIFNHE GAKIVIKQGK IIEADCDVYR VNCKQYEVNA ATDAKFNAPL
	201	VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN ISLRQHPHTD SIGGKTLPAE PA*
	wing p	partial DNA sequence was identified in N. meningitidis <seq 2445="" id="">:</seq>
	1	ATGAGTTTGA GTAAATTGGC GAAAAAAACG GCACAAACTG CTAAAAATAT CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
	101	CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
	151 201	CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
	251	GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
	301	CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
	331 401	GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTACCGG GTTAACTGCA AACAATACGA GGTTAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
	451	GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```
501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
         551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
         601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
         651 ACCGGCGGAA CCGGCATAG
This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:
     a724.pep
              MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VOLSGLADET
              LODLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSO HGSYRIKNLK
              PGETAIFNHE GAKIVIKQGK IIEADCDVYR VNCKQYEVNA ATDAKFNAPL
              VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
         151
              ISLROHPHTD SIGGKTLPAE PA*
a724/m724 100.0% identity in 222 aa overlap
                        10
                                 20
                                           30
                                                    40
                                                             50
                                                                       60
                 MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY
    a724.pep
                 MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLOEY
    m724
                        10
                                 20
                                           30
                                                    40
                                                             50
                                                                       60
                        70
                                 80
                                           90
                                                   100
                                                            110
                                                                      120
                 GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK
    a724.pep
                 GFASHPPDGSEAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK
    m724
                        70
                                 80
                                           90
                                                   100
                                                            110
                                                                      120
                       130
                                140
                                          150
                 I IEADCDVYRVNCKQYEVNAATDAKFNAPLVETSAVLTAQGQINGNGGMAVEGGDGATFS
    a724.pep
                 IIEADCDVYRVNCKQYEVNAATDAKFNAPLVETSAVLTAQGQINGNGGMAVEGGDGATFS
    m724
                       130
                                140
                                          150
                                                   160
                                                            170
                                                                      180
                                200
                                          210
                GDVNOTGGSFNTDGDVVAGNISLROHPHTDSIGGKTLPAEPAX
    a724.pep
                 GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX
    m724
                       190
                                200
                                          210
    q725, seq not found yet
    g725.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2447>:
    m725.seq
             ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
             GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
          51
             TTGAGCCTGC CAGCACCGGC GGCGTATGCG GACGTTATCA GGATACCGCC
         101
             GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
             GCGGCAAGGC GGCATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
             GCGCTGTTCG CCGCCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
         251
             CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
         301
             GCAAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
             ACACCTGCGG GTTGGAAAAT GACCGCTACC CCGAACGCAC CGACAATCCC
             GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
             GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTTACGAC CCGCAATCCG
             CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA
This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:
    m725.pep
             MVRTVKSYNG EADDLAGQIH TLPAVWVTYG GSKVEPASTG GVCGRYQDTA
           1
             EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLL DGQRLGFADS
          51
             RGLVPKAVRA IANHVLVQNA AVSIYAVEYA IRFNTCGLEN DRYPERTDNP
             DDPNHIFTKY QGTLSEPWPD FEGLDGKIYD PQSADEIPVN LTLKDKQ*
```

```
a725.seq not found yet
     a725.pep not found yet
     g726.seq not found yet
     g726.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEO ID 2449>:
     m726.seq
              ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
            1
              CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
           51
          101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
          151 GTTTTAACCC CGCCGCGCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
          201 ATGGAAAATC AGCAAAGCCG CCGCCGCC CCGTTTCGCC AAACAAAAA
          251 CCGCCTTGGC ATTCCGCCTC GCGGAAAAGG CGGACGAACT CAAAAACAGC
          301 CTCTTGGCGG GCTATCCCCA AGTGGAAATC GACAGCTTTT ACAGGCAGGA
          351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
          401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
              AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCCG GCGCGATTAT
              CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
              CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
          601 GGCTGA
This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:
            1 MTIYFKNGFY DDTLGGIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
           51 VLTPPRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
          101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDVLIE
          151 KVIEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
          201
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2451>:
     a726.seg
           1 ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
           51 CCCCGAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
          101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
          151 GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
          201 ATGGGAAATC GGCGAAGCCG CTGCCGCCGC CCGTTTCGCC GAACAAAAA
          251 CCGCCACGGC ATTCCGCCTC GCGGCAAAGG CGGACGAACT CAAAAACAGC
          301 CTCTTGGCGG GCTATCCCCA AGTGGAAATC GACAGCTTTT ACAGGCAGGA
          351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
              TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
              AAAGTTGTCG AAAAATCCGC CCGCCTGGCC GTTGCCGCCG GCGCGATTAT
              CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
              CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
          601
              GGCTGA
This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:
     a726.pep
           1
              MTIYFKNGFY DDTLGSIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
           51 VLTPPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
          101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDVLIE
          151 KVVEKSARLA VAAGAIIGKR QQLEDKLNTI ETAPGLDALE KEIEEWTLNI
          201
              G*
a726/m726 95.5% identity in 201 aa overlap
                                             30
                                                       40
                                                                 50
                 MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTPPRPSEY
     a726.pep
                 m726
                 MTIYFKNGFYDDTLGGIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTPPRPSDY
                         10
                                   20
                                             30
                                                       40
                                                                50
```

a726.pep m726	70 80 90 100 110 120 HEWDGKKWEIGEAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA         : ::       :
a726.pep m726	130 140 150 160 170 180 LARQADNNAPTPMLAQIAAARGVELDVLIEKVVEKSARLAVAAGAIIGKRQQLEDKLNTI !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
a726.pep m726	190 200 ETAPGLDALEKEIEEWTLNIGX
g727.seq	not found yet
g727.pep	not found yet
The following p	artial DNA sequence was identified in N. meningitidis <seq 2453="" id="">:</seq>
1	ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51	CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101	CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151	GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAACT
201	GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251	TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301	GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351	TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401	CTTAA
This correspond	s to the amino acid sequence <seq 2454;="" 727="" id="" orf="">:</seq>
m/2/.pep	MNLVKLLANN WOPIAIIALV GTGLAVSHHO GYKSAFAKQO AVIDKMERDK
51	AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101	DLCKIPFPPD SRNPNTGFRL FSPQIPPNFT QIPP*
The following p	artial DNA sequence was identified in N. meningitidis <seq 2455="" id="">:</seq>
a727.seq	NUCLEUR CO. UCALE COCCUE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE COCCUE DE C
1 51	ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
101	CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151	GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201	GGCGCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
251	TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301	AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351	CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401	CCCTCGGCTA CGGAAATTAA
This correspond	s to the amino acid sequence <seq 2456;="" 727.a="" id="" orf="">:</seq>
a727.pep	
1	MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51	AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101	KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN*
a727/m727 83	.2% identity in 119 aa overlap
a727.pep	10 20 30 40 50 60 MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
a/2/.pep	
•	

WO 99/57280 PCT/US99/09346

1174

```
MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
m727
                                   30
                                            40
                                                             60
                  70
                           80
                                   90
                                           100
                                                     110
                                                            119
           YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
a727.pep
           YARELELARAEAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPPDSRNPNTGF
m727
                           80
                                   90
                                            100
         120
                  130
                           140
           IDGFGHHGLQLYKRALGYGNX
a727.pep
           RLFSPOIPPNFTQIPPX
m727
          120
                   130
```

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2457>: q728.seq

```
ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
      TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
  51
     TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
     GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
 201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
 251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
 301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
 351
     GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
     TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
 451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
 501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
 551 ACGGTTCGGT ATTTGATGCG GCGGGGCGCG GGAAAATCGG GGAAGATGTT
 601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
 651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
 701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
 751 ATGCGGGAAT TGATGCCCCG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
 801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
 851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
 901 ATTGCACAAT CTTCGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
     TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
     TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1051
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA
```

#### This corresponds to the amino acid sequence <SEO ID 2458; ORF 728>; g728.pep

```
1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
 51 AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLALAIRLS
    RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFVNAEYL
101
    YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
    YEHCLGCYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYON
251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2459>: m728.seq

```
ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
    GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
351
    TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
```

501	CGGGGAAAAT	TATGAAACGA	CAGGAGAATA	TCGGGTTGTT	TGGCAACCAG
551	ACGGTTCGGT	ATTTGATGCG	GCGGGGCGCG	GGAAAATCGG	GGAAGATGTT
601	TATGAGCATT	GCCTCGGGTG	TTATCAGATG	GCCCAGGTAT	ATTTGGCGAA
651	ATACCGGGAT	GTCGCGAATG	ACGAGCAGAA	GGTTTGGGAC	TTCCGCAAAG
701	AGAGCAACCG	AATTGCGTCG	GACTCGCGCA	ATTCTGTGTT	TTATCAGAAT
751	ATGCGGGAAT	TGATGCCCCG	AGGGATGAAG	GCGAACAGTC	TTGTGGTCGG
801	CTATGATGCG	GACGGTCTGC	CGCAAAAAGT	CTATTGGAGT	TTCGACAATG
851	GAAAAAAACG	CCAGAGTTTC	GAATATTATT	TGAAAAACGG	AAATCTTTTT
901	ATTGCACAAT	CTTCGACGGT	AGCATTGAAA	GCGGATGGCG	TAACGGCGGA
951	TATGCAGACC	TATCATGCGC	AACAGACGTG	GTATTTGGAT	GGCGGGCGGA
1001	TTGTCCGCGA	AGAGAAACAG	GGAGACAGAC	TGCCTGATTT	TCCTTTGAAC
1051	TTGGAAAATT	TGGAAAAAGA	GGTGCGCCGT	TATGCAGAGG	CTGCGGCGAG
1101	ACGTTCGGGC	GGCAGGCGCG	ACCTTTCTCA	CTGA	

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>: m728.pep

1	MFKKFKPVLL	SFFALVFAFW	LGTGIAYEIN	PRWFLSDTAT	EVPKNPNAFV
51	AKLARLFRNA	DRAVVIVKES	IRTEENLAGT	VDDGPLQSEK	DYLALAIRLS
101	RLKEKAKWFH	VTEQEHGKEV	WLDYHIGEGG	LVAVSLSQRS	PEAFVNAEYL
151	YRNDRPFSVN	VYGGTVHGEN	YETTGEYRVV	WQPDGSVFDA	AGRGKIGEDV
201	YEHCLGCYQM	AQVYLAKYRD	VANDEQKVWD	FRKESNRIAS	DSRNSVFYQN
251	MRELMPRGMK	ANSLVVGYDA	DGLPQKVYWS	FDNGKKRQSF	EYYLKNGNLF
301	IAQSSTVALK	ADGVTADMQT	YHAQQTWYLD	GGRIVREEKQ	GDRLPDFPLN
351	LENLEKEVRR	YAEAAARRSG	GRRDLSH*		

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from N. meningitidis menA with menB

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from N. gonorrhoeae:

m728 / g728

	10	20	30	40	50	60
m728.pep	MFKKFKPVLLSFFA					
		111111111			111111111	111111
g728	MFKKFKPVLLSFFA	LVFAFWLGTG	IAYEINPRWF	LSDTATEVPE	NPNAFVAKLA	RLFRNA
	10	20	30	40	50	60
	70	80	90	100	110	120
m728.pep	DRAVVIVKESIRTE					
	111111111111111111111111111111111111111					
g728	DRAVVIVKESMRTE				KAKWFHVTEÇ	EHGEEV
	70	80	90	100	110	120
	130	140	150	160	170	180
m728.pep	WLDYHIGEGGLVAV				TVHGENYETT	GEYRVV
				,,,,,,,,,,	1:[][[][]	
g728	WLDYYIGEGGLVAV					GEYRVV
•	130	140	150	160	170	180
	190	200	210	220	230	240
m728.pep	WQPDGSVFDAAGRG					
g728	WQPDGSVFDAAGRG					SNRIAS
	190	200	210	220	230	240
	250	260	270	280	290	300
m728.pep	DSRNSVFYQNMREL					
g728	DSRDYVFYQNMREL					KNGNLF
	250	260	270	280	290	300
	310	320	330	340	350	360
m728.pep	IAQSSTVALKADGV					
			111111111111111111111111111111111111111	:	1111111:1	1111

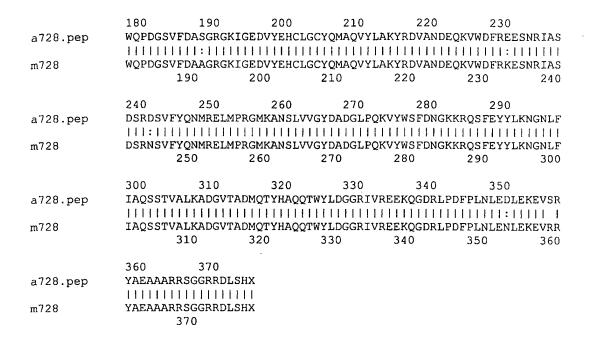
q728

IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR

```
320
                                     330
                                               340
                   370
            YAEAAARRSGGRRDLSHX
m728.pep
            YAEAAARRSGGRRGLSHX
\alpha728
                  370
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2461>:
     a728.seq
              ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
              TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
          51
              TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAAACTT
         101
             GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
         151
         201 GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
         251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
         301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGGAAGAGGT
             TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
         401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
             GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
              TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
              TATTTGATGC GTCGGGGCGC GGGAAAATCG GGGAAGATGT TTATGAGCAT
              TGCCTCGGGT GTTATCAGAT GGCCCAGGTA TATTTGGCGA AATATCGGGA
              TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
              GGATTGCGTC GGACTCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
              TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
              GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
              GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
         851
              TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
         901
         951
              CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
        1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
              TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCGGG
        1051
              CGGCAGGCGC GACCTTTCTC ACTGA
This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:
    a728.pep
              MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
           1
              ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLOSEKDYL ALAVRLSRLK
          51
              EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VSLSORSPEA FVNAEYLYRN
              DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
              CLGCYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
              LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
             SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
             LEKEVSRYAE AAARRSGGRR DLSH*
         351
    a728 / m728
                   96.3% identity in 377 aa overlap
                        10
                                  20
                                           30
                                                     40
                 MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
    a728.pep
                 MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
    m728
                                  20
                        10
                                           30
                                                     40
                                                              50
                                                                        60
                           70
                                     80
                                              90
                                                      100
                 DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV
    a728.pep
                 DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEOEHGKEV
    m728
                        70
                                  80
                                           90
                                                    100
                                                             110
                                                                      120
                                    140
                                             150
                                                       160
                 WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
    a728.pep
                 WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
    m728
                       130
                                 140
                                          150
                                                    160
                                                             170
                                                                      180
```

PCT/US99/09346 WO 99/57280

1177



#### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2463>: q729.seq

```
ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
     ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
  51
 101 TTGCGGAAAC CTTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
 151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
 201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACAGCC GTATTGAACA
     GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCCTGCCC
     ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCgg
     caaTGTCAGC AGCAGCTACA ATGTCGGACT GGGTGCGGca tCTTACGAAC
     TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
     tATTTTGCCA GCGTTGCCAA CcgcGATGCG GCACATTTGa ttCtGATTGC
     CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
 501
 551 CTTTGGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
 601 GAATTGCGGT ACAAGGCAGG CGTGATTTCC GCCGTCGCCC TGCGCCAGCA
     GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCa
     GCCGCGAACA GGCGCGCAAT GCCTTGGCAA CCTTGATTAA CCGTCCGATA
     CCCGAagaCC TGCCCGCCGG TTTGCCGTTG GACAagcAGT TTTTTGTTGA
 751
 801 AAAACTGCCT GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGACA
 851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
 901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
 951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GGCGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATTT TTACTTGGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAAA ACTGCGCCAA CAGGCACAAA TTGTTGCCTA
1101 TGAATCCGCC GTCCAATCCG CCTTTCAAGA CGTGGCAAAC GCATTGGCGG
1151
     CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
     GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
     ATCCGGCGCG CTCGATTTGC TCGATGCGGA ACGCATCAGC TATTCGGCGG
     AAGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
     TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1351
1401
     ATAA
```

#### This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>: g729.pep

- MNTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFQN DTSVSSIRAV 1 51 DLGWHDYFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP
- 101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEAALQG
- 151 YFASVANRDA AHLILIATVA KAYFNERYAE KAMSLAORVL KTREETYKLS

```
201 ELRYKAGVIS AVALRQQEAL IESAKADYAH AARSREQARN ALATLINRPI
251 PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVGTGSV ELGGLFKSGT GVWAFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERIS YSAEGAALSA QLTRAENLAD
451 LYKALDGGLK RDTQTGK*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2465>: m729.seq

```
ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTTGC
  51 ATTGTCTGCC TGCACCATGA TTCCCCAATA CGAGCAGCCC AAAGTCGAAG
 101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGCGCCGTC
 151 GATTTAGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
 201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
 251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
 301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
 351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
     TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
     TATTTCGCCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC
 501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTACGCCGAA GAAGCGATGT
 551 CTTTGGCGCA ACGTGTTTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
 601 GAATTACGTT ACAAGGCAGG CGTGATTTCC GCCGTCGCCC TACGTCAGCA
 651 GGAAGCCCTG ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
 701 GCCGCGAACA GGCGCGCAAT GCCTTGGCAA CCTTGATTAA CCAACCGATA
 751 CCCGAAGACC TGCCTGCCGG TTTGCCGCTG GACAAGCAGT TTTTTGTTGA
 801 AAAACTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
 901 GCACGCGCCG CCTTTTTCCC ATCCATCCGC CTGACCGGAA CCGTCGGTAC
 951 GGGTTCTGCC GAATTGGGTG GGTTGTTCAA AAGCGGCACG GGCGTTTGGT
1001 CGTTCGCGCC GTCTATTACC CTGCCGATTT TTACCTGGGG TACGAACAAG
1051 GCGAACCTTG ATGTAGCCAA GCTGCGCCAA CAGGTACAAA TCGTTGCCTA
1101 TGAATCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGC CTGCGTTACA AGCACGGCGT
1251 ATCCGGCGC CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATGCGGCGG
     AGGGTGCGGC TTTGTCGGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351
     TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401
     ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2466; ORF 729>: m729.pep

```
1 MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDYFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNNLLP
101 TLAANANDSR QGSLSGGNVS SSYKVGLGAA SYELDLFGRV RSSSEAALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQQEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGTVGTGSA ELGGLFKSGT GVWSFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QVQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERSS YAAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*
```

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. meningitidis menA with menB

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from N. gonorrhoeae:

```
m729 / g729 95.7% identity in 467 aa overlap
```

	10	20	30	40	50	60
m729.pep	MDTTLKTTLTSV					
	1:111111111					
g729	MNTTLKTTLTSV	<u>AAAFALSA</u> CTMI	PQYEQPKVEV	AETFQNDTSV	SSIRAVDLGW	HDYFAD
	10	20	30	40	50	60

m729.pep	70 PRLQKLIDIALERNT	80 SLRTAVLNSI	90 EIYRKQYMIER	100 NNLLPTLAAN	110 ANDSRQGSLS	120 GGNVS
g729		SLRTAVLNSE 80	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		 ANGSRQGSLS 110	IIIII GGNVS 120
m729.pep	130 SSYKVGLGAASYELD	140 1.FGRVRSSSF	150	160	170	180
g729	:          SSYNVGLGAASYELD		: :AALQGYFASV	 ANRDAAHLIL		 ERYAE
	130 190	140 200	150 210	160 220	170 230	180 240
m729.pep	EAMSLAQRVLKTREE:	111111111	111111111	[		HIII
9123	190	200	210	220	230	240
m729.pep	250 ALATLINQPIPEDLP	11111111				
g729	ALATLINRPIPEDLP. 250	AGLPLDKQFE 260	VEKLPAGLSSI 270	EVLLDRPDIRA 280	AAEHALKQAN 290	ANIGA 300
m729.pep	310 ARAAFFPSIRLTGTV	320 GTGSAELGGL	330 FKSGTGVWSF7	340 APSITLPIFTW	350 IGTNKANLDV <i>I</i>	360 AKLRQ
g729		IIII:IIIII GTGSVELGGL 320	FKSGTGVWAF <i>I</i> 330			AKLRQ 360
m729.pep	370 QVQIVAYESAVQSAF	380 DVANALAAR	390 EOLDKAYDALS	400 SKOSRASKEAI	410	420 SVSGA
g729	1:                         QAQIVAYESAVQSAFQ	111111111	EQLDKAYDALS			IIIII GVSGA
	430	440	390 450	400 460	410	420
m729.pep	LDLLDAERSSYAAEGA		111111111	11111111	11	
<b>3</b> · · · · ·	430	440	450	460	****	

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2467>:

a729.seq ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC ATTATCCGCC TGCACCATGA TTCCCCAATA CGAGCAGCCC AAAGTCGAAG 101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGCGGTC 151 GATTTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT 201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA 251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC 301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG 351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC 401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC 451 TATTTCGCCA GCACCGCCAA CCGCGATGCG GCACATTTGA GCCTGATTGC 501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT 551 CTTTGGCGCA ACGTGTTTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC 601 GAATTACGTT ACAAGGCAGG CGTGATTTCC GCCGTCGCCC TACGTCAGCA 651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA 701 GCCGCGAACA GGCGCGCAAT GCCTTGGCAA CCCTGATTAA CCAACCGATA 751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTTGTTGA 801 GAAGCTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA 851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG GCACGCGCCG CCTTTTTCCC ATCCATCCGC CTGACCGGAA GCGTCGATAC GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GGCGTTTGGT TGTTCGCACC TTCCATTACC CTGCCGATTT TTACCTGGGG TACGAACAAG

1051 1101 1151 1201 1251 1301 1351	TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA AGCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA ATCCGGCGC CTCGACTTGC TCGATGCGGA ACGCAGCAGC AAGGTGCGGC TTTGTCGGCA CAACTGACC GCGCCGAAAA TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC A	GCATTGACCG ACAAAGCCGC AACACGGCGT FATTCGGCGG CCTTGCCGAT
This correspond	ds to the amino acid sequence <seq 2468;="" id="" orf<="" th=""><th>729.a&gt;:</th></seq>	729.a>:
a729.pep 1		OTADSGTRAV
51	DLGWHDYFAD PRLOKLIDIA LERNTSLRTA VLNSEIYRKO	YMIERNNLLP
101 151		RSSSEAALQG KTREETYKLS
201 251	ELRYKAGVIS AVALRQQEAL IESAKADYAH AARSREQARN A	ALATLINQPI
301	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT 1	LPIFTWGTNK
351 401		AYDALSKQSR
451		ZLIKAENDAD
a729 / m7	729 98.1% identity in 467 aa overlap	
	10 20 30 40	50 60
a729.pep	MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDT	CADSGIRAVDLGWHDYFAD
m729	MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDT	ADSGIRAVDLGWHDYFAD
	10 20 30 40	50 60
a729.pep	70 80 90 100 PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTI	110 120
m729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTI 70 80 90 100	LAANANDSRQGSLSGGNVS 110 120
a729.pep	SSYKVGLGAASYELDLFGRVRSSSEAALQGYFASTANRDAAF	170 180 ILSLIATVAKAYFNERYAE
m729		I SI TATUAKAYENEDYAE
11.723	130 140 150 160	170 180
	190 200 210 220	230 240
a729.pep	EAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQQEALIE 	SAKADYAHAARSREQARN
m729	EAMSLAQRVLKTREETYKLSELRYKAGVISAVALRQQEALIE	SAKADYAHAARSREQARN
	190 200 210 220	230 240
a729.pep	250 260 270 280 ALATLINQPIPDDLPAGLPLDKQFFVEKLPAGLSSEVLLDRE	290 300
		1111111111111111
m729	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRE 250 260 270 280	PDIRAAEHALKQANANIGA 290 300
a729.pep	ARAAFFPSIRLTGSVDTHSAELGGLFKSGTGVWLFAPSITLE	350 360 PIFTWGTNKANLDVAKLRQ
m729		TETWOTHKANI DVAKI BO
E J	310 320 330 340	350 360
	370 380 390 400	410 420
a729.pep	QAQIVAYEAAVQSAFQDVANALTAREQLDKAYDALSKQSRAS  :      :	KEALRLVGLRYKHGVSGA
m729	QVQIVAYESAVQSAFQDVANALAAREQLDKAYDALSKQSRAS	KEALRLVGLRYKHGVSGA
	370 380 390 400	410 420

#### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2469>:

```
GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
      GGCGGTCGCA CTCATACAGC CCGCCCTCGC GGCGGACTTG GCGCAAGACC
  51
     CGTTCATTAC CGATAACACC CAACGGCAGC ACTACGAACC CGGCGGCAAA
 151 TACCACCTCT TCGGcgaCCC GCGCGGCAGC GTTTCCGACC GCACCGGCAA
 201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
 251 AACAGGCGGC AATCCAAGGC AATCTTGGTT ACACCGTCCG CTTTTCCGGA
 301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
 351 AAGCGAAGAA AAAGGCAACG TTGACGACGG CTTTACCGTG TACCGGCTCA
     ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
     GGCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
 501 CGTCAACGGC ACAGCCCGCA GTATCAAACT CAATCCGACC GACACCCGCA
 551 GCATCCGGCA ACGCATATTC GACAACTACA ACAACCTCGG CAGCAATTTC
 601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTCGAGC ACAATGCCAA
 651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TGTCAACGGC GTCGCCGCCG
 701 GCGCGCTCAA CCCCTTTATC AGCGCGGCG AAGCCTTGGG CATAGGCGAC
 751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCGA TGCGCAACAT
 801 CGCCCCTTA CCCGCCGAGG GCAAATTCGC CGCCATCGGC GGCTTGGGCA
 851 GCGCGGCGG CTTTGAAAAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
 901 CAGGAAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
 951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GGCGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG TGGGGATTTT TCTAAATCCT ACACCTGCTC CTTCCACGGC
1051 AGCACCTTGG TCAAAACGGC AGACGGCTAC AAAGCCATTG CCCATATTCA
1101 AGCCGGAGAC CGCGTCCTTT CCAAGGACGA GGCAAGCGGA GAAACGGGAT
1151 ACAAACCCGT TACCGCCCGA TACGGCAATC CGTATCAAGA AACCGTTTAC
1201 ATTGAAGTTT CAGACGGCAT CGGCAACAGC CAAACCCTGA TTTCCAACCG
1251 CATCCACCCG TTTTATTCGG ACGGCAAATG GATTAAGGCG GAAGATTTAA
1301 AAGCGGGAAG CCGGCTGTTA TCCGAAAGCG GCAAAACCCA AACCGTCCGC
1351 AACATCGTTG TCAAACCAAA ACCGCTCAAA GCCTACAATC TGACCGTTGC
1401 CGATTGGCAT ACCTACTTCG TCAAGGGTAA TCAGGCGGAA ACGGAAGGGG
1451 TTTGGGTTCA TAATGATTGT CCGCCTAAAC CAAAACCAAC CAATCATGCC
1501 CAACAAAGAA AAGAAGAAGC TAAAAAACGAT TCTCATCGAA GTGTGGGAGA
1551 TTCCAATCGT GTCGTTCGCG AAGGAAAGCA ATATTTAGAT TCCGACACAG
1601 GAAACCATGT TTATGTAAAA GGAGATAAAG TGGTTATTCT AACTCCTGAT
1651 GGAAGACAGG TAACTCAATT TAAGAACTCG AAAGCCAATA CGTCAAAAAG
1701 GGTAAAAAT GGGAAATGGA CACCAAAATA A
```

### This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

```
9730.pep

1 VKPLRRLTNL LAACAVAAVA LIQPALAADL AQDPFITDNT QRQHYEPGGK
51 YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQQAAIQG NLGYTVRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDDGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIF DNYNNLGSNF
201 SDRADEANRK MFEHNAKLDR WGNSMEFVNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAAIG GLGSAAGFEK NTREAVDRWI
301 QENPNAAETV EALVNVLPFA KVKNLTKAAK PGKAAVSGDF SKSYTCSFHG
351 STLVKTADGY KAIAHIQAGD RVLSKDEASG ETGYKPVTAR YGNPYQETVY
401 IEVSDGIGNS QTLISNRIHP FYSDGKWIKA EDLKAGSRLL SESGKTQTVR
451 NIVVKPKPLK AYNLTVADWH TYFVKGNQAE TEGVWVHNDC PPKPKPTNHA
501 QQRKEEAKND SHRSVGDSNR VVREGKQYLD SDTGNHVYVK GDKVVILTPD
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2471>:

```
m730.seq

1 GTGAAACCGC TGCGCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC
51 GGCGGCCGCA CTCATACAGC CCGCCCTCGC GGCGGACTTG GCGCAAGACC
```

101	CGTTCATTAC	CGATAACGCC	CAACGGCAGC	ACTACGAACC	CGGCGGCAAA
151	TACCACCTCT	TCGGCGACCC	GCGCGGCAGC	GTTTCCGACC	GCACCGGCAA
201	AATCAACGTC	ATCCAAGACT	ATACCCACCA	GATGGGCAAC	CTGCTCATCC
251	AACAGGCAAA	CATCAACGGC	ACAATCGGCT	ACCACACCCG	CTTTTCCGGA
301	CACGGACACG	AAGAACACGC	CCCCTTCGAC	AACCACGCCG	CCGACAGCGC
351	GAGCGAAGAA	AAAGGCAACG	TTGACGAAGG	CTTTACCGTA	TACCGGCTCA
401	ACTGGGAAGG	ACACGAACAT	CATCCCGCCG	ATGCCTACGA	CGGCCCGAAG
451	GGCGGCAATT	ACCCCAAACC	TACGGGCGCA	CGAGACGAAT	ACACCTATCA
501	CGTCAACGGC	ACAGCCCGCA	GTATCAAACT	CAATCCGACC	GACACCCGCA
551	GCATCCGGCA	ACGCATATCC	GACAATTACA	GCAACCTCGG	CAGCAATTTC
601	TCCGACCGCG	CCGATGAAGC	CAACAGAAAA	ATGTTCGAGC	ACAATGCCAA
651	GCTCGACCGC	TGGGGCAACA	GCATGGAGTT	TATCAACGGC	GTCGCCGCCG
701	GCGCGCTCAA	CCCCTTTATC	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC
751	ATACTGTACG	GAACGCGCTA	TGCCATAGAC	AAAGCCGCAA	TGCGCAACAT
801	CGCCCCCTTG	CCCGCCGAGG	GCAAATTCGC	CGTCATCGGC	GGCTTGGGCA
851	GCGTGGCGGG	CTTTGAAAAG	AATACGCGCG	AAGCCGTTGA	CCGGTGGATA
901	CAGGAAAATC	CCAATGCCGC	CGAAACCGTC	GAAGCCGTCT	TCAACGTTGC
951	CGCAGCAGCC	AAAGTCGCGA	AGTTGGCAAA	GGCGGCAAAA	CCAGGGAAGG
1001	CTGCGGTTAG	CGGGGATTTT	GCTGATTCTT	ATAAAAAGAA	ATTGGCTTTG
1051	TCTGATAGTG	CGAGACAGTT	ATATCAAAAT	GCAAAGTATA	GAGAAGCTCT
1101	AGATATACAT	TATGAAGATT	TAATTAGAAG	AAAAACTGAT	GGTTCATCAA
1151	AATTTATTAA	CGGCAGAGAA	ATTGACGCTG	TTACGAATGA	TGCTTTAATA
1201	CAAGCCAAAA	GAACAATTTC	AGCAATAGAT	AAACCTAAAA	ATTTCTTAAA
1251	TCAAAAAAAT	AGAAAGCAAA	TTAAAGCAAC	CATCGAAGCA	GCAAACCAAC
1301	AGGGAAAACG	TGCAGAATTT	TGGTTTAAAT	ACGGTGTTCA	TTCACAAGTT
1351	AAGTCATATA	TTGAATCAAA	AGGCGGCATT	GTTAAAACAG	GTTTAGGAGA
1401	TTAA				

#### This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

This corresponds to the annie acid sequence ADD 15 2472, Old 7505.							
m730.pep							
1	VKPLRRLTNL	LAACAVAAAA	LIQPALAADL	AQDPFITDNA	QRQHYEPGGK		
51	YHLFGDPRGS	VSDRTGKINV	IQDYTHQMGN	LLIQQANING	TIGYHTRFSG		
101	HGHEEHAPFD	NHAADSASEE	KGNVDEGFTV	YRLNWEGHEH	HPADAYDGPK		
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIS	DNYSNLGSNF		
201	SDRADEANRK	MFEHNAKLDR	WGNSMEFING	VAAGALNPFI	SAGEALGIGD		
251	ILYGTRYAID	KAAMRNIAPL	PAEGKFAVIG	GLGSVAGFEK	NTREAVDRWI		
301	QENPNAAETV	EAVFNVAAAA	KVAKLAKAAK	PGKAAVSGDF	ADSYKKKLAL		
351	`SDSARQLYQN	AKYREALDIH	YEDLIRRKTD	GSSKFINGRE	IDAVTNDALI		
401	QAKRTISAID	KPKNFLNQKN	RKQIKATIEA	ANQQGKRAEF	WFKYGVHSQV		
451	KSYIESKGGI	VKTGLGD*					
g730 / m730	g730 / m730 93.0% identity in 344 aa overlap						
<i>5</i>	•	-	20 30	40	50		

VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS g730.pep m730 VKPLRRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS VSDRTGKINVIQDYTHQMGNLLIQQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE g730.pep VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE m730 KGNVDDGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT q730.pep m730 KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT g730.pep DTRSIRQRIFDNYNNLGSNFSDRADEANRKMFEHNAKLDRWGNSMEFVNGVAAGALNPFI DTRSIRQRISDNYSNLGSNFSDRADEANRKMFEHNAKLDRWGNSMEFINGVAAGALNPFI m730 

			•			
				70 28		300
g730.pep	SAGEALO	SIGDILYGTRY <i>A</i>	AIDKAAMRNIAI	PLPAEGKFAAI	GGLGSAAGFEKN	TREAVDRWI
	111111				11111:11111	11111111
m730	SAGEALG				GGLGSVAGFEKN	reavdrwi
		250 2	260 27	70 28	0 290	300
		310 3	320 33	30 34	0 350	360
g730.pep	QENPNAA				FSKSYTCSFHGS'	טסט אממאעגזיו
5 1 - 1	ĪHHH	11111: 11	111:1:11		:	IDVNIADGI
m730	QENPNAA	ETVEAVFNVAA	AAKVAKLAKAA	AKPGKAAVSGD	FADSYKKKLALS	DSARQLYQN
				34		360
		370 3	200 20			
g730.pep	катанто		390 39 390 390 390 390 390 390 390 390 390 390		0 410 YIEVSDGIGNSQ:	420
g/30.pep	1011111112	TODICO BOTODIA	SCHICINEVIA	MIGHEIQEIV.	TTEAPOGTGN2Ö.	LTTSNKTHL
m730	AKYREAL	DIHYEDLIRRK	TDGSSKFINGF	REIDAVTNDAL:	IQAKRTISAIDKI	PKNFLNOKN
		370 3	39 39			420
The following p	partial DNA s	sequence wa	s identified i	in N. mening	gitidis <seq i<="" td=""><td>D 2473&gt;:</td></seq>	D 2473>:
a730.seq						
1	GTGAAACCGC	TGCGAAGACT	CATCAAGCTC	CTTGCCGCCT	GTGCCGTAGC	
51	GGCGGCCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTT	GCGCAAGACC	
101 151	TACCACCTCT	TCCCCCACCC	CAACGGCAGC	CONCORRE	C CGGAGGCAAA C GCACCGGTCA	
201	AATCAACGTCI	ATCCAACACT	· BUBUGGGCAGU	CATCTCCGACC	CTGCTCATCC	
251	AGCAGGCAAA	CATCAACGGC	ACAATCGGCT	' ACCACACCAA(	CTGCTCATCC CTTTTCCGGA	
301	CACGGATACG	AAGAACACGC	CCCCTTCGAC	AACCACGCCG	CCGACAGCGC C	
351	GAGCGAAGAA	AAAGGCAACG	TTGACGAAGG	CTTTACCGTA	TACCGGCTCA	
401	ACTGGGAAGG	ACACGAACAT	CATCCCGCCG	ATGCCTACGA	CGGCCCGAAG	
451	GGCGGCAATT	ACCCCAAACC	TACGGGTGCA	CGCGACGAAT	ACACCTATCA	
501	CGTCAACGGC	ACAGCACGCA	GCATCAAACT	CAATCCGACC	GACACCCGCA	
551	GCATCCGGCA	ACGCATATCC	GACAATTACA	GCAACCTCGG	CAGCAATTTC	
601	TCCGACCGCG	CCGATGAAGC	CAACAGAAAA	ATGTTCGAGC	ACAATGCCAA	
651 701	GCTCGACCGC	TGGGGCAACA	GCATGGAGTT	TATCAACGGC	GTCGCCGCCG	
701 751	ATTA CTCTA CC	CARCCCCTA	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC TGCGCAACAT	
801	CCCCCCTTC	CCCCCCGAGG	CCATAGAC	CCTCATCCC	GGCTTGGGCA	
851	GCGTGGCGGG	CTTTGAAAAA	AATACGCGCG	ABCCCCTTCA	CCGGTGGATA	
901	CAGGAAAACC	CCAATGCCGC	CGAAACCGTC	GAAGCCCTGG	TCAACGTCCT	
951	GCCGTTTGCC	AAAGTCAAAA	ACCTGACAAA	GGCGGCAAAA	CCGGGGAAGG	
1001	CTGCGGTTAG	CGGGGATTTT	TCTGCTGCAT	ACAATACAAG	AACAACTAGA	
1051	AAAGTTACTA	CAGAAACAGA	GGGGTTAAAT	AGAATCAGAC	AGAACCAGAA	
1101	AAATAGTAAT	ATACATGAGA	AAAATTATGG	AAGAGATAAT	CCTAATCATA	
1151	TTAATGTTTT	ATCTGGAAAT	TCTATACAAC	ATATACTGTA	TGGAGATGAA	
1201 1251	CCAAGGAGGTG	GGCATCTTTT	TCCTGGCAAA	CCTGGTAAGA	CAACATTCCC	
1301	CDTCCCCDDD	AACCCAATCC	TATECACACA	TGAAATTAGT	GATATCGTTA CGGCAAATAT	
1351	ATTGCTAAAG	GAAGACCAGC	TAGGTGGGTA	TCATATCAAA	CGAGAGATAT	
1401	AATTCGTATC	AGAACAGTTT	ATGAACCTGC	AACAGGAAAA	GTGGTAACTG	
1451	CATTCCCCGA	TAGAACCTCT	AATCCCAAAT	ATAACCCTGT	AAAATAA	
This correspond	s to the amin	o acid seque	ence <seq i<="" td=""><td>D 2474; OR</td><td>F 730.a&gt;:</td><td></td></seq>	D 2474; OR	F 730.a>:	
a730.pep				•		
1	VKPLRRLIKL	LAACAVAAAA	LIQPALAADL	AQDPFITDNA	QRQHYEPGGK	
51	YHLFGDPRGS	VSDRTGQINV	IQDYTHRMGN	LLIOOANING	TIGYHTRFSG	
101	HGYEEHAPFD	NHAADSASEE	KGNVDEGFTV	YRLNWEGHEH	HPADAYDGPK	
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIS	DNYSNLGSNF	
201 251	SUKADEANRK	MEEHNAKLDR	WGNSMEFING	VAAGALNPFI	SAGEALGIGD	
301	TEIGIKIAID	CAMMINIALP CAMMINIALL	KUKNI DIANA	GLGSVAGFEK	NTREAVDRWI SAAYNTRTTR	
351	KALLELECTN SEMEMATER	RTRONOKNSN	THEKNAGDON	PNHINUTOCH	SAAYNTRTTR SIQHILYGDE	
401	AGGGHLFPGK	PGKTTFPOHW	SASKITHETS	DIALITATION	YAQTGTGGKY	
451	IAKGRPARWV	SYETROGIRI	RTVYEPATGK	VVTAFPDRTS	NPKYNPVK*	

451 IAKGRPARWV SYETRDGIRI RTVYEPATGK VVTAFPDRTS NPKYNPVK*

a730 / m730	88.6% identity in 376 aa overlap	
a730.pep	10 20 30 40 50	60
a/30.pep		
m730	VKPLRRLTNLLAACAVAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHI 10 20 30 40 50	FGDPRGS 60
a730.pep	P VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHA	120 ADSASEE
m730	:  :     :	
111750	70 80 90 100 110	ADSASEE 120
	130 140 150 160 170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTAR	SIKLNPT
m730		 SIKLNPT
	130 140 150 160 170	180
	190 200 210 220 230	240
a730.pep	DTRSIRQRISDNYSNLGSNFSDRADEANRKMFEHNAKLDRWGNSMEFINGVAA	GALNPFI
m730	DTRSIRQRISDNYSNLGSNFSDRADEANRKMFEHNAKLDRWGNSMEFINGVAA	GALNPFI
	190 200 210 220 230	240
a730.pep	250 260 270 280 290	300
a/30.pep		111111
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTR	EAVDRWI
	200 200	300
a730.pep	310 320 330 340 350  QENPNAAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSAAYNTRTTRKVT	360
• •		: :::
m730	QENPNAAETVEAVFNVAAAAKVAKLAKAAKPGKAAVSGDFADSYKKKLA 310 320 330 340 3	ALSDSAR 50
	3.	50
a730.pep	370 380 390 400 410 RIRQNQKNSNIHEKNYGRDNPNHINVLSGNSIQHILYGDEAGGGHLFPGKPGKT	420 TTFPOHW
m730	::         : : :	
111750	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISA 360 370 380 390 400 41	IDKPKNF 10
The following p	partial DNA sequence was identified in N. gonorrhoeae <seq id<="" td=""><td>2475&gt;:</td></seq>	2475>:
g731.seq	1	
1 51	TTTGGACGGC GGCAAAATCG CGTTGCGGCT GGACGGCAGG CGTGCCGTCC	
101 151	TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT	
201	THOCCITII	
251	GTTAA	
This correspond	ds to the amino acid sequence <seq 2476;="" 731.ng="" id="" orf="">:</seq>	
g731.pep		
1 51	THE TOTAL TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL T	
The Calleryin		
The following p	partial DNA sequence was identified in N. meningitidis <seq id<="" td=""><td>2477&gt;:</td></seq>	2477>:
1	ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCGGC	
51 101	CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCCTGCGAG	
151	AACGGTTTGT CTGTGCGCGT CCGCCATTTG GACAGCGGCA AAGTCGCGTT	
201	GCGGCTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG	

251 301 351	CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
This correspond	ds to the amino acid sequence <seq 2478;="" 731="" id="" orf="">:</seq>
1 51 101	NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
g731/m731 95	5.2% identity in 84 aa overlap
g731.pep	10 20 30 DFRAFSCENGLSVRVRNLDGGKIALRLDGR 
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHLDSGKVALRLDGR 20 30 40 50 60 70
g731.pep	40 50 60 70 80 RAVLSSDVAASGERYTAEHGLFGNGTEWHOKGGEAFFGFTDAYGNSVETSCRARX
m731	
The following p	partial DNA sequence was identified in N. meningitidis <seq 2479="" id="">:</seq>
a731.seq 1 51 101 151 201 251 301 351	AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT GCGGTTGGAC GGCAGGCGTG CCGTCCTCT TTCCGACGTT GCCGCATCCG GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA
This correspond	s to the amino acid sequence <seq 2480;="" 731.a="" id="" orf="">:</seq>
a731.pep 1 51 101	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
a731/m731	94.4% identity in 126 aa overlap
a731.pep m731	10 20 30 40 50 60 MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRAFSCENGLSVHVRRL
a731.pep m731	70 80 90 100 110 120 DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE  : ::
a731.pep m731	TSCRARX        TSCRARX
g732.seq 1 ATGTC 51 CAGCC	artial DNA sequence was identified in N. gonorrhoeae <seq 2481="" id="">: CGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT GGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg gegGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG TACGATGGCG</seq>

```
GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
     CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
 251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
 301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
      TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
      TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
      ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
      GATTACTTTG ACGTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
      ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
      GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
     CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
 651
 701 AACCGCTCAA GGGGCTGGTG TTGGATTTGC GCGACGACCC CGGCGGGCTT
      TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
 751
 801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
 851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
 901 ATTCCTGCCG AGTTGAAAAC GATTCCGATG ACGGtaTTGG TcaaTTCCGG
 951 TTCggcttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTC GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTCAGGC ACAGGGGATT GTTCCCGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GGCGGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCttgcCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG
```

# This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>: g732.pep

```
1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDGRDNEV LPVQSIRTMA
51 EVYGQIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAII KVKSVRHHLI
201 EPDYGYIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSAA FLPSEAVVVS TKGRDGKDGM VLKAVPEDYV YGMGGDPLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFGKGSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNKDKKDK K*
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2483>: m732.seq

```
ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
   1
  51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
 101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
 151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
 201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
     ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
     AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
     TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGG
 401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
 451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
 501 GATTACTTTG ACGCTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
 551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
 601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
 651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
 701 AACCGCTCAA GGGGCTGGTG TTGGATTTGC GCGACGACCC CGGCGGGCTT
 751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
 801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
 851 CCATTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
 901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
 951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTC GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
```

1101	TTATACGCCG	AACGACCGTT	CTATTCAGGC	GCAGGGGATT	GTTCCCGATG
1151		AGATAAGGAA			
1201	GTCGGACACA	TCGGCAATCC	CTTGGGCGGC	GAGGATGTGA	ACGGTGAAAC
1251	CCTTGCCGTG				
1301	AAGGTAAAAA	GAAAAAGGAC	GAGGATTTGT	CTTCAAGGCG	GATTCCCAAC
1351	CCTGCCAAAG	ACGACCAGTT	GCGGAAAGCT	TTGGATTTAG	TCAAGTCGCC
1401	CGAGCAGTGG	CAGAAGTCTT	TGGGGCTGGC	GGCGAAAAAG	CCGGTTTCAA
1 4 5 1	ΔΤΑΑΑΚΑΤΑΑ	GAAAGATAAA	AAAGATAAGA	ACTAC	

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>: m732.pep

1	MSKPVFKK <u>IA</u>	LYTLGAISGV	AVSLAVQGFA	AEKDRRDNEV	LPVQSIRTMA
51	EVYGQIKANY	YQDKPDADLF	EGAMKGMVAG	LDPHSEYMDK	KGYAEIKEST
101	SGEFGGLGME	IGQEDGFVKV	VSPIEDTPAE	RAGVKSGDFI	VKIDNVSTRG
151	MTVSEAVKKM	RGKPGTKITL	TLSRKNADKP	IVVNLTRAII	KVKSVRHHLI
201	EPDYGYIRVS	QFQERTVESV	NTAAKELVKE	NKGKPLKGLV	LDLRDDPGGL
251	LTGAVGVSAA	FLPSEAVVVS	TKGRDGKDRM	VLKAIPEDYV	YGMGGDSLAG
301	IPAELKTIPM	TVLVNSGSAS	ASEIVAGALQ	DHKRAVIVGT	QSFGKGSVQT
351	LIPLSNGSAV	KLTTALYYTP	NDRSIQAQGI	VPDVEVKDKE	RIFESREADL
401		EDVNGETLAV			
451	PAKDDQLRKA	LDLVKSPEQW	QKSLGLAAKK	PVSNKDKKDK	KDKK*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from N. meningitidis menA with menB

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from N. gonorrhoeae:

m732/g732 98.2% identity in 491 aa overlap

	10			40	50	60
m732.pep			/AVSLAVQGFA 			
q732	MSKPVFKKI	ALYTLGAISG	/AVSLAVQGFA	AEKDGRDNEV	LPVOSIRTMAE	VYGOIKANY
-	10			40	50	60
	7(	) 80	90	100	110	100
m732.pep			, GLDPHSEYMDKI			COEDGEVKV
m.oz.pcp						
g732			SLDPHSEYMDKI			
	70	) 80	90	100	110	120
	130	) 140	) 150	160	170	100
m732.pep			VKIDNVSTRG1		170	180
m/Jz.pep	111111111					LOKKNADKP
g732			VKIDNVSTRG			
2	130			160	170	180
	190	200	210	220	000	• • •
m732.pep			) 210 EPDYGYIRVS(	220	230	240
m/32.pep	1111111111			7		
g732	IVVNLTRAI	KVKSVRHHLI	EPDYGYIRVS	OFOERTVESV	TAAKELVKEN	KGKPLKGLV
-	190	200	210	220	230	240
	0.54					
-722	250			280	290	300
m732.pep			AFLPSEAVVVS:			_
g732			FLPSEAVVVS:			
	250			280	290	300
	31(			340	350	360
m732.pep	1PAELKTIPN	ITVLVNSGSAS	ASEIVAGALQ	DHKRAVIVGTÇ	SFGKGSVQTL	IPLSNGSAV
g732	TPARIKTTPN	TVI.VNSGSAS		11111111111111111111111111111111111111		TOT CNCCAU
J . V.	310			340	350	360
					550	200

m732.pep	370	380	390	400	410	420
	KLTTALYYTPNDRSI	QAQGIVPD	VEVKDKERIFI	ESREADLVGHI	GNPLGGEDV	NGETLAV
g732	KLTTALYYTPNDRSI	QAQGIVPD	VEVKDKERTFI	ESREADLVGHI	GNPLGGEDV	NSETLAV
	370	380	390	400	410	420
m732.pep g732	430 PLEKDADKPAVKEKG             PLEKDADKPAAKEKG 430		[			111111
m732.pep g732	490 PVSNKDKKDKKDKKX             VSNKDKKDKKX 490					

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2485>:

```
a732.seg
         ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
      51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
     101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
     151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
     201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
     251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
     301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
         TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
         TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
     451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
    501 GATTACTTTG ACGCTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
    551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
    601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
     651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
    701 AACCGCTCAA GGGGCTGGTG TTGGATTTGC GCGACGACCC CGGCGGGCTT
    751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
     801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
     851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTC GTTGGCGGGC
    901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
     951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
   1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTC GGTTCAGACT
   1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
   1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
   1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
   1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
   1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
   1351 CCTGCCAAAG ACGACCAGTT GCGGAAAGCT TTGGATTTAG TCAAGTCGCC
   1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
   1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG
```

### This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

_			-		
.pep					
1	MSKPVFKK <u>IA</u>	LYTLGAISGV	AVSLAVQGFA	AEKDRRDNEV	LPVQSIRTMA
51	EVYGQIKANY	YQDKPDADLF	EGAMKGMVAG	LDPHSEYMDK	KGYAEIKEST
101	SGEFGGLGME	IGQEDGFVKV	VSPIEDTPAE	RAGVKSGDFI	VKIDNVSTRG
151	MTVSEAVKKM	RGKPGTKITL	TLSRKNADKP	IVVNLTRAII	KVKSVRHHLI
201	EPDYGYIRVS	QFQERTVESV	NTAAKELVKE	NKGKPLKGLV	LDLRDDPGGL
251	LTGAVGVSAA				
301	IPAELKTIPM	TVLVNSGSAS	ASEIVAGALQ	DHKRAVIVGT	QSFGKGSVQT
351	LIPLSNGSAV	KLTTALYYTP	NDRSIQAQGI	VPDVEVKDKE	RIFESREADL
401	VGHIGNPLGG	EDVNSETLAV	PLEKDADKPA	VKEKGKKKKD	EDLSSRRIPN
451	PAKDDQLRKA	LDLVKSPEQW	QKSLGLAAKK	PVSNKDKKDK	KDKK*

a732/m732	99.6% identity in 494 aa overlap
a732.pep m732	10 20 30 40 50 60  MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGQIKANY
a732.pep m732	70 80 90 100 110 120 YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
a732.pep m732	130 140 150 160 170 180 VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP
a732.pep m732	190 200 210 220 230 240 IVVNLTRAIIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV
a732.pep m732	250 260 270 280 290 300 LDLRDDPGGLLTGAVGVSAAFLPSEAVVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSLAG
a732.pep m732	310 320 330 340 350 360 IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV
a732.pep m732	370 380 390 400 410 420 KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV
a732.pep m732	430 440 450 460 470 480 PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK
a732.pep m732	490 PVSNKDKKDKKX              PVSNKDKKDKKKX 490

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2487>: g733.seq

ATGATGAATC	CGAAAACCTT	GGGCCGTTTG	TCGCTGTGTG	CGGCGGTCTT
GGCTCTGACC	GCCTGCGCCG	GCGGCGGCA	TAAAAACCTG	TATTATTACG
GCGGTTATCC	CGATACCGTC	TATGAAGGTT	TGAAAAACGa	cgACACTTCG
TTGGGCAAGC	AGACCGAAAA	GATGGAAAAA	TACTTTGCGG	AAGCCGCCAA
	GGCTCTGACC GCGGTTATCC	GGCTCTGACC GCCTGCGCCG GCGGTTATCC CGATACCGTC	GGCTCTGACC GCCTGCGCCG GCGGCGGCA GCGGTTATCC CGATACCGTC TATGAAGGTT	ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG GGCTCTGACC GCCTGCGCCG GCGGCGGCA TAAAAAACCTG GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGa TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG

201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATTTG GGACTGCTGC

```
251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
```

351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>: g733.pep

- 1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
- 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
- 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>: m733.seq

- 1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
- 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
- 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
- 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
- 201 CAAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGACTGCTGC
- 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
- 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
- 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>: m733.pep

- 1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
- 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
- 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from N. meningitidis menA with menB

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from N. gonorrhoeae:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCA	AVLALTACGG	NGQKSLYYY	GGYPDTVYEGI	KNDDTSLGK	QTEKMEK
		11111111111111111	:1:1:111		11111111	
g733	MMNPKTLGRLSLCA	AVLALTACAG	GGHKNLYYY	GGYPDTVYEGI	KNDDTSLGK	OTEKMEK
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAP	GAHAHLGLLL	SRSGDKEGA	FRQFEEEKRLE	PESGVFMDF	LMKTGKG
	11:11:1111111	111111111			111111111	
g733	YFAEAANKKMNAAP	GAHAHLGLLL	SRSGDKEGAI	FRQFEEEKRLE	PESGVFMDF	LMKTGKG
	70	80	90	100	110	120
m733.pep	GKRX					
~ •	1111					
g733	GKRX					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2491>:

a733.seq

- ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT

  51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG

  101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG

  151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA

  201 CAAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGACTGCTGC

  251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG

  301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
- 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

1 51 101	LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE	
a733/m733	3 100.0% identity in 123 aa overlap	
a733.pep	10 20 30 40 50  MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQT	60 EKMEK
m733	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQT 10 20 30 40 50	EKMEK 60
a733.pep		120 KTGKG
m733		 KTGKG 120
a733.pep	GKRX	
m733	 GKRX	
The following p	partial DNA sequence was identified in N. gonorrhoeae <seq 2<="" id="" td=""><td>493&gt;:</td></seq>	493>:
g/54.3eq 1	ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGACTGCGGC	
51	GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC	
101		
151		
201		
251		
301		
351 401		
451	GCTGTTCGCT CCTTAATCCA ACACCTGAAA TAA	
•	ds to the amino acid sequence <seq 2494;="" 734.ng="" id="" orf="">:</seq>	
g734.pep	MMKKILAVSA LCLMTAAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA	
1 51	KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA	
101	MRVENAVVIT SPRFTSVHQV ALNQCIKKYG AQQQCGLETV YCTSSSYYGG	
151	AVRSLIQHLK *	
The following p	partial DNA sequence was identified in N. meningitidis <seq 24<="" id="" td=""><td>195&gt;:</td></seq>	195>:
1	TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTCGCT	
51		
101	GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTTAC GAGCGTTCAT	
151	CAGGTCGCAC TCAACCAGTG CATCAAAAAA TACGGCGTAC AGGGACAATG	
201	CGGCTTGGAA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACTG	
251	TGCGCTCTTT GATTCAAAAT CTCAAATAA	
This correspond	ds to the amino acid sequence <seq 2496;="" 734="" id="" orf="">:  (partial)</seq>	
1	SGIAEDEPTG CRSVVSLNNT CVALAYPKAL GALRVDNAVV ITSPRFTSVH	
51	· · · · · · · · · · · · · · · · · · ·	
m734/g734 92	2.4% identity in 92 aa overlap	20
m734.pep	SGIAEDEPTGCRSVVSLNNTCVALAY :	
g734	VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLA	PKAL

```
60
                 40
                           50
                                             70
                                                       80
                                                                90
                         40
                                  50
                                           60
                                                    70
                                                              80
                                                                       90
                 GALRVDNAVVITSPRFTSVHQVALNQCIKKYGVQGQCGLETVYCTSSSYYGGTVRSLIQN
     m734.pep
                 GAMRVENAVVITSPRFTSVHQVALNQCIKKYGAQGQCGLETVYCTSSSYYGGAVRSLIQH
     q734
                         110
                                   120
                                            130
                                                     140
                 LKX
     m734.pep
                 111
                 LKX
     g734
                160
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2497>:
              ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCGGC
              GGCACGGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
           51
         101 AGAATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCGACG
         151 AAAAGCGAAG CGTTTGCCGA GTTGGAAGCT TTCTGCAAAG GTCAGGACAC
         201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
         251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
         301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
         351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
         401 AATGCGGCTT GGAAACAGTG TATTGCACGT CTTCTTCTTA TTACGGGGGA
              ACTGTGCGCT CTTTGATTCA AAATCTCAAA TAA
This corresponds to the amino acid sequence <SEQ ID 2498; ORF 734.a>:
     a734.pep
              MMKKILAVSA LCLMTAAARA ADTYGYLAVW QNPQNANDVL QVKTTKEDST
              KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV ALAYPKALGA
          51
             MRVENAVVIT SPRFTSVYQV ALNQCIKKYG AQGQCGLETV YCTSSSYYGG
              TVRSLIONLK *
a734/g734 95.6% identity in 160 aa overlap
                                           30
                                                    40
                                                             50
                 MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA
    a734.pep
                 q734
                 MMKKILAVSALCLMTAAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA
                        10
                                 20
                                           30
                        70
                                 80
                                          90
                                                   100
                                                            110
                                                                     120
                 FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVALAYPKALGAMRVENAVVITSPRFTSVYQV
    a734.pep
                 FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV
    q734
                        70
                                 80
                                          90
                                                   100
                                                            110
                       130
                                140
                                         150
                ALNQCIKKYGAQGQCGLETVYCTSSSYYGGTVRSLIQNLKX
    a734.pep
                 g734
                ALNQCIKKYGAQGQCGLETVYCTSSSYYGGAVRSLIQHLKX
                       130
                                140
                                         150
                                                   160
g735.seq
          not found yet
g735.pep
         not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2499>:
m735.seq
         ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
        CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
     51
    101 CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
    151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAACT
        GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
    201
        TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
    251
```

AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAAGCGG

```
351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
401 CCCTCGGCTA CGGAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>: m735.pep

- MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
- 51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
- 101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN*

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2501>:

```
a735.seq
         ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
       1
      51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
     101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
    151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
     201 GGCGCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
     251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
     301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
     351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
     401 CCCTCGGCTA CGGAAATTAA
```

#### This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep					
1	MNLVKLLANN	WQPIAIIALV	GTGLAVSHHQ	GYKSAFAKQQ	AVIEKMKRDK
51	AQALLLSAQN	YARELEQARA	EAKKYEVKAH	AVGMALAKKQ	AEVSRLKTEN
101	KKEIENVLTQ	DRKNAGGGCI	DGFGHHGLQL	YKRALGYGN*	
-725/m725	05 79 10	dontitu in 1	120 22 22221	۱	

a/35/m/35	95.7% identity	1n 139 aa	overlap			
	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPI	AIIALVGTGL	AVSHHQGYKS	SAFAKQQAVIE	KMKRDKAQAL	LLSAQN
				[]]]]];	11:1111111	11111
m735	MNLVKLLANNWQPI	AIIALVGTGL	AVSHHQGYKS	SAFAKQQAVII	KMERDKAQAL	LLSAQN
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKK'	YEVKAHAVGM	ALAKKQAEVS	RLKTENKKEI	ENVLTQDRKN	AGGGCI
					111111111	1:1111
m735	YARELELARAEAKK	YEVKAHAVGM	ALAKKQAEVS	RLKTENKKEI	ENVLTQDRKN	ASGGCI
	70	80	90	100	110	120
	130	140				

```
DGFGHHGLQLYKRALGYGNX
a735.pep
          m735
          DGFGSHGLOLYNRALGYGNX
               130
```

#### The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 2503>: g736.seq

```
ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT
```

```
601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>: g736.pep

- MNFIRSVGAK TLGLIQSFGS ITLFLLNILA KSGTAFARPR LSVRQVYFAG
- 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMAVNPVAR VVAPRFWAGV
- 151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMQNN ITIHYDVING
- 201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
- 251 LTAWMFTD*

The following partial DNA sequence was identified in N. meningitidis <SEO ID 2505>: m736.seq

ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC 1 51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA 101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCGTG 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT 551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA 701 CGCGCACGGT GGTTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEO ID 2506; ORF 736>: m736.pep

- MNFIRSVGAK TLGLIQSLGS ITLFLLNILA KSGTAFVRPR LSVRQVYFAG
- 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
- 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
- 151 FSMPLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMQNN ITIHYDVING
- 201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
- 251 LTAWMFTD*

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. meningitidis menA with menB ORF 736 shows 97.7% identity over a 258 as overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*: m736/g736

m736.pep	10 MNFIRSVGAKTLGI	20 JQSLGSITLF			-	60 LIVAVS
g736	MNFIRSVGAKTLGI					LIVAVS 60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYT	'QLSKFKSADI	LGYMVAASLL	RELGPVLAAI	LFASSAGGAM	ITSEIGL
		3	1111111111		1 1 1 1 1 1 1 1 1 1	11111
g736	GLFVGMVLGLQGYT	'QLSKFKSADI	LGYMVAASLL	RELGPVLAAI	LFASSAGGAM	1TSEIGL
	70	80 .	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMA	VNPVARVVAP	RFWAGVFSMP	LLASIFNVAG	IFGAYLVGVT	WLGLDS
g736	MKTTGQLEAMNVMA	VNPVARVVAP	RFWAGVFSMP	LLASIFNVAG	IFGAYLVGVS	WLGLDS

		130	140	150	160	170	180
		190	200	210	220	230	240
m736	.pep (	GIFWSQMQNNIT:	IHYDVINGLIK	SAAFGVAVTLI	AVHQGFHCVPT	rsegilrast	RTVVSS
q736	(	 GIFWPQMQNNIT:					
9,50	·	190	200	210	220	230	240
		250	259				
m736	.pep A	ALTILAVDFILTA					
g736	I	ALTILAVDFILT/ 250	AWMFTDX				
		200		•			
The		partial DNA s	sequence was	identified i	n N. mening	ritidis <se< td=""><td>Q ID 2507&gt;:</td></se<>	Q ID 2507>:
	a736.seq 1	7 m C 7 7 m m m m 7	TCCGTTCCGT		7.CCC#0000		m.a.
	51	TCTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	TATTCTGGC	: TTATTCAA : AAATCCGG	TC TA
	101	CGGCTTTCGT	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	A TTTTGCCG	GC
	151	GTGCTGTCGG	TGTTGATTGT	TGCCGTTTCA	GGGCTGTTTC	TCGGCATG	GT
	201 251	CTTGGGTTTG	CAGGGCTATA TATGGTCGCG	CGCAGTTGTC	GAAATTCAAA	A TCCGCCGA	TA
	301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GCCGCGAACT	T GGGTCCGG	TG Ca
	351	AATCGGTTTG	ATGAAAACGA	CCGAACAGCT	CGAAGCGATG	AACGTGAT	GG GG
	401	CGGTAAACCC	CGTCGCCCGA	GTGGTTGCGC	CGCGCTTTTC	GGCGGGCG	TG
	451	TTTTCCATGC	CGCTTTTGGC	TTCGATTTTC	AACGTGGCGG	GTATTTTC	GG
	501.		GTCGGTGTAA				
	551	GGTCGCAAAT	GCAGAACAAC	ATCACGATAC	ATTACGATGT	AATCAACG	GT
	601 651	TCAGGGCTTC	CCGCCGCGTT CACTGCGTCC	CGACCTCGGA	ACCOMPAND	TIGCCGIG	CA
	701	CGCGCACGGT	GGTTTCGTCC	GCCCTGACGA	TTTTGGCGGT	г ССССССКО Г	CA TΔ
	751		GGATGTTTAC				•••
This	correspond	is to the amin	o acid seque	nce <seq i<="" td=""><td>D 2508; OR</td><td>F 736.a&gt;:</td><td></td></seq>	D 2508; OR	F 736.a>:	
	a736.pep						
	1	MNFIRSVGAK	TLGLIQSLGS	ITLFLLNILA	KSGTAFVRPR	LSVRQVYF	AG
	51	VLSVLIVAVS	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELG	PV
	101 151	ESMPLIASSA	GGAMTSEIGL NVAGIFGAYL	MKTTEQLEAM	NVMAVNEVAR	VVAPRFWA	GV
	201	LIKSAAFGVA	VTLIAVHQGF	HCVPTSEGII.	BYZLAZČMÕNN	TITHIDVI	NG ET
	251	LTAWMFTD*			Talorni vvbb	THITTHYD	1. 1.
	a736/m736	100 08 10	dentity in 2	50 22 0100	lan		
	a130/11130	100.04 10	rentity in 2	Jo da OVEL	Lap		
				30			
	a736.pep	MNFIRSVO	SAKTLGLIQSLO	SITLFLLNIL	AKSGTAFVRPR	LSVRQVYFA	GVLSVLIVAVS
	m736	MNFTRSVO				1 6/10/0/17/27	
	111750	11112 2110 40		0 30			
				_	-		00
				0 90			
	a736.pep	GLFVGMVI	LGLQGYTQLSKE	KSADILGYMV	AASLLRELGPV	LAAILFASS	AGGAMTSEIGL
	m736	[	GLQGYTQLSKE				
	111/20	GHFVGHVI		0 90			
					100	**	J 120
			.30 14				
	a736.pep		CAMNVMAVNPVA				
	m736			IIIIIIIIII	IIIIIIIIIIIIIII	111111111	1111111111
	m/20		CAMNVMAVNPVA .30 14				
		-		- 13(	, ,,00	170	7 100
			.90 20				
	a736.pep	GIFWSQMQ	NIVOYHITINMO	GLIKSAAFGV	AVTLIAVHQGF	HCVPTSEGII	LRASTRTVVSS
			111111111				
		11111111		1111111111			

GIFWSQMQNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS m736 200 210 220 230 250 259 ALTILAVDFILTAWMFTDX a736.pep 1111111111111111111111111 m736 ALTILAVDFILTAWMFTDX 250 The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2509>:

g737.seq

- 1 atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
- 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
- 101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
- 151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
- 201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
- 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
- 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEO ID 2510; ORF 737>: g737.pep

- 1 MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAAHO HGKODKIISR
- 51 AQAEKAAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
- 101 VISSRRDD*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2511>: m737.seq..

- 1 ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG 51 CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
- 101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
- 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
  201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
  251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
  301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>: m737.pep

- MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAAHO HNKODKIISR
- 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
- 101 VISSRRDD*

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. meningitidis menA with menB

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from N. gonorrhoeae:

m737/g737

m737.pep	10 MNIKHLLLTSAAT 	20 ALLSISAPALA    :	30 HHDGHGDDDH 	40 GHAAHQHNK	50 QDKIISRAQAE	60 KAALAR
g737	MNIKHLLTAAAT	ALLGISAPALA	HHDGHGDDDH	<b>GHAAHQHGK</b>	QDKIISRAOAE	KAAWAR
	10	20	30	40	50	60
	70	80	90	100	109	
m737.pep	VGGKITDIDLEHDI	NGRPHYDVEIV	KNGQEYKVVV	DARTGRVIS	SRRDDX	
		:111111111	1111111111	11111111	11111	
g737	VGGKITDIDLEHDI	OGRPHYDVEIV	KNGQEYKVVV	DARTGRVIS	SRRDDX	
	70	80	90	100		

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2513>:

```
a737.seq
             ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
             CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
          51
         101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
         151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
         201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
         251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
         301 GTGATTTCCT CCCGCCGCGA CGACTGA
This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:
    a737.pep
             MNFKRLLLTA AATALMGISA PALAHHDGHG DDDHGHAAHQ HSKQDKIISR
             AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
          51
         101 VISSRRDD*
    a737/m737
                94.4% identity in 108 aa overlap
                                20
                                         30
                MNFKRLLLTAAATALMGISAPALAHHDGHGDDDHGHAAHQHSKQDKIISRAQAEKAALAR
    a737.pep
                MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAAHQHNKQDKIISRAQAEKAALAR
    m737
                       10
                                20
                                         30
                                                  40
                                                           50
                       70
                                80
                                         90
                VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
    a737.pep
                VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
    m737
                       70
                                80
                                         90
                                                 100
```

# The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2515>: g738.seq

```
ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCCG CCAAACTGCC
     GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
 101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
 151 GCGGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
 201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
 251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
 301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
 351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtT ACCCTGTTTG
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
 451 CAGTTTGCCG GCTGGGAAAA CACCCCCCTG CTTCAAAACA TCATCGTTCA
 501 CAGAGGGCAA GGCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA
 601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
 801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
 851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC
     GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
     CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACTTC CTCAGCACCT TGTTCACCCA TTCCCACAAC
1051 ATCATCCTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTITICCTG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCCTCA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCCGCCGCT GACGACAGTG CCAAAACCCT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCCTAC TCCGCCACCT
```

```
1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
1801 AAACCCTGCA AATGA
```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>: g738.pep

```
1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
     AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWWLQAR LMNLIYPGMN
 51
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
     QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGOR
     KIPAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
     TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
301
     IILQLLAEMG ISGTLLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
351
     SMLEYPLWYV YFLIPFGLML FLSPAEASDG IAFKKAANLG ILTASAAIFA
401
     GLLHLDWTYT RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEEA TLKALKYRPY SATYRIALYL MRQGKVAEAK
551 QWMRATQSYY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2517>: m738.seq

```
ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACTGCC
   1
      GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
  51
      TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
 101
      GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAACTGTT
      TGATGTCAAA ATCCCCGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
      TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
      GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
 351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
 451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
 501 CAGCGGGCAA GGCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
 601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
 801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
 851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAATC
     GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
      CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCCACAAC
     ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1051
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCCTCA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAAACCCT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCGTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
     TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1751
1801 AAACCCTGCA AATGA
```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>: m738.pep

¹ MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```
1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
1801 AAACCCTGCA AATGA
```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>: g738.pep

```
1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLFL TAGKKLFDVK IPAISFLFA MAAFWWLQAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
351 IILQLLAEMG ISGTLLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAEASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWTYT RLVNSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEEA TLKALKYRPY SATYRIALYL MRQGKVAEAK
551 QWMRATQSYY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2517>: m738.seq

```
ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACTGCC
   1
      GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
  51
      TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
 101
     GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAACTGTT
     TGATGTCAAA ATCCCCGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
     TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
     GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
     CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
     CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
     CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
     CAGCGGGCAA GGCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
 601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
 651
     TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
     CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
 701
     ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
     TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
     CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAATC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
 951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCCACAAC
1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCCTCA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAAACCCT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCGTACCTGA TGCCCCGATA
     CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
     TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1751
1801 AAACCCTGCA AATGA
```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>: m738.pep

¹ MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

51		TAGKKLFDVK			
101	DIVSWIFILL	AVSAWACRSL	VAHFGQERIV	TLFAWSLLIG	SLLQSCIVVI
151		FQNIIVYSGQ			
201	KIPAALGVIC	LIMQTAVLGL	VNSRTILTYI	AAIALILPFW	YFRSDKSNRR
251	TMLGIAAAVF	LTALFQFSMN	TILETFTGIR	YETAVERVAN	GGFTDLPRQI
301	EWNKALAAFQ	SAPIFGHGWN	SFAQQTFLIN	AEQHNIYDNL	LSNLFTHSHN
351	IVLQLLAEMG	ISGTLLVAAT	LLTGIAGLLK	RPLTPASLFL	ICTLAVSMCH
401	SMLEYPLWYV	YFLIPFGLML	FLSPAEASDG	IAFKKAANLG	ILTASAAIFA
451	GLLHLDWTYT	RLVNAFSPAT	DDSAKTLNRK	INELRYISAN	SPMLSFYADF
501	SLVNFALPEY	PETQTWAEEA	TLKSLKYRPH	SATYRIALYL	MRQGKVAEAK
551	QWMRATQSYY	PYLMPRYADE	IRKLPVWAPL	LPELLKDCKA	FAAAPGHPEA
601	KPCK*				

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from N. meningitidis menA with menB

ORF 738 shows 95.0% identity over a 604 as overlap with a predicted ORF (ORF738.a) from N. gonorrhoeae:

m738/g738

	10	20	30	40	50	60
m738.pep	MPAETTVSGAHP	AAKLPIYILPCE	LWIGIVPFT	ALKLKPSPD	FYHDAAAAAG	LIVLLFL
		111111111111	11111:111	11:11111	HIMMAN	111111
g738	MSAETTVSGARP	AAKLPIYILPCE	LWIGIIPFT	ALRLKPSPD	FYHDAAAAAG	LIVLLFL
,	. 10	20	30	40	50	60
						0.0
	70	80	90	100	110	120
m738.pep	TAGKKLFDVKIP	AISFLLFAMAAF	WYLOARLMNI	LIYPGMNDIV		AWACRSI.
		111111111111	1:1111111		11:111111	1111111
q738	TAGKKLFDVKIP	AISFLLFAMAAF	WWLOARLMNI	IYPGMNDTA	SWVFTI.I.AVS	AWACKSI
<b>3</b> ·	70	80	90	100	110	120
				200	110	120
	130	140	150	160	170	180
m738.pep	VAHFGQERIVTL	FAWSLLIGSLIC				CHICODN
		1111111111		11.111111	111. 11111	IIII JAN
g738	VAHYGQERIVTL	FAWSLLIGSLLO	SCTVVIOFAC	WENTPLION	TTVHRCOCVT	CHICODN
9,50	130	140	150	160	170 170	180
	150	110	130	100	170	100
	190	200	210	220	230	240
m738.pep	NLGHYLMWGILA					
m/30.pep		•		CNATOTANT	CITTIIITAAT.	ALILPEW
g738	NLGHYLMWGILA	SAALMCUBKLDA	ALCATCLEMO	ייין אין אין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין איייין  1		
g / 30	190	200	210	220	230	ALILPIW 240
	130	200	210	220	230	240
	250	260	270	280	290	300
m738.pep	YFRSDKSNRRTM					טטכ
m/30.pep				ILLIGIKIEL	IIIIIIIIII	IDTEKÕT
g738	YFRSDKSNRRTM	Τ.GΤΔΔΔV.FT.ͲΔΤ.	FORSMNATIR	╵╵╎╎╎╎╎ ╵╙┎┰СТБУ╏┰		
9730	250	260	270	280	290	
	250	200	270	200	290	300
	310	320	330	340	350	360
m738.pep	EWNKALAAFQSA:					360
m/30.pep		IIIIIIIIIIIII	TILLIIII Öledinweðu	.	PETHONNIAT	ZLLAEMG
g738	EWNKALAAFQSA			: :  :  :	[ ]	!
9/30	310	320	330			
	310	320	330	340	350	360
	370	380	390	400	410	
m738.pep	ISGTLLVAATLL				410	420
m/38.pep	12GILLVAAILL.	I G T W G P P V K L P I	PASEFEICTE	AVSMCHSMLI	SYPLWYVYFL.	LPFGLML
g738	TECTITIVA ARTIS			Nichtonian		11111
9/38	ISGTLLVAATLL	380	390			
			190	400	410	420
	370	300	330	100	110	
m720	430	440	450	460	470	480
m738.pep	430 FLSPAEASDGIA	440 FKKAANLGILTA	450 SAAIFAGLLH	460 LDWTYTRLVN	470 VAFSPATDDS	480 AKTLNRK
• •	430 FLSPAEASDGIA	440 FKKAANLGILTA	450 SAAIFAGLLH	460 LDWTYTRLVN	470 NAFSPATDDS/	480 AKTLNRK
m738.pep	430 FLSPAEASDGIA	440 FKKAANLGILTA	450 SAAIFAGLLH	460 LDWTYTRLVN	470 NAFSPATDDS/	480 AKTLNRK

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPMLS	SFYADFSLVN	IFALPEYPETQ	TWAEEATLKS	LKYRPHSATY	RIALYL
			11111111	11111111:	11111:1111	111111
g738	INELRYISANSPMLS	SFYADFSLVN	FALPEYPETQ	TWAEEATLKA	LKYRPYSATY	RIALYL
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQGKVAEAKQWMRA	TQSYYPYLM	PRYADEIRKL	PVWAPLLPEL		PGHPEA
		11111111	11111111111	1111111111		11111.
g738	MRQGKVAEAKQWMRA	TQSYYPYLM	PRYADEIRKL	PVWAPLLPEL	IKOCKAFAAA	PCHDET
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2519>:

```
a738.seq
         ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACTGCC
      1
         GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
     51
         TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
         GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
         TGATGTCAAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
         TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
    251
    301
        GACATCGTCT CTTGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCCTG
        CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
    351
         CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
    401
         CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATTGTTTA
    451
         CAGCGGGCAA GGCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
         ACTACCTCAT GTGGGGCATA CTCGCCGCCG CCTACCTCAA CGGACAACGA
         AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
    601
         TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
    651
         CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
    701
         ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
    751
         TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
    801
         CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACCTGCC GCGCCAAATC
    851
    901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
    951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
   1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCCACAAC
   1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
   1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
   1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
   1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCCTCA TCCCCTTCGG
   1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
        AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTCGCA
   1351
        GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
         CCCCGCCACT GACGACAGTG CCAAAACCCT CAACCGGAAA ATCAACGAGT
         TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
         TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
   1501
         GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCCAC TCCGCCACCT
   1551
        ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
   1601
        CAATGGATGC GGGCGACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
   1651
        CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
   1701
        TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
   1751
   1801
        AAACCCTGCA AATGA
```

### This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

a738.pep

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAA
51 AAGLIVLLFL TAGKKLFDVK IPPISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

201 251 301 351 401 451 501 551 601	KIPPALGAIC LIMOTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI EWRKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIHDNL LSNLFTHSHN IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH SMLEYPLWYV YFLIPFGLML FLSPAEASDG IAFKKAANLG ILTASAAIFA GLLHLDWTYT RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF SLVNFALPEY PETQTWAEEA TLKSLKYRPH SATYRIALYL MRQGKVAEAK QWMRATQSYY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
a738/m738	98.3% identity in 604 aa overlap
a738.pep	10 20 30 40 50 60  MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQPSPDFYHDAAAAAGLIVLLFL
a738.pep	70 80 90 100 110 120 TAGKKLFDVKIPPISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL                                   TAGKKLFDVKIPAISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL 70 80 90 100 110 120
a738.pep	130 140 150 160 170 180 VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN    :
a738.pep	190 200 210 220 230 240 NLGHYLMWGILAAAYLNGQRKIPPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW
a738.pep	250 260 270 280 290 300 YFRSDKSNRRTILGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI
a738.pep	310 320 330 340 350 360  EWRKALAAFQSAPIFGHGWNSFAQQTFLINAEQHNIHDNLLSNLFTHSHNIVLQLLAEMG
a738.pep	370 380 390 400 410 420 ISGTLLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML
a738.pep	430 440 450 460 470 480 FLSPAEASDGIAFKKAANLGILTASAAIFAGLLHLDWTYTRMVNAFSPATDDSAKTLNRK
a738.pep	490 500 510 520 530 540 INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEEATLKSLKYRPHSATYRIALYL

```
560
                               570
                                       580
                                               590
          MRQGKVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA
a738.pep
          m738
          MRQGKVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA
                               570
                                               590
a738.pep
          KPCKX.
          \Box
m738
          KPCKX
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2521>: g739.seq

```
1 ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51 ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCCGTA CTGCCCACAA ACGCCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCCGAAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACAC CCGAAAAACA
551 CGCCGGCCAA ACCCCCATAAA GAGATTCTCG ACAACCTCTT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>: g739.pep

```
1 MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51 PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAOPD GTEESGSGLP
```

- 101 SPAAPKKNRV KPRPSDAARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
- 151 RKETPEKQAQ PKETPKEKET PKENHTKPDT PKNTPAKPHK EILDNLF*

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2523>: m739.seq

```
1 ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51 ACGCGCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACG CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCCGTA CTGCCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCCGAAAA ACAGGCGCAG CCCAAAGAA CGCCCAAAGA
501 AAACCATACC AAACCGGACA CCCCGAAAAA CACGCCGCC AAACCCCATA
551 AAGAAATTCT CGACAAACTC TTC
```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>: m739.pep

```
1 MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51 PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQPADTAQT DRQPDDAGTQ AENTLKETPV LPTNVPRPEP
```

151' RKETPEKQAQ PKETPKENHT KPDTPKNTPP KPHKEILDKL F

Computer analysis of the amino acid sequences gave the following results: Homology with a predicted ORF from N. meningitidis menA with menB

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from N. gonorrhoeae:

m739/g739

	10 20 30 40 50 60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPQHTDSPRET 
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPQHTDSPRET
<b>9</b>	10 20 30 40 50 60
	70 80 90 100 110 120
m739.pep	70 80 90 100 110 120 EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSPAAPKKNRVKPQPADTAQT
m/39.pep	
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSGLPSPAAPKKNRVKPRPSDAARA
	70 80 90 100 110 120
	130 140 150 160 170
m739.pep	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKENHTKPDT
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPDT 130 140 150 160 170 180
	130 140 150 160 170 180
	180 190
m739.pep	PKNTPPKPHKEILDKLF
700	
g739	190
The following	g partial DNA sequence was identified in N. meningitidis <seq 2525="" id="">:</seq>
a739.se	pq
	1 ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
	1 ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
10 15	
20	
25	
30	
35	1 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
40	
45	
50 55	
55	T CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA
This correspo	nds to the amino acid sequence <seq 2526;="" 739.a="" id="" orf="">:</seq>
a739.pe	
_	1 MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAIGIVSTFN PNGDKTLOTE
5	1 POHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
10	
15	1 RKETPEKQAQ PKETPKEKET PKENHTKPDT PKNTPPKPHK EILDNLF*
a739/m7	39 93.9% identity in 197 aa overlap
u133/11.	55 55.50 Idoneley in 157 dd Overlap
	10 20 30 40 50 60
a739.pe	
m739	
m/39	10 20 30 40 50 60
	70 80 90 100 110 120
a739.pe	
720	
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSPAAPKKNRVKPQPADTAQT 70 80 90 100 110 120
	70 80 90 100 110 120
	130 140 150 160 170 180
a739.pe	P DRQPDDAGAQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPDT
5.5.5	
m739	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKENHTKPDT
	130 140 150 160 170

PCT/US99/09346

1204

190 PKNTPPKPHKEILDNLFX a739.pep m739 PKNTPPKPHKEILDKLF 180 The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 2527>: g740.seq ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCCAGC 51 101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa 151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATTT 201 GAAACgtcaa ACCATGTTTC TGTTTATTCC GATTGTTTTG CTGGTTGTGT 251 ATTTGTTCCA CTATTTCGGC GCGTTTTag This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>: g740.pep MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK FVLFETIKHH LKQGFDLKRQ TMFLFIPIVL LVVYLFHYFG AF* The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2529>: m740.seq ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACTCCAGC 51 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAA 101 151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT 251 ATTTGTTCCA CTATTTTGGC GCGTTTTAG This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>: m740.pep MSRNLLVRWL AVCLIPLATL AVFAANPPED KLQHLINGII LACEATFLFK FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLFHYFG AF* 51 93.5% identity in 92 aa overlap m740/q740 10 20 30 40 50 60  ${\tt MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLQHLINGIILACEATFLFKFVLFDTIKHH}$ m740.pep MSRNLLVRWLAVCLIPLATLAVFAANPPEDKPQHLINGIILACEATFLFKFVLFETIKHH a740 10 20 30 40 70 80 LKQEFDLKRQTMLLFIPIILLIVYLFHYFGAFX m740.pep 111 | 11111111111111111111111111111 q740 LKQGFDLKRQTMFLFIPIVLLVVYLFHYFGAFX 70 80 90 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2531>: a740.seq ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT 1 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCCAGC 51 101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTT GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT 251 ATTTGTTCCA CTATTTTGGC GCGTTTTAG This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>: a740.pep MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHLINGII LACEATFLFK FVLFDTIKHH LKQEFDLKRQ TMLLFIPIIL LIVYLFHYFG AF* a740/m740 97.8% identity in 92 aa overlap 10 20 30 40 50 60

```
MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPQHLINGIILACEATFLFKFVLFDTIKHH
      a740.pep
                 MSRNLLVRWLAVCLIPLATLAVFAANPPEDKLQHLINGIILACEATFLFKFVLFDTIKHH
      m740
                        10
                                 20
                                          30
                                                   40
                                                            50
                                                                     60
                        70
                                 80
                 LKQEFDLKRQTMLLFIPIILLIVYLFHYFGAFX
      a740.pep
                 LKQEFDLKRQTMLLFIPIILLIVYLFHYFGAFX
      m740
                        70
                                 80
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2533>:
      g741.seg
                GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
             1
               TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTC GCCGCCGACA
            51
               TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
           101
               AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
               ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
          201
               AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
           251
               TTCGACTTCG TGCAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
          301
          351
               AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
               TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
               CAACGCTCCT TCCTTGTCAG CGATTTGGGC GGAGAACATA CCGCCTTCAA
          451
               CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
          501
               ACGATGCCGA CGGAAAACTG ACCTATACCA TAGATTTCGC CGCCAAACAG
          551
               GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
          601
               TGCCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
          651
               GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACTTACCG CCTCGCCCTT
               TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
               GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG
This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:
     g741.pep
               VNRTTFCCLS LTAGPDSDRL QQRRGGGGGV AADIGTGLAD ALTAPLDHKD
            1
               KGLKSLTLEA SIPONGTLTL SAQGAEKTFK AGGKDNSLNT GKLKNDKISR
               FDFVQKIEVD GQTITLASGE FQIYKQDHSA VVALRIEKIN NPDKIDSLIN
               QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
          151
               GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
          201
          251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2535>:
     m741.seq
               GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
               GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
           51
               GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
          101
               CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
               GGCGGCACAA GGTGCGGAAA AAACTTATGG AAACGGTGAC AGCCTCAATA
              CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
          251
              ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
          301
              ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
          351
          401 AAGATTCGGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
              GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
          451
              CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
          551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAAATC
          601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
          651 CAAGCCGGAT GGAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
              ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
               CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
              TATCGGCCTT GCCGCCAAGC AATAA
This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:
     m741.pep
              VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT APLDHKDKGL
              QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRFDFIRO
           51
              IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMVAKRQFRI
```

```
151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQGNGKI
              EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA
              QEVAGSAEVK TVNGIRHIGL AAKO*
m741/g741 61.4% identity in 280 aa overlap
                                              30
                 VNRTAFCCLSLTT---ALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQ
     m741.pep
                  1111:1111111: : ;
                                       VNRTTFCCLSLTAGPDSDRLQQRRGGGGGVAADIGTGLADALTAPLDHKDKGLKSLTLEA
     g741
                                  20
                                                     40
                  60
                                        80
                                                 90
                                                         100
                                                                   110
                 SVRKNEKLKLAAQGAEKTY---GNGDSLNTGKLKNDKVSRFDFIRQIEVDGQLITLESGE
     m741.pep
                       SIPQNGTLTLSAQGAEKTFKAGGKDNSLNTGKLKNDKISRFDFVQKIEVDGQTITLASGE
     g741
                         70
                                  80
                                           90
                                                    100
                    120
                             130
                                       140
                                                         160
                                                                   170
                 FQVYKQSHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGT
     m741.pep
                 FQIYKQDHSAVVALRIEKINNPDKIDSLINQRSFLVSDLGGEHTAFNQLPDG-KAEYHGK
     q741
                                 140
                                          150
                                                   160
                    180
                             190
                                       200
                                                210
                                                                   230
                 AFGSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYN
     m741.pep
                 AFSSDDADGKLTYTIDFAAKQGHGKIEHLKTPEQNVELASAELKADEKSHAVILGDTRYG
     g741
               180
                        190
                                  200
                                           210
                                                    220
                             250
                                      260
                                                270
                 QAEKGSYSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAAKQX
     m741.pep
                   111:1 1::11 :111:111 11 : :::|1:| 111
     q741
                 GEEKGTYRLALFGDRAQEIAGSATVKIGEKVHEIGIADKQX
               240
                        250
                                  260
                                           270
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2537>:
     a741.seq
              GTGAACCGAA CTGCCTTCTG CTGCCTTTCT TTGACCGCCG CCCTGATTCT
           1
              GACCGCCTGC AGCAGCGGAG GCGGCGGTGT CGCCGCCGAC ATCGGCGCGG
          51
              TGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAAGTTTG
              CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAAACGAGA AACTGAAGCT
              GGCGGCACAA GGTGCGGAAA AAACTTATGG AAACGGCGAC AGCCTCAATA
         201
              CGGGCAAATT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAA
         251
             ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGCGGAG AGTTCCAAGT
         301
             GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC
         351
         401 AAGATTCGGA GCATTCAGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
             GGCGATATAG CGGGTGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
         451
         501 CAGGGCGACA TATCGCGGGA CGGCATTCGG TTCAGACGAT GCCAGTGGAA
         551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGACA CGGCAAAATC
             GAACATTTGA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT
         601
         651 CAAGCCGGAT AAAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
         701 ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC
         751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAACG GCATACGCCA
         801 TATCGGTCTT GCCGCCAAGC AGTAA
This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:
    a741.pep
              VNRTAFCCLS LTAALILTAC SSGGGGVAAD IGAVLADALT APLDHKDKSL
           1
             QSLTLDQSVR KNEKLKLAAQ GAEKTYGNGD SLNTGKLKND KVSRFDFIRQ
          51
         101 IEVDGQLITL ESGEFQVYKQ SHSALTALQT EQVQDSEHSG KMVAKRQFRI
         151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD ASGKLTYTID FAAKQGHGKI
         201 EHLKSPELNV DLAASDIKPD KKRHAVISGS VLYNQAEKGS YSLGIFGGQA
         251 QEVAGSAEVE TANGIRHIGL AAKO*
```

a741.pep	10 VNRTAFCCLSLTAA	20 LILTACSSGO				
m741	VNRTAFCCLSLTTA				)	
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAAQGAEK	TYGNGDSLNI	GKLKNDKVSF	RFDFIRQIEV	OGQLITLESG	EFQVYKQ
m741	KNEKLKLAAQGAEK		GKLKNDKVSF	RFDFIRQIEVI	OGQLITLESG	EFQVYKQ
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQ					TAFGSDD
/ m741	SHSALTAFQTEQIQ					
	130	140	150	160	170	180
	190	200	210	222	000	
a741.pep				220	230	240
a/41.pep	ASGKLTYTIDFAAK				IAVISGSVLYN	IQAEKGS
m741	:				1	
ш/41	AGGKLTYTIDFAAK 190	QGNGKIERLK 200				
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVA	<del>-</del>		ıχ		
~ · · - · Þ ~ Þ						
m741	YSLGIFGGKAQEVA					
	250	260	270	,	•	

g742.seq not found yet

g742.pep not found yet

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2539>: m742.seq

0 1		,			2241
2.seq					
1	ATGGTTTACG			GGCGACAGCA	GTGTGCTTAC
51		ATGTATCAGA			TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAAT	CAGAAAACTG	CCCCGTTCAG	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TTAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA			CCGAAGTGTC	
301	AATGAATCCG	ATGCGAAGGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG		ATGCGGTAGG	CTTTTTGACT	GAAAAAAACG
401	AAGTCATCCC		AAAGATAAGG	CATTGGAGAA	
451	TATCGTGATG			GAGCGCAAAG	
501	TAAAAACCGT			ACAGTATCGC	AGCCGCCGTG
551	CCGCAGAACG		TTTGACAAGT	GTATGAGTGA	CCCTTTCGCG
601	CTGGACTTTA			GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA			GAAGGAGGC	ATCTTTAATA
701		ACGTTTTCCA			CTTTAATCGG
751	AAGGCTACCG			ATGCCGTTGC	GGCATACCAA
801	AGACGACCGC			CCTGACCGGC	ACATATGGGC
851	TGTTCGGGCG	GGAGCATGAT		GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT		AGAAATCTAC		ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACGG	CGATTTGTCG	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG		AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT		GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCGAC	GGCACGCCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCGG
1301	TTTGGAAAAC	CGTCAAAGTG		ATGTTCCTGC	
1351		ACCTCAACAC		CATTCGCTGA	
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA

1451	CGCGCTATGA	GACTTCGCAA	ACCAAAGATA	TGCCTGTCCG	CTATGGGCAG
1501	CCGGCAAGCG	ATTTTCAGAC	GGCATCGAGC	ATTAGGGCGG	ATCAGGACCA
1551	TTACACGGCC	AAGATGCAAG	GTCATAAATT	GACGCCCTAT	GCAGGCATTA
1601	CCTATGACTT	GACACCGCAA	CAGAGTATTT	ACGGAAGTTA	TACCAAAATC
1651	TTCAAACAGC	AGGATAATGT	CGATGTCAGT	GCCAAAACCG	TTTTACCGCC
1701	TTTGGTCGGC	ACAAACTATG	AGGTAGGCTG	GAAAGGCGCG	TTCTTGCAAG
1751		TGCTTCGTTC		ACCTCGAACA	GAAAAACCGC
1801			TGTTCCCGGA		AGCAGGGGTC
1851	GTTCCAAACC		CGATAGGCAA		AGGGGTGCGG
1901	AATTCGAGTT		TTGAACGAAG		CTTTGCGGGT
1951			CTACAAAAAC		TCAACGCCGA
2001			GTGCAGACCC		AGCAATTTCA
2051			TTCGGAACGA		ACCGAATACG
2101			CGTGTCCGCA	CAAAGCGGCA	CAAGCAGTCT
.2151	GTATAACATC			GATAGACGGT	TTCGTCCGTT
2201	ACGAATTGGG	CAAACACGCC	AAATTGAGCC	TCATCGGTAC	GAACTTAAAC
2251			CAACTACAAC		GCGCAAACAA
2301	CTTCTACGGA	GAGCCGCGCA	ÇTGTCAGCAT	GAAACTGGAT	TGGCAGTTTT
2351	AA				

#### This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```
m742.pep
         MVYGIAEADA GDSSVLTLGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
         ACNRPLOLPR NTYLGEDWSR LSADKYNLFS GFKHVFDNGW QLNAEVSYTK
     51
         NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
         YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSDPFA
         LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAAQRFP NSLYDSSFNR
         KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FFVGYAYGDE
    251
    301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEPDGDLS SPLVRGHKEP
         DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
    351
         YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN
    401
    451
         YAKYLNTNKT HSLTASTRFN VTGRLHLLGG LHYTRYETSQ TKDMPVRYGQ
         PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
    551
         FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRLNASF ALFYLEQKNR
         TVVDFGYVPG AGGKQGSFQT VAKPIGKVVS RGAEFELSGE LNEDWKVFAG
    601
    651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
    701
         GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
         GRTYFENNYN RTRGANNFYG EPRTVSMKLD WOF*
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2541>:

```
a742.seq
         ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCGACAGCA GTGTGCTTAC
      1
    ′ 51
         TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
         TTATTTTGTC CTGTGAAAAT CAGAAAACTG CCCCGTTCAG TTCAACGCCT
         GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
         TTGGTCGCGG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTTCAAAC
    251
         ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
    301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
    351 GGCGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAAACG
    401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
    451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
    501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTG
    551 CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
    601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
    651 CAAGTCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
    701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
    751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
    801 AGACGACCGC CAATGGGGAA TTAAACTTGA CCTGACCGGC ACATATGGGC
         TGTTCGGGCG GGAGCATGAT TTCTTTGTCG GCTATGCCTA CGGCGATGAA
    901 AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
         TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAGGGGG
   1001
         AGCCGGACGG TGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
   1051
         GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
         ATGCAGGAAT GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
   1101
         GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA
   1151
```

1201	TATGTCGATG	TATATGAACT	GGATGAAAAA	GGCAATAAGA	TTCAGGAGAC	
1251	CAATCCCGAC	GGCACGCCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCGG	
1301	TTTGGAAAAC	CGTCAAAGTG	GCCGACGACC	ATGTTCCTGC	GCTGTATAAC	
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTCGCTGA	CTGCCGGCAC	
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCATCT	TTTGGGCGGG	CTGCACTACA	
1451	CGCGCTATGA	AACCTCGCAA	ACCAAAGATA	TGCCTGTCCG	CTATGGGCAG	
1501	CCGGCAAGCG	ATTTTCAGAC	GGCATCGAGC	ATTAAGGCGG	ATCAGGACCA	
1551	TTATACGGCC.	AAGATGCAAG	GTCATAAATT	GACGCCCTAT	GCAGGCATTA	
1601	CCTATGATTT	GACACCGCAA	CAGAGTATTT	ACGGAAGTTA	TACCAAAATC	
1651		AGGATAATGT		GCCAAAACCG	TTTTACCGCC	
1701	TTTGGTCGGC	ACAAACTATG	AGGTAGGCTG	GAAAGGCGCG	TTCTTGCAAG	
1751	GACGGCTGAA	TGCTTCGTTC	GCATTGTTTT	ACCTCGAACA	GAAAAACCGC	
1801	ACGGTCGTCG	ATTTTGGCTA	TGTTCCCGGA	GCAGGCGGCA	AGCAGGGGTC	
1851	GTTCCAAACC	GTTGCCAAAC	CGATAGGCAA	AGTGGTCAGC	AGGGGTGCGG	
1901	AATTCGAGTT	GTCGGGTGAG	TTGAACGAAG	ATTGGAAAGT	CTTTGCGGGT	
1951	TACACCTACA	ACAAGAGCCG	CTACAAAAAC	GCCGCCGAAG	TCAACGCCGA	
2001	ACGCCTCGCC	AAAAACACAG	GCGCAGACCC	GTACAACTTC	AGCAATTTCA	
2051	CACCCGTGCA	CATATTCCGT	TTCGGAACGA	GCTTCCATAT	ACCGAATACG	
2101	GGGCTGACCG	TCGGCGGCGG	CGTGTCCGCA	CAAAGCGGCA	CAAGCAGTCT	
2151	GTATAACATC	AGGCAGGGCG	GCTACGGGCT	GATAGACGGT	TTCGTCCGTT	
2201	ACGAATTGGG	CAAACACGCT	AAATTGAGCC	TCATCGGTAC	GAACTTAAAC	
2251			CAACTACAAC		GCGCAAACAA	
2301	CTTCTATGGA	GAGCCGCGCA	CTGTCAGCAT	GAAACTGGAT	TGGCAGTTTT	
2351	AA					
esponds to the amino acid sequence < SEO ID 2542: OPE 742						

# This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

42.pep					
1	MVYGIAEADA	GDSSVLTLGG	MYQKSREVPD	FSGIILSCEN	QKTAPFSSTP
51	ACNRPLQLPR	NTYLGEDWSR	LSADKYNLFS	GFKHVFDNGW	QLNAEVSYTK
101	NESDAKVGQF	FLKNEHAAGL	SDEDAVGFLT	EKNEVIPFEP	KDKALEKLKA
151	YRDETAKEYR	ERKDDFVKNR	FDNTAFEQYR	SRRAAERKAG	FDECMSAPFA
201	LDFICQGSWG	DPGVDADKSE	FVDKALAKEG	IFNNAAQRFP	NSLYDSSFNR
251		$\mathtt{MPLRHTKDDR}$		TYGLFGREHD	FFVGYAYGDE
301	KIRSEYLEIY	ERRHRVRPNT	GATHGVYAGS	CQGEPDGDLS	SPLVRGHKEP
351				DAEGKQVYYY	
401				TVPVWKTVKV	
451				LHYTRYETSQ	TKDMPVRYGQ
501	PASDFQTASS	IKADQDHYTA	KMQGHKLTPY	AGITYDLTPQ	QSIYGSYTKI
551	FKQQDNVDVS	AKTVLPPLVG	TNYEVGWKGA	FLQGRLNASF	ALFYLEQKNR
601	TVVDFGYVPG	AGGKQGSFQT	VAKPIGKVVS	RGAEFELSGE	LNEDWKVFAG
651	YTYNKSRYKN	AAEVNAERLA	KNTGADPYNF	SNFTPVHIFR	FGTSFHIPNT
701	GLTVGGGVSA	QSGTSSLYNI	RQGGYGLIDG	FVRYELGKHA	KLSLIGTNLN
751	GRTYFENNYN	RTRGANNFYG	EPRTVSMKLD	WOF*	

# a742/m742 98.5% identity in 783 aa overlap

	•	- <b>T</b>				
	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSS	VLTLGGMYQK	SREVPDFSGI	ILSCENOKTA	PESSTPACNE	RPLOLPR
	11111111111111	1111111111	1111111111			
m742	MVYGIAEADAGDSS	VITLGGMYOK	SREVPDESCT	TIDOFNORMA	DECCUDACNE	וווווו
	10					
	10	20	30	40	50	60
	70	80	90	100	110	120
a742.pep	NTYLGEDWSRLSAD	KYNLFSGFKH	VFDNGWQLNA	EVSYTKNESD	AKVGOFFLKN	EHAAGL
	- 11111111111111	1111111111		111111111		
m742 '	NTYLGEDWSRLSAD	KYNLESGEKH	VEDNGWOLNA	EVSYTKNESD	AKUCOPPI KK	1・11:1
	70	80	90			
	70	00	90	100	110	120
	130	140	150	160	170	180
a742.pep	SDEDAVGFLTEKNE	VIPFEPKDKA	LEKLKAYRDE	TAKEYRERKD	DFVKNRFDNI	'AFEOYR
		11111111111		1111111111		
m742	SGEDAVGFLTEKNE	VIPFEPKDKA	LEKLKAYRDE	TAKEYRERKD	DEVKNDEDNT	A EEOVD
	130	140	150	160	170	
	100	130	130	100	170	180
	100	000				
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDEC	MSAPFALDFI	CQGSWGDPGV	'DADKSEFVDK	ALAKEGIFNN	AAORFP

WO 99/57280 PCT/US99/09346

1210

m742	 SRRAAERKAGF 190	:		:       ADKAEFVDKA 220		IIIII AQRFP 240
a742.pep	250 NSLYDSSFNRK	260 ATANRRYSYMPLRH'	270	280	290	300
m742					111111111	1111
a742.pep		320 RRHRVRPNTGATHG				
m742	KIRSEYLEIYE 310	:	/YAGSCQEEPI 330		  GHKEPDWQAY    350	DEKGN 360
a742.pep		380 KKIKTEPKLDAEGK(				
m742	RTVYAEECRNA 370	KKIKTEPKLDAEGK( 380	QVYYYDEYSGS 390	SRTPVYVDVY 400	ELDEKGNKIQI 410	ETNPD 420
a742.pep		440 VPVWKTVKVADDHVI				
m742	GTPAFTGFSGT 430	VPVWKTVKVADDHVI 440	PALYNYAKYLN 450	NTNKTHSLTA 460	STRFNVTGRLI 470	HLLGG 480
a742.pep		500 KDMPVRYGQPASDFÇ				
m742	LHYTRYETSQT 490	KDMPVRYGQPASDFÇ 500	TASSIRADQI 510	DHYTAKMQGH 520	KLTPYAGITYI 530	DLTPQ 540
a742.pep		560 KQQDNVDVSAKTVLE             KQQDNVDVSAKTVLE 560	11111111111	111111111	1111111111	1111
a742.pep m742	610 TVVDFGYVPGA	620 GGKQGSFQTVAKPIG             GGKQGSFQTVAKPIG	630 KVVSRGAEFE	640 ELSGELNEDW	650 KVFAGYTYNKS	660 GRYKN
7.10	610 670	620 680	630 690	640 700	650 710	660 720
a742.pep.	11111111111	NTGADPYNFSNFTPV  ::              SSADPYNFSNFTPV   680	111111111	  IPNTGLTVG		LYNI
a742.pep	730	740 VRYELGKHAKLSLIG	750	700 760 NNYNRTRGAI	710 770 NNFYGEPRTVS	720 780 MKLD
m742			11111111111		[][]	1111
a742.pep	WQFX					
m742	WQFX					
a742/ p25184 sp P25184 P >gi 94923 pi		FERRIC-PSEUDO	BACTIN	358 RI	ECEPTOR	PRECURSOR

```
ferric-pseudobactin receptor precursor - Pseudomonas putida >gi|45723 (X56605)
      pseudobactin uptake protein [Pseudomonas putida]Length = 819
       Score = 152 bits (381), Expect = 6e-36
       Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)
      Query: 436 KTVKVADDHV-PALYNYAKYLNTNKTHSLTAGTRFNVTGRLHLLGGLHYTRYETSQTKDM 494
                +T K DD + P + + Y + N+ + RFN+T LHL+ G + Y
      Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDDLHLILGARASNYRFDYAL-- 564
     Ouery: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
                                 ++ +TPYAGI YDLT +QS+Y SYT IFK O
     Sbjct: 565 -WRIGNEPAPYKM------VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609
     Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLQGRLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
                +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N
     Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRLNANIALYMVKRDNLAESTNEVVPDSGGL 668
     Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
                       + +
                              ++G + ELSGE+
                                            W VF GY++ ++
     Sbjct: 669 IAS-----RAVDGAETKGVDVELSGEVLPGWNVFTGYSHTRTE------D 707
     Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
                     + P+ FRF ++ +P
                                          LT+GGGV+ S ++ + YN + O Y +
     Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGEWEKLTLGGGVNWNSKSTLNFARYNSHVTQDDYFV 767
     Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
                     RY + +
                             +L N+ + Y Y G+ YG PR ++ L + F
     Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819
     q743.seq not found yet
     g743.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2543>:
     m743.seq
            1 ATGAATCAAA ATCATTTTTC ACTTAAAATT CTGACCGTTA TGCTGTTATC
           51 GGCTTACGGT GGTTCTTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
          101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
          151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
          201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
              TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
              ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTCAG GCTTGCAGAC
              GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
              TGACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
              TCTCCGAGTA CCGATTTGGC GGTTTATGAC CATATTGAAG TTGTACGGGG
              TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
          551 TGATCCGTAA GTGA
This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:
     m743.pep
            1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
           51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSRLD DKAVHTLEEA
          101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
          151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2545>:
     a743.seq
           1 ATGAATCAAA ATCATTTTTC ACTTAAAATT CTGACCGTTA TGCTGTTATC
          51 GGCTTACGGT GGTTCTTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
         101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTCG
         151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCCACCGC
         201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
```

TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
ATGAAAAACA CGACGGTGT CAACGTTGTG CGCGATTCAG GCTTGCAGAC

```
GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
                TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
                TCTCCGAGTA CCGATTTGGC GGTTTATGAC CATATTGAAG TTGTACGGGG
                TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
                TGATCCGTAA GCGA
This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:
                MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
            51
                GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSRLD DKAVHTLEEA
                MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
               SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR
a743/m743 98.9% identity in 187 aa overlap
                           10
                                     20
                                               30
                                                         40
                                                                    50
                   MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
     a743.pep
                   MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT
     m743
                           10
                                     20
                                                         40
                                                                   50
                                                                              60
                           70
                                     80
                                               90
                                                        100
                                                                  110
                                                                            120
                   IDRMSTATGMRIAGKDTPQSVSVITRSRLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL
     a743.pep
                   IDRMSTATGMRIAGKDTPQSVSVITRSRLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFL
     m743
                           70
                                     80
                                               90
                                                        100
                                                                            120
                          130
                                    140
                                              150
                                                        160
                                                                  170
                                                                            180
                   SRGFYIDQIGEDGITVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
     a743.pep
                   m743
                  SRGFYIDQIGEDGMTVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
                          130
                                    140
                                              150
                                                        160
     a743.pep
                  TVNLIRKR
                  111111
     m743
                  TVNLIRKX
g744.seq not found yet
g744.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2547>:
m744.seq
        ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
        CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
     51
        AATATTTGGA TGAATTATGT GAACCAAATA TTTCGTTTTT AATCGGAGAA
    101
    151 AAGGGAACTG GAAAGACAGC ATATGCTGTT TATTTAACTA ATAACTTCTA
        TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
    201
        AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
        AGTATTTGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
    301
        TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
    401
        ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTTGATCC GGAAATTGTA
        CAAGCAATAA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
    451
    501
        TGGAAAATTT GTTAAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTTA
        CAGAAAGTAA ATTCCAAGCA AATTTAGGTT TTATTGAAAG AAAATTTAAA
    601
        GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
        TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
        GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTTAAATAA TGATATCTTC
    701
        CCTTCCATTA AAGATAGTAA GGGAAGGATG AGAGTTGTGT TATTGATTAG
        ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAAT ACCAAACTTC
    801
        AAGATAATTC AGTATTTTTA GACTGGAGGA CGGATTATAA ATCTTATAGA
    851
    901 AGTTCAAAGA TTTTTGGCGT TTTTGATCAT CTTTTGAGAA CCCAGCAAGA
    951
        AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
        GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTTATT
   1001
        AGCTTCCTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
   1051
        TACTTTGCTA CAAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
   1101
   1151
        AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTTACTT
        GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAAA GTGATTATCA
```

1251 AAATTTCCTG AAATTTTTTG AATTTTTAAA CGGGAAAGAT AGATTTAAAT

PCT/US99/09346 WO 99/57280 1213

```
1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
     ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
     ATTTTTATTT GACTTGAATG TTATTGCTTA TTTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAT
1501 ATTTCTCCTA AAATAAAAAC TGAAACTGAA TATTTAATAT TTTCAGGATT
     ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGAACAAA CAGTAA
```

### This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>: m744.pep

```
MKPLKTLEFG FVDAANYRRR ENKDLFNRIF VKGEYLDELC EPNISFLIGE
     KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
 51
     SIWKVILYLL ISNQIKCKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEEESQQ ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQNQN TKLQDNSVFL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNSWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLFY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
     TSVEIPKFMS TANEFLQFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPFKNK O*
```

```
g745.seq
         not found yet
g745.pep
        not found yet
```

## The following partial DNA sequence was identified in N. meningitidis <SEO ID 2549>:

```
m745.seq
         ATGTTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGG
      1
      51 GACAATATTC ATCAATAAGA AAACTTCAAA GCAAAAGGCG ACATTAGATG
    101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
    151 ATTTCGCCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
    201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
    251 GAGGGCATTT ACTTACCGTA ATCAATCGGC ACGAGTTTTA TGCGTGCGCA
    301 ATCAACTCGG GAGTATTGGA TGAGGATTTG TTTAAACGGC TGCATTGCAC
    351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
    401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGGTT
     451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTTGT GA
```

#### This corresponds to the amino acid sequence <SEO ID 2550; ORF 745>:

```
m745.pep
      1 MFWQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
      51 ISPYIRGTAV DDNNARIDLY EIYONKGGOW EKERGHLLTV INRHEFYACA
     101 INSGVLDEDL FKRLHCTNFI KLWNAVSPLV MKIREEERKD TIFRELEILV
     151 ALWKANPLKA SDL*
a745.seq not found yet
a745.pep not found yet
```

#### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2551>: q746.seq

```
1 ATGTCCGAAA ACAAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
 51 ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGGCGA AACCGGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCCTGCCT TGAAATCCGC CGCCGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAAAACGTA GGCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
    CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAAACCAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG
```

PCT/US99/09346

1214

```
751 GCGCAAAAAA CCGACAAAGC GGACAAAACC AAAACCGCCG AGAAGGAAAA
     ATCCGGCAAG GCGGGCAAAA AAGCCGCCAT TCAGGCAGGT TATGCCGAAA
851 AAGAACGCGC CTTGAGCCTC CAGCGCAAAA TGAAGGCGGC GGGTATCGAT
901 TCGACCATCA CCGAAATCAT GACCGACAAC GGCAAAGTTT ACCGCGTCAA
951 ATCAAGCAAC TATAAAAACG CAAGGGATGC CGAACGCGAT TTGAACAAAC
     TGCGCGTGCA CGGCATCGCC GGCCAGGTAA CGAATGAATA G
1001
```

This corresponds to the amino acid sequence <SEQ ID 2552; ORF 746.ng>: g746.pep

```
MSENKQNEVL TGYEQLKRRN RRRLVTASSL VAASCILLAA ALSSDPADSN
    PAPQAGETGA TESQTANTAQ TPALKSAAEN GETAADKPQD LAGEDKPSAA
51
    DSEISEPENV GAPLVLINDR LEDSNIKGLE ESEKLQQAET AKTEPKQAKQ
101
151 RAAEKVSATA DSTDTVAVEK PKRTAEPKPQ KAERTAEAKP KAKETKTAEK
201 VADKPKTAAE KTKPDTAKSD SAVKEAKKAD KAEGKKTAEK DRSDGKKHET
    AQKTDKADKT KTAEKEKSGK AGKKAAIQAG YAEKERALSL ORKMKAAGID
251
301 STITEIMTDN GKVYRVKSSN YKNARDAERD LNKLRVHGIA GQVTNE*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2553>: m746.seq

```
ATGTCCGAAA ACAAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
    ACGGCGCAAC CGCCGCCC TCGTAACGGC AAGTTGCCTG GTTGCCGCCT
 51
    CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
101
151 GCCGGCGAAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCCG CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGAGCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAAACCG ACAAAGCGGA CAAGACCAAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATTC GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATTT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2554; ORF 746>: m746.рер

```
MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEOT
  1
 51 AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINERL EDSNIKGLEA SEKLQQAETA KTAPKQAKQR AAEKVPATAD
151 STDTVAVEKP KRTAETKPQK AERTAKAKPK AKETKTAEKV ADKPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALSLQRKM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from N. gonorrhoeae:

```
89.9% identity in 346 aa overlap
m746/g746
                         20
          MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQT----AGETSG
m746.pep
          MSENKQNEVLTGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA
g746
                 10
                         20
            60
                    70
                                  80
                                                 100
                                                         109
          VENKAAGAAQTPALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
m746.pep
          :1:::1::1111111111
                              TESQTANTAQTPALKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
q746
                 70
                         80
                                 90
                                        100
```

PCT/US99/09346 WO 99/57280

```
1215
```

```
130
                120
                               140
                                       150
         LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPO
m746.pep
          LEDSNIKGLEESEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPO
g746
                       140
               130
                              150
                                      160
                                              170
        170
                180
                       190
                               200
                                       210
                                              220
                                                     229
         KAERTAKAKPKAKETKTAEKVADKPKTAAEKTKPDTAKSDSAVKEAKKADKAESKKTAEK
m746.pep
         KAERTAEAKPKAKETKTAEKVADKPKTAAEKTKPDTAKSDSAVKEAKKADKAEGKKTAEK
q746
                       200
               190
                              210
                                      220
                       250
        230
                240
                                 260
                                         270
         DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALSLQRKMKAAGID
m746.pep
         DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKKAAIQAGYAEKERALSLQRKMKAAGID
q746
               250
                       260
                              270
                                      280
                                             290
          290
                  300
                          310
                                 320
                                         330
         STITEIMTDNGKVYRVKSSNYKNARDAERDLNKLRVHGIAGQVTNEX
m746.pep
         STITEIMTDNGKVYRVKSSNYKNARDAERDLNKLRVHGIAGQVTNEX
g746
                       320
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2555>: a746.seq

```
ATGTCCGAAA ACAAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
 1
    ACGGCGCAAC CGCCGCCGC TCGTAACGGC AAGTTGCCTG GTTGCCGCCT
51
    CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
101
    GCCGGCGAAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
151
201 CCCTGCCTTG AAATCCGCCG CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
    GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
    TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
351
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451
    AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAAA GCCAAAGAAA
    CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACTGC CGCCGAAAAA
551
    ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
601
    AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
    GCAAAAAACA CGAAACGGCA CAAAAAACCG ACAAAGCGGA CAAGACCAAA
701
    ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCCGCCATTC AGGCAGGTTA
    TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
801
    GTATCGATTC GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATTT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

- MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT 1
- AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG 51
- 101 APLVLINDRL EDSNIKGLEA SEKLQQAETA KTAPKQAKQR AAEKVPATAD
- STDTVAVEKP KRTAETKPQK AERTAKAKPK AKETKTAEKV ADKPKTAAEK
- TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK 201 251 TAEKEKSGKK AAIQAGYAEK ERALSLQRKM KAAGIDSTIT EIMTDNGKVY
- RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from N. meningitidis

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from N. meningitidis:

```
a746/m746; 99.7% identity in 332 aa overlap
```

	10	20	30	40	50	60
a746.pep	MSENKQNEVLSO	YEQLKRRNRRR	LVTASCLVAAS	CILLAAALSS	GPAEQTAGET	SGVENK
			1111111111	[]]]]	111111111	
m746	MSENKQNEVLSO	SYEQLKRRNRRR	LVTASCLVAAS	CILLAAALSS	GPAEQTAGET	SGVENK
	10	20	30	40	5.0	60

```
80
                               90
                                      100
          AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
a746.pep
          AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA
m746
                                      100
               130
                       140
                              150
                                      160
                                              170 .
          SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQKAERTAKAKPK
a746.pep
          SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQKAERTAKAKPK
m746
               130
                       140
                              150
                                      160
               190
                       200
                              210
                                      220
                                              230
                                                     240
          AKETKTAEKVADKPKTAAEKTKPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
a746.pep
          AKETKTAEKVADKPKTAAEKTKPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
m746
                              210
                                      220
                                             230
               250
                       260
                              270
                                      280
                                             290
          QKTDKADKTKTAEKEKSGKKAA1QAGYAEKERALSLQRKMKAAGIDSTITEIMTDNGKVY
a746.pep
          QKTDKADKTKTAEKEKSGKKAAIQAGYAEKERALSLQRKMKAAGIDSTITEIMTDNGKVY
m746
               250
                       260
                              270
                                      280
               310
                       320
                              330
a746.pep
         RVKSSNYKNARDAERDLNKLRVHGIAGQVTNEX
          m746
         RVKSSNYKNARDAERDLNKLRVHGIAGQVTNEX
                       320
                              330
```

q747, seg not found yet

g747.pep not found yet

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2557>: m747.seq

- 1 CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
- 51 GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
- 101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
- 151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
- 201 CCGTGAGATT GTCTTGGACG GTGACAAAAC CAAAATGGGC CGCTCCAAAT
- 251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
- 301 TCAAAATAG

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>: m747.pep

- 1 LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
- 51 VGLEFDPYYR HKTIYKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
- 101 SK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2559>: a747.seq

- 1 CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
- 51 GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAAA AGCGCCAAAG
- 101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
- 151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
- 201 CCGTGAGATT GTTTTGGACG GCGACAAAAC CAAAATGGGC CGCTCCAAAT
- 251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCTATAG TCAATTAAAA
- 301 TCAAAGTAG

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>: a747.pep

- 1 LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
- 51 VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
- 101 SK*

Computer analysis of this amino acid sequence gave the following results:

## Homology with a predicted ORF from N. meningitidis

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from N. meningitidis:

```
a747/m747
            97.1% identity in 102 aa overlap
                            20
                                     30
                                              40
                                                       50
           \verb|LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR
a747.pep
            m747
            LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR
                   10
                            20
                                     30
                                              40
                   70
                            80
                                     90
           HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
a747.pep
            HKTIYKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
m747
                            80
                                     90
a747/m80195
qi|150271 (M80195) outer membrane protein [Neisseria meningitidis] Length = 272
 Score = 59.3 bits (141), Expect = 6e-09
 Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)
         LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR 60
          + PW++ DL + K+ T
                              +D+++ GW G+G N+GK+L +S +E P+Y+
Sbjct: 174 INPWSEVKFDLNSRYKLNTGVTNLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233
Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
             + E + GD
                             + ++
                                   EYG RV
Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272
```

## The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2561>: g748.seq

```
ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTTCAAAAC
   1
      CGCCCTTGCC GTCGGCGCAA TCGGCGCAAT CGGAGGTTAT TTCGGCGGCA
 101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
 151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCCGCG
 201 GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
      AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
 251
 301 ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAAACTCC CGTCAGCCGG
 351 CAGCGGCATT TTGGGTAAAG CCTTCAACCC CGACGGATTG ACCGTTACCG
      TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
 401
 451
      AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCCAACG ATAAGCTGCA
 501 AAAAAGCTGG TGCGACGGCG ATTTGAGCCT GCAAATCTGC GCCTTCACCC
     CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAAACA CACCGCCCAA
 551
      ACCGCCGTCA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
 651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCCGAGAC GGCACGGGCA
 701 ACCCCAAGGT TTCCGATCCC AAAACCGCCG ACGAGGTTTT ATGGACGGGC
     GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
 751
 801 TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTTGG GACAGGACGC
     CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGAAAATA CAGCGGGGCG
 901 CCGATGGACG GCAAAAAGA AGCCGACCAA CCGGATTTCG CCAAAGACCC
     CGAGGGTGAT ATCACGCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCCTCAAA AAACACTGCC TCTTCCGCCG CGCCTACAGC
     TATTCTCGCG GACCCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101
     CGTCTGCTAT CAGGCAAATC TTGCCGACGG TTTCATCTTC GTGCAAAACC
     TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCCTT CGGCGGCGGC
     TATTTCTTCG TCTTGCCCGG CGTGGGAAAA GGCGGATTCT TGGGACAAGG
1201
1251
     GCTGCCGGGC GTATAA
```

## This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>: g748.pep

```
1 MSQNQPAQPT KRNLFKTALA VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPRQAF SIMCAFDVTA QSAKQLENLF RTLTARIEFL
101 TQGGEYQDGD DKLPSAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KTVHLQEMRD FPNDKLQKSW CDGDLSLQIC AFTPETCQTA LRDIIKHTAQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLQEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRRAYS
351 YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLLNGEPL EEYISPFGGG
```

```
401 YFFVLPGVGK GGFLGOGLPG V*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2563>: m748.seq

```
ATGAGCAAAA AACAACCCGC ACAACCGACC AGGCGCACTC TTTTTAAAAC
      CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
  51
      AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
 101
      CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
 201 GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
      AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
 251
      ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
 301
      CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTTG ACCGTTACCG
 351
      TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
 401
      AAACCGATTC ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
 451
      AAAAAGCTGG TGCGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
 501
      CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
     ACCGCCGTTA TCCGTTGGAG TATCGACGGG TGGCAGCCCA AATCCGAACC
 601
      CGGCGCGATG GCGGCGCGA ACCTGTTGGG CTTCAGGGAC GGCACGGGCA
 701 ACCCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTTT GTGGACGGGG
      GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
 801
     TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTTGG GACAGGACGC
      CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGCAAATA CAGCGGTGCG
 851
 901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
     CGAGGGTGAT ATCACGCCCA AAGACAGCCA TATACGCCTG GCGAATCCGC
 951
     GCGATCCCGA ATTCCTCAAA AAACACCGCC TCTTCCGCCG CGCCTACAGC
1001
     TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1051
     CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCATCTTC GTGCAAAACC
1101
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCCTT CGGCGGCGGC
1201 TATTTCTTCG TCTTGC
1251 GCTGCTGGGC GTATAA
     TATTTCTTCG TCTTGCCCGG CGTGGAAAAA GGCGGCTTTT TGGGGCAAGG
```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>: m748.pep

```
1 MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RTLTARIEFL
101 TQGGEYQDGD DKLPPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLSLQIC AFTPETCQAA LRDIIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHIRL ANPRDPEFLK KHRLFRRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLLNGEPL EEYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae* 

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from N. gonorrhoeae

```
m748/g748
           95.0% identity in 421 aa overlap
                         20
          {\tt MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKQGETAERTAESQHSPQAYPCYGEHQ}
m748.pep
           g748
          MSQNQPAQPTKRNLFKTALAVGAIGAIGGYFGGKKQGETAERTAESQHSPQAYPCYGEHQ
                 10
                         20
                                          40
                                                  50
                 70
                         80
                                         100
                                                 110
          {\tt AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGDDKLPPAGSGI}
m748.pep
          {\tt AGIVTPRQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGDDKLPSAGSGI}
g748
                 70
                         80
                                         100
                                                 110
                130
                        140
                                150
          LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSLQIC
m748.pep
          LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKTVHLQEMRDFPNDKLQKSWCDGDLSLQIC
g748
                130
                        140
                                150
                                                 170
                                                         180
                        200
                                210
                                        220
                                                         240
m748.pep
          AFTPETCQAALRDIIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
```

```
AFTPETCQTALRDIIKHTAQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
q748
               190
                       200
                              210
                                      220
               250
                       260
                              270
                                      280
          KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDIFGRRKYSGA
m748.pep
          KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRRFVEFWDRTPLQEQTDIFGRRKYSGA
a748
               250
                       260
                              270
                                      280
               310
                       320
                              330
                                      340
                                             350
                                                     360
          PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
m748.pep
          {	t PMDGKKEADQPDFAKDPEGDITPKDSHMRLANPRDPEFLKKHCLFRRAYSYSRGPASSGQ}
g748
               310
                      320
                              330
                                     340
                      380
                              390
                                      400
         \verb|LDVGLVFVCYQANLADGFIFVQNLLNGEPLEEYISPFGGGYFFVLPGVEKGGFLGQGLLG|
m748.pep
         a748
         LDVGLVFVCYQANLADGFIFVQNLLNGEPLEEYISPFGGGYFFVLPGVGKGGFLGQGLPG
               370
                      380
                              390
                                     400
                                             410
m748.pep
         ٧X
         11
q748
         νx
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2565>: a748.seq

```
ATGAGCAAAA ACCAACCGC ACAACCGACC AGGCGCACTC TTTTTAAAAC
   1
      CGCGATCGCA GCTGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
  51
      AAAAACGGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
 101
      CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
 151
      GCAGGCGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
 251
      AGCAGCTGGA AAACCTGTTC CGCACGCTGA CCGCCCGCAT CGAGTTTCTC
      ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
 301
      CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTTG ACCGTTACCG
      TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
      AAACCGATTC ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
 451
 501 AAAAAGCTGG TGCGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
      CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
      ACCGCCGTTA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
      CGGCGCGATG GCGGCGCGA ACCTGTTGGG CTTCCGCGAC GGCACGGGCA
 651
     ACCCCAAAGT TTCCGACCCC AAAACTGCCG ACGAGGTTTT GTGGACGGGG
 701
     GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
 751
     TCAGGCAGTC CGCCTTATCC GCCACTTTGT TGAGTTTTGG GACAGGACGC
 801
     CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GGCGCAAATA CAGCGGCGCG
 851
     CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
     CGAGGGGAAT ACCACGCCCA AAGACAGCCA TATACGCCTG GCGAATCCGC
 951
     GCGATCCCGA GTTCCTTAAA AAACACCGCC TCTTCCGCCG CGCCTACAGC
1051
     TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
     CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCATCTTC GTGCAAAACC
     TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCCTT CGGCGGCGGC
1151
     TATTTCTTCG TCTTGCCCGG CGTGGAAAAA GGCGGCTTTT TGGGGCAAGG
1201
1251 GCTGCTGGGC GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2566; ORF 748.a>: a748.pep

```
1 MSKNQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKRGETA ERTAESQHSP
51 QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RTLTARIEFL
101 TQGGEYQDGD DKLPPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNDKLQKSW CDGDLSLQIC AFTPETCQAA LRDIIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLWTG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLQEQTD IFGRRKYSGA
301 PMDGKKEADQ PDFAKDPEGN TTPKDSHIRL ANPRDPEFLK KHRLFRRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLLNGEPL EEYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*
```

Computer analysis of this amino acid sequence gave the following results:

WO 99/57280 PCT/US99/09346 1220

## Homology with a predicted ORF from N meningitidis

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from N. meningitidis:

a748/m748	99.0% identity in 421 aa overlap
a748.pep m748	10 20 30 40 50 60  MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGGKKRGETAERTAESQHSPQAYPCYGEHQ    :
a748.pep	70 80 90 100 110 120 AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGEYQDGDDKLPPAGSGI
a748.pep m748	130 140 150 160 170 180 LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSLQIC IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
a748.pep	190 200 210 220 230 240 AFTPETCQAALRDIIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
a748.pep	250 260 270 280 290 300 KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRHFVEFWDRTPLQEQTDIFGRRKYSGA
a748.pep	310 320 330 340 350 360  PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
a748.pep m748	370 380 390 400 410 420 LDVGLVFVCYQANLADGFIFVQNLLNGEPLEEYISPFGGGYFFVLPGVEKGGFLGQGLLG LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
a748.pep m748	vx    vx

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2567>: g749.seq

1	ATGAGAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTGGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCCGCGCCG	GCCGCGTCCG
101	GTGAGACCCA	ATCCGCCAAC	GAAGGCGGTT	CGGTCGGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCGAT	GAATCTGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AGGGCGTGAT	GGTGGTGGAC	GAACGCGAAA	ATATCGCCCC	GGGGCTTTCC
301	GACAAAATGA	CCGTAAccct	GCTGCCGGGC	GAATACGAAA	TGACCTGCGG
351	CCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAGCCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGCCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTACGTTCA	AGGCGAGGTT	AAAGAGCTGG	CGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGCCACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGTGTG	AAGACGACTT
651	CAAAGACGGT	GCGAAAGATG	CCGGGTTTAC	CGGCTTCCAC	CGTATCGAAC
701	ACGCCCTTTG	GGTGGAAAAA	GACGTATCCG	GCGTGAAGGA	AACCGCGGCC
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC

```
801 GttcctCCG GGCAAAGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
      851 CGGCGGGCAG TAAAATCAGC GGCGAAGAAG ACCGttaCAG CCACACCGAT
      901 TTGAGCGACT TCCAAGCTAA TGCGGACGGA TCTAAAAAAA TCGTCGATTT
      951 GTTCCGTCCG TTGATTGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
     1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCAAA
     1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
     1151 TACTCGGCTT GAAATAA
 This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:
           MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIAVN DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
       51
      101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
      151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
           ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
      251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
      301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
      351 DGFETYDKLS EADRKALQAP INALAEDLAO LRGILGLK*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2569>:
m749.seq
           ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
       51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
      101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
     151 GACAATGCCT GCGAACCGAT GGAACTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
      251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
      301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
     351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
      451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
      501 CAAAACTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
      551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
      601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
      651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTCAC CGTATCGAAT
     701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
     751
          AAACTGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
     801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
     851 TGGCGGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
     901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
     951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
    1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
    1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
    1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
    1151 TACTCGGCTT GAAATAA
This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:
m749.pep
          MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
          DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
      51
     101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
     151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
     201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
     251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
     351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from
N. gonorrhoeae
```

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNS	GRKLEWEILE	KGVMVVDEREN	IAPGLSDKM	VTLLPGEYE	MTCGLLT
	- [ [ [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [	111111111	111111111	1111111111	111111111	111111
g749	VPSGQVVFNIKNNS	GRKLEWEILK	GVMVVDEREN	IAPGLSDKM	VTLLPGEYE	MTCGLLT
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTDSGFK	DTANEADLEK	KLSQPLADYKA	YVQGEVKELV	'AKTKTFTEAV	JKAGDIE
	111111111:11111	111111111	1 11111111	111111111:	111111111	111111
g749	NPRGKLVVADSGFK	DTANEADLEK	LPQPLADYKA			/KAGDIE
	130	140	150	160	170	180
	190	200	210	000		
m240 man			210	220	230	240
m749.pep	KAKSLFADTRVHYE					
~740	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			111111111	11111111:	
g749	KAKSLFAATRVHYE	200				
	190	200	210	220	230	240
	250	260	270	280	200	
m749.pep	DVSGVKEIAAKLMT				290	300
м/45.рер	1111111 111111	IIIIIIIIII		GGW2FTTFFA	AGSKISGEEL	RYSHTD
g749`	DVSGVKETAAKLMT	DVEALOKETD	AT.AFPPCKUV		VCCA16CEEL	
9,15	250	260	270	280	290	300
	200	200	270	200	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKI				AKYRTKDGFF	יייטעגיכ. 200
		111111111	11111111	11111111	111111111	IIIIII
q749	LSDFQANADGSKKI	VDLFRPLIEA:	KNKALLEKTD'	INFKOVNETT	AKYRTKDGFF	TYDELS
•	310	320	330	340	350	360
					550	300
	370	380	389			
m749.pep	EADRKALQASINAL	AEDLAQLRGI	LGLKX			
		111111111	1111			
g749	EADRKALQAPINALA	AEDLAQLRGI	LGLKX			
	370	380				

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2571>: a749.seq

```
ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
  51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
 151 GACAATGCCT GCGAACCGAT GGAACTGACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351
     TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
     AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
 401
 451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGGCGAAAAC
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
     CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
     AAACTGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
851 TGGCGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAA TCGTCGATTT
951
     GTTCCGTCCG TTGATCGAGA CCAAAAACAA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051
     GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
     ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA
```

# This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>: a749.pep

1 MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA

251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N meningitidis* 

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from N. meningitidis:

a749/m749	99.7% identity in 388 aa overlap
a749.pep m749	10 20 30 40 50 60  MRKFNLTALSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIAVNDNACEPMELT
a749.pep m749	70 80 90 100 110 120  VPSGQVVFNIKNNSGRKLEWEILKGVMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
a749.pep m749	130 140 150 160 170 180  NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
a749.pep m749	190 200 210 220 230 240 KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
a749.pep	250 260 270 280 290 300  DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD
a749.pep m749	310 320 330 340 350 360 LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDTNFKQVNEILAKYRTKDGFETYDKLG [
a749.pep	370 380 389  EADRKALQASINALAEDLAQLRGILGLKX                          EADRKALQASINALAEDLAQLRGILGLKX 370 380

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2573>: g750.seq

1	GTGAAACCGC	GTTTTTATTG	GGCAGcctGC	GCCGTCCTGC	CGGCCGCCTG
51	TTCGCCCGAA	CCTGCCGCCG	AAAAAACTGT	ATCCGCCGCA	TCCCAAGCCG
101	CATCCACACC	TGTCGCCACG	CTGACCGTGC	CGACCGCGCG	GGGCGATGCC
151	GTTGTGCCGA	AGAATCCCGA	ACgcgtcgcc	gtgtAcgaCt	ggGCGGCGTt
201	ggaTACGCTG	ACCGAGCCGG	GCGTGAATGT	GGGCGCAACC	ACCGCGCCGG
251	TGCGCGTGGA	CTATTTGCAG	CCTGCATTTG	ACAAGGCGGC	AACGGTGGGG
301	ACGCTGTTTG	AGCCCGATTG	CGAATCCCTG	CACCGCCACA	ATCCGCAGTT
351	TGTCATTACC	GGCGGGCCGG	GTGCGGAAGC	GTATGAACAG	TTGGCGAAAA
401	ACGCGACCAC	CATAGATTTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC
451	GGCGAGAAGC	AGATGGAGAC	CCTGTCGCGG	ATTTTCGGTA	AGGAAGCGCG
501	CGTGGCGGAA	TTGAATGCGC	AGATTGACGC	GCTGTTCGCC	CAAAAGCGCG
551	AAGCCGCCAA	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCGGT	TACAGGCAAC
601	AAGGTGTCCG	CCTTCGGCAC	GCAATCGCGG	TTGGCAAGTT	GGATACACGG
651	CGACATCGGC	CTGCCGCCCG	TGGACGAATC	TTTACGCAAC	GAAGGGCACG
701	GGCAGCCCGT	TTCCTTCGAA	TACATCAAAG	AGAAAAACCC	CGGCTGGATT
751	TTCATCATCG	ACCGCACCGC	CGCCATCGGG	CAGGAAGGGC	CGGCTGCCGT

```
801 GGAAGTGTTG GATAACGCGC TGGTATGCGG CACGAACGCT TGGAAGCGCA
      851 AGCAAATCAT CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCGCG
          CGGCAGTTGA TACAGGCGGC GGAACAGTTG AAGGCGGCGT TTGAAAAGGC
      951 AGAACCCGTT GCGGCGCAGT AG
 This corresponds to the amino acid sequence <SEQ ID 2574; ORF 750.ng>:
 g750.pep
          VKPRFYWAAC AVLPAACSPE PAAEKTVSAA SQAASTPVAT LTVPTARGDA
     51 VVPKNPERVA VYDWAALDTL TEPGVNVGAT TAPVRVDYLQ PAFDKAATVG
101 TLFEPDCESL HRHNPQFVIT GGPGAEAYEQ LAKNATTIDL TVDNGNIRTS
     151 GEKQMETLSR IFGKEARVAE LNAQIDALFA QKREAAKGKG RGLVLSVTGN
     201 KVSAFGTQSR LASWIHGDIG LPPVDESLRN EGHGQPVSFE YIKEKNPGWI
          FIIDRTAAIG QEGPAAVEVL DNALVCGTNA WKRKQIIVMP AANYIVAGGA
     301 RQLIQAAEQL KAAFEKAEPV AAQ*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2575>:
m750.seq
          GTGAAACCGC GTTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
      51
          TTCGCCCGAA CCTGCCGCCG AAAAAACTGT ATCCGCCGCA TCCGCATCTG
     101 CCGCCACGCT GACCGTGCCG ACCGCGGGG GCGATGCCGT TGTGCCGAAG
     151 AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
          CGAATTGGGC GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
     251 ATTTGCAGCC TGCATTTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTCGAG
     301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
     351 CGGGCCGGGC GCGGAAGCGT ATGAACAGTT AGCGAAAAAC GCGACCACCA
401 TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
     451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
     501 GAAGGCGCAG ATTGACGCGC TGTTCGCCCA AACGCGCGAA GCCGCCAAAG
     551 GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCCGCC
     601 TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
     651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
     701 CCTTCGAATA CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
     751 CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTCG AAGTATTGGA
     801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
     851 TCATGCCTGC CGCGAACTAC ATTGTCGCGG GCGGCGCGCG GCAGTTGATT
         CAGGCGGCGG AGCAGTTGAA GGCGGCGTTT AAAAAGGCAG AACCCGTTGC
     901
     951 GGCGGGGAAA AAGTAG
This corresponds to the amino acid sequence <SEQ ID 2576; ORF 750>:
m750.pep
         VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
      51 NPERVAVYDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
     101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
     151 METLARIFGK EARAAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
     201 FGTQSRLASW IHGDIGLPPV DESLRNEGHG QPVSFEYIKE KNPDWIFIID
     251 RTAAIGQEGP AAVEVLDNAL VRGTNAWKRK QIIVMPAANY IVAGGARQLI
     301 QAAEQLKAAF KKAEPVAAGK K*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from
N. gonorrhoeae
m750/g750
            93.8% identity in 322 aa overlap
                                        30
                              20
            VKPRFYWAACAVLLTACSPEPAAEKTVSAASASA---ATLTVPTARGDAVVPKNPERVA
m750.pep
            VKPRFYWAACAVLPAACSPEPAAEKTVSAASQAASTPVATLTVPTARGDAVVPKNPERVA
q750
                                        30
                                                  40
                                  80
                                            90
                                                     100
            VYDWAALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVIT
m750.pep
            VYDWAALDTLTEPGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDCESLHRHNPQFVIT
a750
                    70
                                        90
                                                 100
                                                          110
```

m750.pep

150

GGPGAEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFA

160

```
GGPGAEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
q750
                                         150
                                                   160
              180
                         190
                                   200
                                             210
                                                       220
             QTREAAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFE
m750.pep
             î 1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940) (1940)
g750
             QKREAAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSFE
                    190
                               200
                                         210
                                                   220
                                                              230
              240
                        250
                                   260
                                             270
                                                       280
                                                                  290
             YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGA
m750.pep
             YIKEKNPGWIFIIDRTAAIGQEGPAAVEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGA
q750
                    250
                              260
                                         270
                                                   280
              300
                        310
                                   320
             RQLIQAAEQLKAAFKKAEPVAAGKKX
m750.pep
             1111111111111111111111111111111
a750
             RQLIQAAEQLKAAFEKAEPVAAQX
                    310
                              320
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2577>: a750.seq

```
GTGAAACCGC GTTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCGCCTG
  1
     TTCGCCCGAA CCTGCCGCCG AAAAAACTGT ATCCGCCGCA TCCGCATCTG
 51
     CCGCCACACT GACCGTGCCG ACCGCGCGGG GCGATGCCGT TGTGCCGAAG
101
    AATCCCGAAC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
151
     CGAATTGGGT GTGAATGTGG GCGCAACCAC CGCGCCGGTG CGCGTGGATT
251
    ATTTGCAGCC TGCATTTGAC AAGGCGGCAA CGGTGGGGAC GCTGTTCGAG
     CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
301
    CGGGCCGGGC GCGGAAGCGT ATGAACAGTT GGCGAAAAAC GCGACCACCA
351
    TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCAGCGG CGAAAAGCAG
451 ATGGAGACCT TGGCGCGGAT TTTCGGCAAG GAAGCGCGCG CGGCGGAATT
    GAAGGCGCAG ATTGACGCGC TGTTCGCCCA AACGCGCGAA GCCGCCAAAG
    GCAAAGGACG CGGGCTGGTG CTGTCGGTTA CGGGCAACAA GGTGTCCGCC
551
    TTCGGCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651 ACCGCCTGTA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
    CCTTCGAATA CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
701
751
    CGTACCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTCG AAGTATTGGA
    TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAAATCATCG
801
    TCATGCCTGC CGCGAACTAC ATTGTCGCGG GCGGCTCGCG GCAGTTGATT
851
901
    CAGGCGGCGG AGCAGTTGAA GGAGGCGTTT GAAAAGGCAG AACCCGTTGC
    GGCGGGGAAA GAGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2578; ORF 750.a>: a750.pep

```
1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
51 NPERVAVYDW AALDTLTELG VNVGATTAPV RVDYLQPAFD KAATVGTLFE
101 PDYEALHRYN PQLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
151 METLARIFGK EARAAELKAQ IDALFAQTRE AAKGKGRGLV LSVTGNKVSA
201 FGTQSRLASW IHGDIGLPPV DESLRNEGHG QPVSFEYIKE KNPDWIFIID
251 RTAAIGQEGP AAVEVLDNAL VRGTNAWKRK QIIVMPAANY IVAGGSRQLI
301 OAAEOLKEAF EKAEPVAAGK E*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from N. meningitidis:

```
a750/m750
         98.8% identity in 321 aa overlap
                       20
                               30
                                       40
a750.pep
         VKPRFYWAACAVLLTACSPEPAAEKTVSAASASAATLTVPTARGDAVVPKNPERVAVYDW
          m750
         VKPRFYWAACAVLLTACSPEPAAEKTVSAASASAATLTVPTARGDAVVPKNPERVAVYDW
                               30
                                      40
                                              50
                70
                       80
                               90
                                      100
                                             110
         AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG
a750.pep
         m750
         AALDTLTELGVNVGATTAPVRVDYLQPAFDKAATVGTLFEPDYEALHRYNPQLVITGGPG
```

```
90 -
                70
                        80
                                       100
                                               110
                                                       120
                       140
               130
                               150
                                       160
                                               170
          AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFAOTRE
a750.pep
          AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTRE
m750
                       140
                               150
                                       160
                       200
                               210
               190
                                       220
                                               230
                                                       240
          AAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESLRNEGHGOPVSFEYIKE
a750.pep
          AAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESLRNEGHGOPVSFEYIKE
m750
               190
                       200
                               210
                                       220
                                               230
                                                       240
               250
                       260
                               270
                                       280
                                               290
                                                       300
a750.pep
          KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGSROLI
          KNPDWIFIIDRTAAIGQEGPAAVEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLI
m750
                       260
                               270
                                       280
                                               290
               310
                       320
          QAAEQLKEAFEKAEPVAAGKEX
a750.pep
          m750
          QAAEQLKAAFKKAEPVAAGKKX
               310
                       320
```

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>: m751.seq..

```
1 ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
    TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
51
     AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTTGGTC ATTGAATGAT
101
    TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
151
     TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
201
     ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTTATTGCA
251
     GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
301
351
     AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTTCTGAA CTGATGTATG
     TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
401
    ACCAATTCAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
451
    GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
501
    CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
551
    ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
601
     GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
651
    CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
701
    GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
751
801
    CACACAAGGT ACATGTAAGG GGTTGTGCTA TTCGCATAGC AGTTATTTTG
     CGGAGGTGCC AAAAGCAGGT ACAAAAGAAT TTGATGACTA TGTAAAAATA
851
901
     TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAATCTAA
    ACCCATACTG GTAGAACCAA ACAAAACAAA AGATAATGAA AAATATGAAA
951
    AAGAAGCTTT CTAA
```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>: m751.pep..

```
1 MAWSMFATTQ ADRAVRSATA PKEMWFHKKI IDEKTGKVSF DTRQIWSLND
51 LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAKQNR NSTNGSGVIA
101 VMNPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVQKMGNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFVGNKWIPF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKEFDDYVKI
```

301 WGEVEYDAQG KPINKSKPIL VEPNKTKDNE KYEKEAF*

a751.seq not found yet

a751.pep not found yet

WO 99/57280 PCT/US99/09346

1227

```
g752.seq not found yet
q752.pep not found yet
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2581>: m752.seq.

```
1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
  51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCTT
 101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
 151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
 201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
     CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
     GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
 351
     TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
 401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
 451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
 551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
 601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTGC ACCGCATTGC
 651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
 701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
 751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
 801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
 851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
 901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
 951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001. CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
     GATTTAACCT ATTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1051
     TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
     TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
     CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG
```

## This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

```
m752.pep
       1 MKISRPPEFT LLQQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
         DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRAVKESRK KIQKPIDFPF
         EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLLKSLIM
         EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
    201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
    251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAIILHF LIGYIHPFGD
    301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
    351 DLTYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
    401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
    451 SGNALEYVAP ODLLERLEKK *
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2583>: m752-1.seq

```
1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
 51 GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
    GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
    GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
    TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
351
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTGC ACCGCATTGC
```

```
1228
```

```
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
     701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
     751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
     801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
     851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
     901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
    1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
    1051 GATTTAACCT ATTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
          TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
    1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
    1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
    1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
    1351 TCAGGAAATG CTTTAGAGTA TGTTGCTCCT CAGGATTTAT TGGAAAGGTT
    1401 AGAAAAAAA TAG
This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:
m752-1.pep
       1 MKISRPPEFT LLQQEYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
      51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRAVKESRK KIOKPIDFPF
     101 EHQFWFCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLLKSLIM
     151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
     251 PPHGOVHTLM EEVCAFANNT YDGVENPFIH PVVOAIILHF LIGYIHPFGD
     301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
          DLTYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
     401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
     451 SGNALEYVAP QDLLERLEKK *
a752.seq not found yet
a752.pep not found yet
      q753.seq not found yet
      q753.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2585>:
                 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
             51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
            101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
            151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
            201 CCAACCAATC GGTTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
            251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTTCCTAGT ACGACAGTAC
                  TCATCAAATG CGCTCAGCTG TGCGCCAGTT ATTTCCTAGT ACGACAGTAC
            401
                  GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
            451 AAAACTTGA
This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:
      m753.pep
              1 MPITPPLNII SPKLYPNEQW NESEALGAIT WLWYQSPTHR QVPIVEMMTY
             51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNSDWN
            101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
            151 KT*
      a753.seg not found yet
      a753.pep not found yet
```

g754.seg not found yet

q754.pep not found yet

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2587>:
```

```
m754.seq
         ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
      1
     51 AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
    101 AAAAGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
    151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
    201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTTG GATGCACACA
    251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTTGAAGA CAATGAGATG
    301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
         CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
         ATCCAAGAAT ATTGACTGAA CGGGATTTGC TGGGCATAAA TGCCCGACAG
         GTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
    501
         TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
    551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
    601 CCTTGCTTGG CTGCCAATGA ATTTTTATGC ATGCAGACCA TCAAACAAGC
    651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
    701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
    751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
    801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
    851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
    901 AACGGCGATG CACACCTCAA AAATTTTTCA GTACTCTATC ATGACGAATA
    951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
         GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTA
   1001
         AACCTGACTA ACCACGGTAA GAAAACATAT CCTTCCAAGA ATACATTGTT
   1051
   1101 GGATTTTGCT GAGAAATATT GCGATTTGGG AAGAGAAGAT GCATCCTTTA
         TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
   1151
         GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
   1201
         GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG
```

## This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
         MMKSILTVSG NRMRKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
      51 LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
     101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
     151 VFQQYMAEIF HHGRFVSVSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
     201 PCLAANEFLC MQTIKQAGIA VAQTSLSEDS SVLLVRRFDV SEQGYFLGME
     251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
     301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDT SIYRVGTQGI FDAYDDTLAL
     351 NLTNHGKKTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
         DVLRENEWLA OKWHFIPDEN EEGLPFTFR*
a754.seq not found yet
a754.pep not found yet -
g755.seq not found yet
g755.pep not found yet
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2589>: m755.seq..

```
1 ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
    CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTAAAACCA
    TCTTGGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
    CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
    CGCTCGGTTT GATTGGTTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
201
251 GCCTTGAAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

```
This corresponds to the amino acid sequence <SEO ID 2590; ORF 755>:
      m755.pep..
             1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
                REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLESDLN AQFIADGVYQ
            51
           101 AKQAFLQRVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*
      a755.seq not found yet
      a755.pep not found yet
 g756.seq
         not found yet
 g756.pep
         not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2591>:
 m756.seq
       1
         ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
         CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
      51
     101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
         TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
     201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
     251
         CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
     301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
     351 TGCCGTCGAC CGTCTTGCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
         TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
     451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
     501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
     551 TAGGGGATTA A
This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:
m756.pep
         MTANFAQTLV EIQDSLYRVV STVQYGDDNL KRLTADKRKQ YELNFKISEG
         STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLLV GGALGYGYLE
      51
         YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
     151 SREDISEANR RAERVPYGAE LVSDGNFTAV LSDIGD*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2593>:
     a756.seq
                ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
            1
               NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
           51
               CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
               TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
          201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
               CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
          251
          301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
          351 TGCCGTCGAC CGTCTTGCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
          401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
          451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
               TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
          551 TAGGGGATTA A
This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:
     a756.pep
            1 MTANFAQTLV EIQDSLXRVV STVQYGDDNL KRLTADKRKQ YELNFKISEG
           51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLLV GGALGYGYLE
               YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DFVQIGRRSY
               SREDISEANR RAERVPYGAE LVSDGNFTAV LSDIGD*
m756 / a756 99.5% identity in 186 aa overlap
                                               30
                                                         40
                  MTANFAQTLVEIQDSLYRVVSTVQYGDDNLKRLTADKRKQYELNFKISEGSTRVESDFKE
     m756.pep
                  MTANFAQTLVEIQDSLXRVVSTVQYGDDNLKRLTADKRKQYELNFKISEGSTRVESDFKE
     a756
                          10
                                     20
                                               30
                                                         40
                                                                   50
                                                                              60
```

```
70
                                     80
                                               90
                                                        100
                                                                  110
                   TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
      m756.pep
                   TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
      a756
                           70
                                     80
                                               90
                                                                  110
                          130
                                    140
                                              150
                                                        160
                                                                  170
                   RLAESQERITSAILKGARGADFVQIGRRSYSREDISEANRRAERVPYGAELVSDGNFTAV
     m756.pep
                   a756
                   RLAESQERITSAILKGARGADFVQIGRRSYSREDISEANRRAERVPYGAELVSDGNFTAV
                          130
                                    140
                                              150
                                                        160
     m756.pep
                   LSDIGDX
                   111111
     a756
                   LSDIGDX
g757.seq not found yet
g757.pep not fiund yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2595>:
         ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
      1
         TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
     51
         CACAATCCGA ATTAAAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
     101
         GCAGCCAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
         ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
     201
     251
         TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
     301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
     351 GGAAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
         AAGACCGCAC AATGCTGCGT GATACCGGCG ACCAAATCGA AATGGCGATT
     451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
     501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
    551 CAAAAGCTGA GTAA
This corresponds to the amino acid sequence <SEO ID 2596; ORF 757>:
m757.pep (lipoprotein)
        MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
     51 AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHDFSDGLTI LTVDTDKADK
    101 ITAVRVVWNT DAMPQKAEKL SKAAAALIAA TAPEDRTMLR DTGDOIEMAI
    151 DSHNAQKEPT REWARGGIAY KVTVTNLPSV VLTAKAE*
     a757.seq not found yet
     a757.pep not found yet
     g758.seq not found yet
     g758.pep not fiund yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2597>:
     m758.seq
               ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
               TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
           51
          101
               AGGGCAAACT GGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
               GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
          151
          201
               CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
               CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
          251
               CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
              CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
          401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
```

451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC

501

ATGA

401

```
This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:
     m758.pep
               MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
            1
               DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
           51
               RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
               LLAAGDQVRF VAERIEP*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2599>:
     a758.seg
            1
               ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
              TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
           51
              AGGGCAAACT GGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
          101
              GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
              CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
          201
          251
              CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
          301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
          351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
              TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
              CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
          501 ATGA
This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:
     a758.pep..
            1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
              DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
           51
              RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPT
          151 LLAAGDQVRF VAERIEP*
m758 / a758 100.0% identity in 167 aa overlap
                         10
                                  20
                                            30
                                                     40
                 MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ
     m758.pep
                 MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ
     a758
                         10
                                  20
                                            30
                                                     40
                                                               50
                                                                        60
                         70
                                  80
                                            90
                                                    100
                                                              110
                                                                       120
                 TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAGSVGIGGSQT
     m758.pep
                 a758
                 TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAGSVGIGGSOT
                         70
                                  80
                                            90
                                                    100
                                                              110
                        130
                                 140
                                           150
                                                    160
    m758.pep
                 GVYPFASPGGWQIIGRTELPLFRADLNPPTLLAAGDQVRFVAERIEPX
                 a758
                 GVYPFASPGGWQIIGRTELPLFRADLNPPTLLAAGDQVRFVAERIEPX
                        130
                                 140
                                           150
                                                    160
     g759.seg not found yet
    g759.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2601>:
    m759.seg
              ATGCGCTTCA CACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
           1
              TCTTTTTGCC GTTTCCCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
          51
         101 ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCACCGTA
         151
              GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
         201
              GGTTCTCAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
         251
              CCGCCATCGC CACCCTGGTT CACCCCCAAT ACGTCAACAG TGTCAAACAC
              AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
         301
              AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGGACT
```

ACGACTACCA CCTTCCCCGC CTCAACAAC TGGTTACCGA AATCTCACCT

451	ACCGCACTCA	GCAGCGTACC	CTTGCTTGGA	AACGGCCAGC	CAAAGGCCAA
501	TGCCTACCTC	GATACCGACC	GCTTCCCCTA	CTTTGTACGA	CTCGGCTCAG
551	GCACGCAACA	AGTCCGCAAA	GCAGACGGCA	CGCGTACACG	AACCGCCCCG
601	GCATACCAAT	ACCTGACCGG	CGGCACGCCG	CTGAAAGTAT	TGGGGTTCCA
651	AAACCACGGC	TTACTCGTCG	GCGGCAGCCT	GACCGACCAA	CCCCTTAACA
701	CCTACGCAAT	CGCCGGAGAC	AGCGGTTCCC	CCCTGTTTGC	CTTCGACAAG
751	CATGAAAACC	GCTGGGTGCT	TGCGGGCGTA	CTCAGCACCT	ACGCCGGCTT
801	CGATAATTTC	TTCAACAAAT	ACATCGTCAC	GCAACCCGAA	TTCATCCGTT
851	CCACCATCCG	CCAATACGAA	ACCCGGCTGG	ATGTCGGGCT	GACCACCAAC
901	GAACTCATAT	GGCGCGACAA	CGGTAATGGC	AACAGCACCC	TGCAAGGGCT
951		ATCACCCTGC			
1001		GCACATGCCG		CCGGCAAAAC	
1051	TCCAGCAGGT				ATATCAACCA
1101		GCATTGCAGT			GTCGGTAAAA
1151					CAAACGCGTC
1201					AACTGGGCGC
1251					GACATCAGCA
1301					AGACGGCAGC
1351	AAACAAGCAT				GCACGGCCGT
1401	CCTCGCCGAC	AGCCAGCAAA			
1451	GGGGCGGACG		AACGGCAACA		
1501		ACGGCGCGC		AATCACAACC	
1551		ACGCTGACCG			
1601		ATGGGGCAAC			
1651		CGCACCGCAA			
1701	CGGCGGCAAC	CCGCGCGAAT			AACTCAACAA
1751	GCTGGCAATT				ACAAGTCGCC
1801		ATGCCCGCCC			
1851		CAAACGGGCA			
1901		AGAAAAAACC ACCGTTACAA			
1951 2001		AGCACGCTGT			
2051	AAGTCTTGAT				GCCCGTACCC
2101		ACCACCAGGC			
2151		ACCACCAGGC			
2201		AGGGCGCAAT			CATAACCGCA
2251		CCGGCATCGA			
2301	ATGCTACCGC		GCGGCAGCAC		
2351	TTTTAAAAGC		CGTGCACTAC		
2401	GACATTACCC	TTAACGACCG		CGCCTGGGCA	
2451		ATCCGTGCCG			
2501		GACACTTTCC			
2551		AAATTACCCT			
2601		AACACACTGA			
2651	CATTCCGATT	CCTGACCGGC	ATCGTCCGAA	AACAAAATGC	CCCCCCCCTC
2701		GGGACAGCCG			
2751		CCTCAAACAA			
2801		CCACCAAGCC			
2851		ACCGCTACAT			
2901	GTACAACCCG	CTCAAAGAGG	CCGAACTTCA	AATTGAAGCC	ACGCGTGCGG
2951		CAACCAACAG			
3001		TTCAACATGA			
3051	CTGGCAGAAC	AGTCAAACCG	AACTTGCCCG	CATCGACAGC	CAAGTCCAAT
3101	ATCTGTCCGC	CCAATTGAAA	CAGACAGACC	CGCTGACCGG	CATTCTGACG
3151	CGTGCCCAAA	ACCTGTGTGC	CGCACAAGGA	TACAGTGCCG	ATATCTGCCG
3201	TCAGGTTGCC	AAAGCCGCCG	ACACGAACGA	CCTGACACTC	TTCGAAACCG
3251	AACTGGATAC	GTATATAGAA	CGTGTAGAAA	TGGCCGAATC	CGAACTTGAC
3301		AAGGCGGCGA			
3351	CTACCTGAAC	GCACTCAACC	GTCTGTCCCG	ACAAATCCAC	AGTTTGAAAA
3401	CCGGCGTTGC	CGGCATCCGT	ATGCCGAACC	TGGCCGAACT	GATCAGCCGG
3451	TCGGCCAACA	CCGCCGTTTC	CGAACAGGCC	GCCTACAATA	CCGGCCGGCA
3501	ACAGGCGGGA	CGCCGCATCG	ACCGCCACCT	TACCGATCCG	CAGCAGCAAA
3551	ACATCTGGCT	GGAAACCGGT	ACGCAACAAA	CCGACTACCA	TAGCGGCACA
3601	CACCGTCCCT	ACCAACAAAC	TACCAACTAT	GCACATATCG	GCATCCAAAC
3651	CGGCATCACC	GACCGTCTCA	GTGTCGGTAC	GATTTTAACC	GATGAGCGCA
3701	CAAACAACCG	TTTTGATGAA	GGCGTATCCG	CCCGAAACCG	CAGCAACGGC

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1234

```
3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAAATC
3901 GATACCGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCGCCAC AAACAGGCAG GAATCAAAAT AGGCTACAAC TGGTAA
```

## This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```
m759.pep
       1 MRFTHTTPFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
      51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
          NVGYGSIQFG NDTQNPEEQA YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
          TALSSVPLLG NGQPKANAYL DTDRFPYFVR LGSGTQQVRK ADGTRTRTAP
     201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
     251 HENRWVLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
     301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNDSRHMP SEDAGKTLIL
     351 SSRFDNKTLM LADNINQGAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
     401 FWOVSNPKGD RLSKLGAGTL IANGOGINOG DISIGEGTVV LAOKAASDGS
     451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRLDL NGNNLAFTHI
     501 RHADGGAQIV NHNPDQAATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
     551 YINPHRNRRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAAEQVA
     601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
     651 RPEYRYNGAL NLHYRPKRTD STLLLNGGMN LNGEVLIEGG NMIVSGRPVP
     701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
     751 YDLSGIDLGF TQGKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
     801 DITLNDRSEL RLGKAHLYGS IRAGKDTAVR MEADSNWTLS QSSHTGALTL
851 DGAQITLNPD FANNTHNNRF NTLTVNGTLD GFGTFRFLTG IVRKQNAPPL
901 KLEGDSRGAF QIHVKNTGQE PQTTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNNGYSLYNP LKEAELQIEA TRAEHERNQQ AYNQLQATDI
    1001 SRQVQHDSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
    1051 RAONLCAAOG YSADICROVA KAADTNDLTL FETELDTYIE RVEMAESELD
    1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAELISR
    1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQQTDYHSGT
    1201 HRPYQQTTNY AHIGIQTGIT DRLSVGTILT DERTNNRFDE GVSARNRSNG
    1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
    1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
    1351 LGQAKLTPAF SSDYYHTRQN SGSALSVNDR TLLQQAAHGT LHTLQIDAGY
```

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2603>:

```
g760.seq
         (partial)
      1 AACAACCGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
      51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
    101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
    151 GACGACGCA TCTTCCTGCT GGTGCCCAAA CACAGCGCAA ACCTGTGGAC
    201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
    251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
         TTCGATGCGA TGGCGGCATA CCGCTTCACG CCCAAGCTGA AGCTGCAAAT
    351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
         CGAACACCTT TAACATTCCC GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
    451 CGTTACAGTT TTTAA
```

### This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```
g760.pep
         (partial)
         NNRNTRYAAL GKRVMEGVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
         DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
     101 FDAMAAYRFT PKLKLQINAD NIFNRHYYAR VGGTNTFNIP GSERSLTANL
     151 RYSF*
```

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2605>:

m760.seq ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG 51 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC 201 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG 251 CCCGGCCTGC GCGTGTTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA TGCAGAGTAT CAACGGCACG CTGCCCAACC TGTTCGCCTT CGACCGCGTG 401 451 GAAGTGATGC GCGGGCCGAG CGGACTGTTC GACAGCAGCG GCGAGATGGG CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC 651 GCAGACCGTC GGCGCGTCTC CGCGTCCCGC CGAGAAAAAC AACCGGCGCG 701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG GGCGCGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT 751 801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG TCGGCGCGGA TTGGAACAAA TTTAAAATGC ACAGCCACGA CGTGTTCGCC 851 901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG CTATTCCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAC TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCCGT TTGCCTTGGG 1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA 1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT 1201 GGTTTCCGCG CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG 1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG 1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAGGTTT GTCGTTGATT GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC 1351 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GGCGCGGTTT 1401 1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTCTAC 1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC 1551 TCAATACCCG GGTTTCGTTC TACCGCATGA AGGATAAAAA CGCCGCCGCA 1601 1651 CCGCTGGACT CAAACAACAA AAAAACCCGT TACGCCGCAT TGGGCAAACG 1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT 1751 GGCAAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC TCCAATTCGC GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC 1801 1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC 1901 1951 GGTTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAACT GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTCGGA GCGCAGCCTG ACGGCAAACC TGCGTTACAG TTTTTAA

#### This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

m760.pep MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQQVKDRNV DTFDQLARKT 101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFAFDRV 151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAEAD 201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL GAGYLYQQRR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHSHDVFA DLKHYFGNGG YGKVGMRYSD RKADSNYTFA GSKLNNTGQA DVAGLGTDIK QKAFAVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLSKSVALD GFRALPYNGI LQNARAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI AGGRVGHHKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA 501 551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA 601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSERSL 651 701 TANLRYSF*

```
m760 / g760 91.6% identity in 154 aa overlap
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                                540
                                         550
                                                   560
                                                             570
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     m760.pep
                                                11::1111111111111111111111111111111
     g760
                                                NNRNTRYAALGKRVMEGVETEISGAITPKW
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                                                                  20
                                                                           30
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                               600
                                         610
                                                   620
                                                             630
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     m760.pep
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     g760
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                                                       70
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                                                  680
                                                            690
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     m760.pep
                  g760
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                         100
                                   110
                                            120
                                                      130
                    709
     m760.pep
                  RYSFX
                  11111
     g760
                  RYSFX
     g761.seq not found yet
     g761.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2607>:
     m761.seq
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           51
              CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
              AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
              CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
          251
              AAAATTACGG TACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
          301
              ATCGACGCTG CCTACGATAT GCGCGGTGAA AGCATTTTCC TGCGCGGTTT
          351
              TCAAGCCGAC GCATCCGATA TTTACCGCGA CGGCGTGCGC GAAAGCGGAC
              AAGTGCGCCG CAGTACTGCC AACATCGAGC GCGTGGAAAT CCTGAAAGGC
              CCGTCTTCCG TGCTTTACGG CCGCACCAAC GGCGGCGGCG TCATCAACAT
          451
          501
              GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGCAACATC GGAGCGGTTT
              ACGGCTCATG GGCAAACCGC AGCCTGAATA TGGACATTAA CGAAGTGCTG
          551
          601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC
          651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
          701 CCGTCAAACT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
              AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
         801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA
         851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
         901 AAATGGCGTG CCCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT
              TGATCATTTC TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT
        1001
              ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
        1051
              AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT
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              TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
              AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
              CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTTG AAATTCGTCC
              TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
              GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
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        1401
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        1451
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              TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC
        1501
              CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
        1551
        1601
              CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC
              AACCCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA
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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA
```

## This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

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m761.pep
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         NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
         NVERTPDRSP TKSVYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
         KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQTD NKTLSSNLTL
         NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
         RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
    451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAPYGG RGGYLSIDTL
         SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
    551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGSLGVMQA KVVEDKENPD
    601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
    651 LPGFARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
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        YRF*
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## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2609>:

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a761.seq
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         CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
    151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
    201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
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    351
         TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
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         CCGTCCTCCG TGCTTTATGG GCGTACCAAC GGCGGCGGTG TCATCAACAT
         GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
    501
    551 ATGGTTCGTG GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
    601 AACAAAAACG TCGCCATCCG TCTCACCGGC GAAGTCGGGC GCGCCAATTC
    651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
    701 CCGTCAAACT CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
    751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
    801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA
    851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
    901 AAATGGCGTG CCCAATGGCA GCTCGCCCAC CGCACGGCGG CGCAGGATTT
   951 TGATCATTTC TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAACT
   1001
        ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCCAA CTTAACGCTC
   1051
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         TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
         AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACGG
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         TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCCGAAAA CAAACTCACC
   1301
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   1401
        GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG
   1451
        TCTTCCGCCG TGTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC
   1501
   1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
   1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC
   1651 AACCCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA
   1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
```

			•			
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1801	CGAGTGGGCA					
1851	TTTCCGTTAT	ACCCCGACCG	AAAACCTCTA	CGGCGAAATC	GGCGTAACCG	
1901	GTACAGGCAA					
1951	CTTCCAGGCT					
2001	TGTTAACGTT					
	GTTCGGACTC					
2051			AATCCGCGCG	GCIAIACIGC	CCGGGTAAAT	
2101	TACCGTTTCT	GA				
~ ·		• •	-OFO II	D 0/10 ODI	77/1	
This correspond	is to the amino	o acid seque	nce <seq ii<="" td=""><td>D 2610; ORI</td><td>' /61.a&gt;:</td><td></td></seq>	D 2610; ORI	' /61.a>:	
a761.pep						
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101	IDAAYDMRGE					
151	PSSVLYGRTN					
201	NKNVAIRLTG					
251	NVERTPDRSP					
301	KWRAQWQLAH					
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401	RLQPILTQNR					
451	GSSRQYSGHS					
501	SSAVFNADPE			<del>-</del>		
551	NPYIYAVSGK					
601	RVGIHLNNTS					
651	LPGFARVDAM	LGWNHKNVNV	TFAAANLFNQ	KYWRSDSMPG	NPRGYTARVN	
701	YRF*					
m761 / a761 99	6% identity in	n 703 aa ove	erlap			
111/01/ 11/01/	_		20 30	) 40	50	60
7.61						
m761.pep				EHYTATLPTVS		
						1111111
a761	MKISFHLA	LLPTLIIASF	PVAAADTQDNGE	EHYTATLPTVSV	VGQSDTSVLKG	YINYDEAA
a761	MKISFHLA	LLPTLIIASF		EHYTATLPTVSV		
a761	MKISFHLA	LLPTLIIASFI 10 2	PVAAADTQDNGE 20 30	EHYTATLPTVSV ) 40	VGQSDTSVLKG 50	YINYDEAA
a761	MKISFHLA	LLPTLIIASFI 10 2 70 8	PVAAADTQDNGE 20 30 30 90	EHYTATLPTVSV 0 40 0 100	VGQSDTSVLKG 50 110	SYINYDEAA 60 120
a761 m761.pep	MKISFHLA	LLPTLIIASFI 10 2 70 8	PVAAADTQDNGE 20 30 30 90	EHYTATLPTVSV ) 40	VGQSDTSVLKG 50 110	SYINYDEAA 60 120
	MKISFHLA VTRNGQLI	LLPTLIIASFI 10 2 70 & KETPQTIDTLN	PVAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE	EHYTATLPTVSV 0 40 0 100	VGQSDTSVLKG 50 110 DAAYDMRGESI	SYINYDEAA 60 120 FLRGFQAD
	MKISFHLA VTRNGQLI 	LLPTLIIASFI 10 2 70 8 KETPQTIDTLN	PVAAADTQDNGE 20 30 30 90 NIQKNKNYGTNI	EHYTATLPTVSV 0 40 100 DLSSILEGNAGI	VVGQSDTSVLKG 50 110 DAAYDMRGESI	SYINYDEAA 60 120 FLRGFQAD
m761.pep	MKISFHLA VTRNGQLI         VTRNGQLI	LLPTLIIASFI 10 2 70 6 KETPQTIDTLN                       KETPQTIDTLN	PVAAADTQDNGE 20 30 30 90 NIQKNKNYGTNI	EHYTATLPTVSV  0 40  100  DLSSILEGNAGI           DLSSILEGNAGI	VVGQSDTSVLKG 50 110 DAAYDMRGESI	SYINYDEAA 60 120 FLRGFQAD
m761.pep	MKISFHLA VTRNGQLI         VTRNGQLI	LLPTLIIASFI 10 2 70 8 KETPQTIDTLN	PVAAADTQDNGE 20 30 NIQKNKNYGTNE           NIQKNKNYGTNE	EHYTATLPTVSV  0 40  100  DLSSILEGNAGI           DLSSILEGNAGI	VGQSDTSVLKG 50 110 DAAYDMRGESI 	YINYDEAA 60 120 FLRGFQAD 
m761.pep	MKISFHLA VTRNGQLI         VTRNGQLI	LLPTLIIASFI 10 2 70 8 KETPQTIDTLN	PVAAADTQDNGE 20 30 NIQKNKNYGTNE            NIQKNKNYGTNE 80 90	EHYTATLPTVSV  100  100  DLSSILEGNAGI	VGQSDTSVLKG 50 110 DAAYDMRGESI 	YINYDEAA 60 120 FLRGFQAD 
m761.pep a761	MKISFHLA  VTRNGQLI           VTRNGQLI	LLPTLIIASFI 10 2 70 8 KETPQTIDTLN            KETPQTIDTLN 70 8	PVAAADTQDNGE 20 30 80 90 NIQKNKNYGTNE HIIIIIIIIII NIQKNKNYGTNE 80 90	EHYTATLPTVSV  100  LSSILEGNAGI  LIIIIIIIIIIIIII  DLSSILEGNAGI  100  160	VGQSDTSVLKG 50 110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110	TINYDEAA 60 120 FLRGFQAD         FLRGFQAD 120
m761.pep	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG	LLPTLIIASFI 10 2 70 6 KETPQTIDTLN            KETPQTIDTLN 70 6 30 14 VRESGQVRRST	PVAAADTQDNGE 20 30 NIQKNKNYGTNE HIIIIIIIIII NIQKNKNYGTNE 30 90 TANIERVEILKO	EHYTATLPTVSV  100  LSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNO	VGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIIII DAAYDMRGESI 110 170 GGGVINMVSKYA	TELEGENAL SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECTION SELECT
m761.pep a761 m761.pep	MKISFHLA  VTRNGQLI           VTRNGQLI  1  ASDIYRDG	LLPTLIIASFI 10 2 70 6 KETPQTIDTLN            KETPQTIDTLN 70 8 30 14 VRESGQVRRST	PVAAADTQDNGE 20 30 NIQKNKNYGTNE HIIIIIIIIIII NIQKNKNYGTNE 30 90 TANIERVEILKO	EHYTATLPTVSV  100  LSSILEGNAGI  LIIIIIIIIIIIII  DLSSILEGNAGI  100  160  GPSSVLYGRTNG	VGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110  170 GGGVINMVSKYA	TINYDEAA 60  120 FLRGFQAD         FLRGFQAD 120  180 ANFKQSRNI
m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG	LLPTLIIASFI 10 2 70 8 KETPQTIDTLN            KETPQTIDTLN 70 8 30 14 VRESGQVRRST	PVAAADTQDNGE 0 30 80 90 NIQKNKNYGTNE	EHYTATLPTVSV  100  LSSILEGNAGI  LIIIIIIIIIIIII  DLSSILEGNAGI  100  160  GPSSVLYGRTNG  LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	VGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110  170 GGGVINMVSKYA	TINYDEAA 60  120 FLRGFQAD         FLRGFQAD 120  180 ANFKQSRNI
m761.pep a761 m761.pep	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG	LLPTLIIASFI 10 2 70 6 KETPQTIDTLN            KETPQTIDTLN 70 8 30 14 VRESGQVRRST	PVAAADTQDNGE 0 30 80 90 NIQKNKNYGTNE	EHYTATLPTVSV  100  LSSILEGNAGI  LIIIIIIIIIIIII  DLSSILEGNAGI  100  160  GPSSVLYGRTNG  LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	VGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110  170 GGGVINMVSKYA	TINYDEAA 60  120 FLRGFQAD         FLRGFQAD 120  180 ANFKQSRNI
m761.pep a761 m761.pep	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG	LLPTLIIASFI 10 2 70 6 KETPQTIDTLN            KETPQTIDTLN 70 8 30 14 VRESGQVRRST            VRESGQVRRST	PVAAADTQDNGE 20 30 NIQKNKNYGTNE HIIIIIIIIII NIQKNKNYGTNE 30 90 TANIERVEILKO	EHYTATLPTVSV  100  CLSSILEGNAGI  IIIIIIIIIIIIII  CLSSILEGNAGI  100  160  GPSSVLYGRTNGI  IIIIIIIIIIIIIIII  GPSSVLYGRTNGO  160	VVGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110 170 GGGVINMVSKYA IIIIIIIIIIII	TINYDEAA 60  120 FLRGFQAD         FLRGFQAD 120  180 ANFKQSRNI
m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1  1	LLPTLIIASFI 10 2 70 6 KETPQTIDTLN            KETPQTIDTLN 70 8 30 14 VRESGQVRRST            VRESGQVRRST 30 14	PVAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE                         NIQKNKNYGTNE 30 90 10 150 PANIERVEILKO                         PANIERVEILKO 10 150	EHYTATLPTVSV ) 40 ) 100 DLSSILEGNAGI              DLSSILEGNAGI ) 100 O 160 GPSSVLYGRTNG             GPSSVLYGRTNG ) 160 ) 220	VVGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110 170 GGGVINMVSKYA IIIIIIIIIIII GGGVINMVSKYA 170 230	TYINYDEAA 60  120 FLRGFQAD         FLRGFQAD 120  180 ANFKQSRNI         ANFKQSRNI 180 240
m761.pep a761 m761.pep	WKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1  GAVYGSWAI	LLPTLIIASFI 10 2 70 6 KETPQTIDTLN            KETPQTIDTLN 70 8 30 14 VRESGQVRRST            VRESGQVRRST 30 14 VRESGQVRST 30 14	PVAAADTQDNGE 20 30 30 30 30 30 30 30 30 30 30 30 30 30 3	EHYTATLPTVSV  100  LSSILEGNAGI  LIIIIIIIIIIIII  DLSSILEGNAGI  100  160  GPSSVLYGRTNG  LIIIIIIIIIIIIIIII  GPSSVLYGRTNG  160  220  GEVGRANSFRSG	VGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110  170 GGGVINMVSKYA IIIIIIIIIII GGGVINMVSKYA 170  230 GIDSKNVMVSPS	TYINYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI 180 240 EITVKLDNG
m761.pep a761 m761.pep a761	WKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1  GAVYGSWAI	LLPTLIIASFI 10	PVAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE 111111111111111111111111111111111111	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNG              GPSSVLYGRTNG  160  220  GEVGRANSFRSG	VVGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110 170 GGGVINMVSKYA IIIIIIIIIII GGGVINMVSKYA 170 230 GIDSKNVMVSPS	TYINYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI 180 240 EITVKLDNG
m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1  GAVYGSWAI   :        GTVYGSWAI	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE NIQKNKNYGTNE 30 90 TANIERVEILKO NIERVEILKO 10 150 VLNKNVAIRLTO VLNKNVAIRLTO	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  160  220  GEVGRANSFRSG	JOSCHNINGS STORY LKG  110  DAAYDMRGESI  IIIIIIIIIIII  DAAYDMRGESI  110  170  GGVINMVSKYA  IIIIIIIIIII  GGVINMVSKYA  170  230  GIDSKNVMVSPS  IIIIIIIIIII  GIDSKNVMVSPS	TYUNYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI          ANFKQSRNI 180  240 GITVKLDNG
m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1  GAVYGSWAI   :        GTVYGSWAI	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE NIQKNKNYGTNE 30 90 TANIERVEILKO NIERVEILKO 10 150 VLNKNVAIRLTO VLNKNVAIRLTO	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  160  220  GEVGRANSFRSG	VGQSDTSVLKG 50  110 DAAYDMRGESI IIIIIIIIIII DAAYDMRGESI 110  170 GGGVINMVSKYA IIIIIIIIIII GGGVINMVSKYA 170  230 GIDSKNVMVSPS	TYINYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI 180 240 EITVKLDNG
m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1  GAVYGSWAI   :       GTVYGSWAI	LLPTLIIASFI 10 2 70 6 KETPQTIDTLN             KETPQTIDTLN 70 8 30 14 VRESGQVRRST             VRESGQVRRST 30 14 VRESGQVRRST             VRESGQVRRST 30 14 VRESGQVRRST 30 20 NRSLNMDINEN	2VAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  160  220  GEVGRANSFRSG               GEVGRANSFRSG  220	JOSCH STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STR	SYINYDEAA 60  120 FLRGFQAD          FFLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI          ANFKQSRNI 180  240 EITVKLDNG
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m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1  GAVYGSWAI   :       GTVYGSWAI  1  LKWTGQYT	LLPTLIIASFI 10	PVAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE                         NIQKNKNYGTNE 30 90 10 150 PANIERVEILKO                         PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                         PANIERVEILKO                         PANIERVEILKO                         PANIERVEILKO                         PANIERVEILKO                         PANIERVEILKO                             PANIERVEILKO                                   PANIERVEILKO	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  1100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  160  220  GEVGRANSFRSG  111           GEVGRANSFRSG  220  280  LPYRMGFAHRNG	JOSCHANDER DE STORT DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONT	SYINYDEAA 60  120 FLRGFQAD          FFLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI          ETVKLDNG          ETVKLDNG 240 300 EDLEYAFND
m761.pep a761 m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1  GAVYGSWAI   :       GTVYGSWAI  1  LKWTGQYT	LLPTLIIASFI 10	PVAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE                         NIQKNKNYGTNE 30 90 10 150 PANIERVEILKO                         PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                       PANIERVEILKO                         PANIERVEILKO                         PANIERVEILKO                         PANIERVEILKO                         PANIERVEILKO                         PANIERVEILKO                             PANIERVEILKO                                   PANIERVEILKO	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  160  220  GEVGRANSFRSG                GEVGRANSFRSG  220  280	JOSCHANDER DE STORT DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONTROL DE LA CONT	SYINYDEAA 60  120 FLRGFQAD          FFLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI          ETVKLDNG          ETVKLDNG 240 300 EDLEYAFND
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m761.pep a761 m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1:        GAVYGSWAI   :        GTVYGSWAI  1  LKWTGQYT           LKWTGQYT	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 NIQKNKNYGTNI NIQKNKNYGTNI 30 90 10 150 TANIERVEILKO 10 150 VLNKNVAIRLTO VLNKNVAIRLTO VLNKNVAIRLTO 00 210 VLNKNVAIRLTO 00 210 SPTKSVYDRFGI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  220  GEVGRANSFRSG  220  280  LPYRMGFAHRNG  LPYRMGFAHRNG	VVGQSDTSVLKG 50  110  DAAYDMRGESI            DAAYDMRGESI 110  170  GGGVINMVSKYA            GGVINMVSKYA 170  230  SIDSKNVMVSPS            GIDSKNVMVSPS 230  290  PFVKDKLQVWRS	SYINYDEAA 60  120 FLRGFQAD          FFLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI           ETVKLDNG           ETVKLDNG 240 300 EDLEYAFND
m761.pep a761 m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG  1:        GAVYGSWAI   :        GTVYGSWAI  1  LKWTGQYT           LKWTGQYT	LLPTLIIASFI 10	PVAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE 111111111111111111111111111111111111	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  220  GEVGRANSFRSG  220  280  LPYRMGFAHRNG  LPYRMGFAHRNG	JOSCH STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDA	TYNYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI          ANFKQSRNI 240 SITVKLDNG          SITVKLDNG 240 300 BLEYAFND
m761.pep a761 m761.pep a761 m761.pep a761	VTRNGQLI:           VTRNGQLI:           VTRNGQLI:  ASDIYRDG'          ASDIYRDG'          GAVYGSWAN  :       GTVYGSWAN     LKWTGQYT'         LKWTGQYT'	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 31QKNKNYGTNE 31 11111111111111111111111111111111111	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI  100  100  160  EPSSVLYGRTNE  11           EPSSVLYGRTNE  220  EEVGRANSFRSE  11            EEVGRANSFRSE  220  280  LPYRMGFAHRNE  11           LPYRMGFAHRNE	JOSCH STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDARD STANDA	TYNYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI          ANFKQSRNI 240 SITVKLDNG          SITVKLDNG 240 300 BLEYAFND
m761.pep a761 m761.pep a761 m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI:           VTRNGQLI:          ASDIYRDG           ASDIYRDG           GAVYGSWAN   :       GTVYGSWAN   :       LKWTGQYT          LKWTGQYT	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 31QKNKNYGTNE 31 11111111111111111111111111111111111	EHYTATLPTVSV  100  100  DLSSILEGNAGI               DLSSILEGNAGI               DLSSILEGNAGI  100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  220  GEVGRANSFRSG  220  280  LPYRMGFAHRNG  11           LPYRMGFAHRNG  280  340	VGQSDTSVLKG 50  110  DAAYDMRGESI            DAAYDMRGESI 110  170 GGGVINMVSKYA             GGGVINMVSKYA 170  230 GIDSKNVMVSPS             GIDSKNVMVSPS 230  290 OFVKDKLQVWRS            OFVKDKLQVWRS 290 350	120 120 151 160 120 151 161 161 171 171 180 180 180 180 180 180 180 180 180 18
m761.pep a761 m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG            GAVYGSWAI   :        GTVYGSWAI  1  LKWTGQYT           LKWTGQYT  2  3  KWRAQWQLI	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE NIQKNKNYGTNE 30 90 10 150 TANIERVEILKO 10 150 TANIERVEILKO 10 150 VLNKNVAIRLTO VLNKNVAIRLTO 10 210 VLNKNVAIRLTO 50 270 50 270	EHYTATLPTVSV  100  100  DLSSILEGNAGI                DLSSILEGNAGI                DLSSILEGNAGI  100  160  GPSSVLYGRTNG               GPSSVLYGRTNG  220  GEVGRANSFRSG  220  160  280  LPYRMGFAHRNG  11           LPYRMGFAHRNG  280  140  140  140  140  140  140  140  1	JOSCHTSVLKG 50  110  DAAYDMRGESI            DAAYDMRGESI            DAAYDMRGESI 110  170  GGVINMVSKYA             GGVINMVSKYA 170  230  SIDSKNVMVSPS 230  290  PVKDKLQVWRS            DFVKDKLQVWRS 290  350  KTLSSNLTLNG	SYINYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI          ANFKQSRNI 180  240 FITVKLDNG          FITVKLDNG 240  300 FDLEYAFND          FDLEYAFND 300  360 FDYTIGRFE
m761.pep a761 m761.pep a761 m761.pep a761 m761.pep	MKISFHLA  VTRNGQLI:           VTRNGQLI:          ASDIYRDG           ASDIYRDG           GAVYGSWAN   :       GTVYGSWAN   :       LKWTGQYT          LKWTGQYT          LKWTQQYL	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE NIQKNKNYGTNE NIQKNKNYGTNE 30 90 10 150 TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO TANIERVEILKO T	EHYTATLPTVSV  100  100  DLSSILEGNAGI                DLSSILEGNAGI                DLSSILEGNAGI  100  100  160  EPSSVLYGRTNO  11            EPSSVLYGRTNO  220  EVGRANSFRSO  11             EVGRANSFRSO  220  280  LPYRMGFAHRNO  11            LPYRMGFAHRNO  280  KRNYAWQQTDN	JOSCHTSVLKG 50  110  DAAYDMRGESI            DAAYDMRGESI            DAAYDMRGESI 110  170  GGVINMVSKYA             GGVINMVSKYA 170  230  SIDSKNVMVSPS 230  290  PVKDKLQVWRS            DFVKDKLQVWRS 290  350  KTLSSNLTLNG	SYINYDEAA 60  120 FLRGFQAD          FFLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI 180 240 EITVKLDNG          EITVKLDNG 240 BOLEYAFND          EDLEYAFND 300 BOLTIGRFE
m761.pep a761 m761.pep a761 m761.pep a761 m761.pep a761	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG            GAVYGSWAN   :        GTVYGSWAN  1  LKWTGQYT           LKWTGQYT           KWRAQWQLI	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	EHYTATLPTVSV  100  100  DLSSILEGNAGI                DLSSILEGNAGI                DLSSILEGNAGI  100  160  GPSSVLYGRTNG                GPSSVLYGRTNG  220  GEVGRANSFRSG  220  160  280  LPYRMGFAHRNG  11           LPYRMGFAHRNG  280  140  150  150  160  160  160  160  160  16	JOSCH STEEL STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE	TYINYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI 180  240 SITVKLDNG          SITVKLDNG 240 SITVKLDNG 1        SITVKLDNG 300 SDLEYAFND          SDLEYAFND 300 360 SDYTIGRFE
m761.pep a761 m761.pep a761 m761.pep a761 m761.pep	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG           ASDIYRDG            GAVYGSWAN   :        GTVYGSWAN  1  LKWTGQYT           LKWTGQYT           KWRAQWQLI	LLPTLIIASFI 10	2VAAADTQDNGE 20 30 30 90 NIQKNKNYGTNE HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	EHYTATLPTVSV  100  100  DLSSILEGNAGI                DLSSILEGNAGI                DLSSILEGNAGI  100  160  GPSSVLYGRTNG                GPSSVLYGRTNG  220  GEVGRANSFRSG  220  160  280  LPYRMGFAHRNG  11           LPYRMGFAHRNG  280  140  150  150  160  160  160  160  160  16	JOSCHTSVLKG 50  110  DAAYDMRGESI            DAAYDMRGESI            DAAYDMRGESI 110  170  GGVINMVSKYA             GGVINMVSKYA 170  230  SIDSKNVMVSPS 230  290  PVKDKLQVWRS            DFVKDKLQVWRS 290  350  KTLSSNLTLNG	SYINYDEAA 60  120 FLRGFQAD          FFLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI 180 240 EITVKLDNG          EITVKLDNG 240 BOLEYAFND          EDLEYAFND 300 BOLTIGRFE
m761.pep a761 m761.pep a761 m761.pep a761 m761.pep	MKISFHLA  VTRNGQLI            VTRNGQLI  1  ASDIYRDG            ASDIYRDG            GAVYGSWAN   :        GTVYGSWAN  1  LKWTGQYT           LKWTGQYT           KWRAQWQLI            KWRAQWQLI	LLPTLIIASFI 10	PVAAADTQDNGE 20 30 30 30 90 NIQKNKNYGTNE 111111111111111111111111111111111111	EHYTATLPTVSV  100  100  DLSSILEGNAGI                DLSSILEGNAGI                DLSSILEGNAGI  100  160  EPSSVLYGRTNO                EPSSVLYGRTNO  220  EVGRANSFRSO  11             EVGRANSFRSO  220  280  LPYRMGFAHRNO  11            LPYRMGFAHRNO  280  EKRNYAWQQTDN                 EKRNYAWQQTDN  340  340	JOSCH STEEL STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE	TYINYDEAA 60  120 FLRGFQAD          FLRGFQAD 120  180 ANFKQSRNI          ANFKQSRNI 180  240 SITVKLDNG          SITVKLDNG 240 SITVKLDNG 1        SITVKLDNG 300 SDLEYAFND          SDLEYAFND 300 360 SDYTIGRFE

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m761.pep	NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
a761	NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
	370 380 390 400 410 420
	400
	430 440 450 460 470 480
m761.pep	QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
<b></b>	
a761	QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
	430 440 450 460 470 480
	490 500 510 520 530 540
m761.pep	YNKGFAPYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
m/or.pcp	1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.
a761	YNKGFAPYGGRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
3.52	490 500 510 520 530 540
	550 560 570 580 590 600
m761.pep	NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761	NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
	<b>550 560 570 580 590</b> 600
	610 620 630 640 650 660
m761.pep	RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
a761	RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
	610 620 630 640 650 660
m761 nen	670 680 690 700
m761.pep	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
• •	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
m761.pep a761	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
• •	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761 <b>g762.seq</b>	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761 g762.seq g762.pep	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761 g762.seq g762.pep	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761 g762.seq g762.pep	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p	670 680 690 700 LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq	670 680 690 700  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq	670 680 690 700  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51	670 680 690 700  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101	670 680 690 700  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101 151 201 251	670 680 690 700  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101 151 201 251 301	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101 151 201 251 301 351	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101 151 201 251 301	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq  1 51 101 151 201 251 301 351 401	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101 151 201 251 301 351 401  This correspond	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq  1 51 101 151 201 251 301 351 401	G70 680 690 700  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101 151 201 251 301 351 401  This correspond	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101 151 201 251 301 351 401  This correspond	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
a761  g762.seq g762.pep  The following p m762.seq 1 51 101 151 201 251 301 351 401  This correspond	LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2613>: a762.seq

```
ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
  1
51 AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAAATCTA TCTATATGGC
201 AATTATTAT CCTATTTTAT ATTTTTTAC GATAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
```

```
301 AGTTTTATGG ACTTTTACTT TTTTTCCATA TATTCAGATA ACCTTAGCTA
              TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT
              CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA
This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:
     a762.pep
              MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
            1
           51
              LFLLFIFNFV TKSIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
          101
              SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*
m762 / a762 100.0% identity in 147 aa overlap
                         10
                                            30
                 MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV
     m762.pep
                 MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV
     a762
                         10
                                   20
                                            30
                                                      40
                                                                50
                                                                         60
                         70
                                   80
                                            90
                                                     100
                                                               110
                                                                        120
                 TKSIYMAIIYPILYFFTIKKYYPYSRKVIILLSLALSIYFSFMDFYFFSIYSDNLSYETE
     m762.pep
                 a762
                 TKSIYMAIIYPILYFFTIKKYYPYSRKVIILLSLALSIYFSFMDFYFFSIYSDNLSYETE
                         70
                                   80
                                            90
                                                     100
                                                               110
                                                                        120
                        130
                                  140
                 PLHLYIPIIINFFSLLVSNFILSFINKX
     m762.pep
                 a762
                 PLHLYIPIIINFFSLLVSNFILSFINKX
                        130
                                  140
     g763.seg not yet found
     q763.pep not yet found
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2615>:
    m763.seq
              ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
           1
              CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
          51
              CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTTAC CTTGCCACTA
              TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
              GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
         201
              CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
         251
              TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
         351
              CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
              CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
         401
         451
              CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
              TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
         501
              AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
         551
              AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
         601
              CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
         651
              AAAACCAGTT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
         701
              ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
              CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
         851
              GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
         901
              CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
             CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
         951
        1001
              GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
              TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
        1051
              ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
        1101
        1151
              ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
```

TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC

AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT

TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA

1201

1251 1301

1351

1401

ATAA

```
This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:
```

```
m763.pep

1 MTLLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51 SLSPSVSAFT LPEAWRAQQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIAVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYQNNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLAV RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
```

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2617>: a763.seq

```
ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
  51
      CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101
      CCTATTTTC CAAATATATC CTACCCGTTT CACTTTTTAC CTTGCCACTA
 151
      TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
     GGCGCAGCAA CATTCGGCTG ATTTTCAAGC GTCCCATTAC CAGCGTGATG
      CAGTGCGCGC ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
      TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG
     CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
 401
     CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
     CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 451
     TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
     AAAAAGAGGC TTATGCCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
     AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
      CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
      AAAACCAGTT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
     ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
     CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851
     GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901
     CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
     CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 951
     GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1001
     TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
     ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151
     ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT
1201
     TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
     CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC
     AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
     TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA
1351
1401
     ATAA
```

## This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

1					LPVSLFTLPL
51	SLSPSVSAFT	LPEAWRAAQQ	HSADFQASHY	QRDAVRARQQ	QAKAAFLPHV
101				FDAAKFAQYR	
151	QRFDAAREEL	LLKVAESYFN	VLLSRDTVAA	HAAEKEAYAQ	QVRQAQALFN
201	KGAATALDIH				
251	IDTANLLARY	LPKLERYSLD	EWQRIALSNN	HEYRMQQLAL	QSSGQALRAA
301				RGKGMSVGVQ	
351				RQAYTESGAA	
401	LESSRLKLKS	TETGQQYGIR	NRLEVIRARQ	EVAQAEQKLA	QARYKFMLAY
451	LRLVKESGLG	LETVFAE*			

#### m763 / a763 99.8% identity in 467 aa overlap

	10	20	30	40	50	60
m763.pep	MTLLNLMIMQDYGI	SVCLTLTPYL	QHELFSAMKSY	FSKYILPVS:	LFTLPLSLSP	SVSAFT
		111111111	1111111111	11111111	1111111111	
a763	MTLLNLMIMQDYGI					
	10	20	30	4.0	50	60

	70	80	90	100	110	120
m763.pep	LPEAWRAAQQHSA	DFQASHYQRD	avrarqqqak <i>i</i>	AAFLPHVSAN	ASYOROPPST	CTRETO
	11111111111		111111111		1111111111	1111111
a763	LPEAWRAAQQHSAI	DFQASHYQRD	AVRARQQQAKA	AFLPHVSAN	ASYOROPPST	SSTRETO
	70	. 80	90	100	110	120
						120
	130	140	1.50	160	-170	180-
m763.pep	GWSVQVGQTLFDAA	AKFAQYRQSRI	FDTQAAEQRFD	AAREELLLK	VAESYFNVLL	SRDTVAA
						IIIIIII
a763	GWSVQVGQTLFDAA	AKFAQYRQSRI	TOTQAAEQRFD	AAREELLLK	/AESYFNVI.I.	SRDTVAA
	130	140	150	160	170	180
					- · ·	2.00
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQ	AQALFNKGA <i>A</i>	ATALDIHEAKA	GYDNALAOE	AVLAEKOTY	ENOLNDY
		111111111		1111111111		FILLIT
a763	HAAEKEAYAQQVRQ	AQALFNKGAA	TALDIHEAKA	GYDNALAOE	AVLAEKOTY	ENOLNDY
	190	200	210	220 ~	230	240
						2.10
	250	260	270	280	290	300
m763.pep	TDLDSKQIEAIDTA	NLLARYLPKL	ERYSLDEWOR	IALSNNHEYE	MOOLALOSS	SOAT.RAA
		1111111111	111111111		11111111	
a763	TGLDSKQIEAIDTA	NLLARYLPKL	ERYSLDEWOR	IALSNNHEYR	MOOLALOSS	CALRAA
	250	260	270	280	290	300
					230	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGY	QNNLYTSSAQ	NNDYHYRGKGI	MSVGVOLNLP	LYTGGELSG	774TX
		111111111	111111111			IIIIII
a763	QNSRYPTVSAHVGY	QNNLYTSSAO	NNDYHYRGKGI	MSVGVOLNLP	LYTGGELSGE	THEAFA
	310	320	330	340	350	360
					330	300
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATER	HIKLAVROAY			RI.KI.KSTETC	OZF GTOVOO:
	Тинийний				IIIIIIIIII	IIIIII
a763	QYGAAEAQLTATER	HIKLAVROAY	TESGARRYOT	MAOERVIESS	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	COVCID
	370	380	390	400	410	420
	- · ·		550	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAQ				FAEX	
• •					1111	
a763	NRLEVIRARQEVAQ	AEOKLAOARYI	KEMI.AYI.RI.VE	CESCLCLETY	IIII Fary	
	430	440	450	460	r viiv	
		1.0	100	400		

```
g764.seq not found yet g764.pep not found yet
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2619>: m764.seq

```
ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTACTGTATG
   1
      GCGCAATGTT TGGGCGGTGC GCGACCAGTT GAAACCGCCC AAACGCACGG
  51
 101 CGGAAGAACA GGCGTTTTTG CCCGCGCATT TGGAACTGAC CGATACGCCG
 151 GTCTCTGCCG CTCCGAAATG GGCGGCGCGT TTTATTATGG CGTTTGCGCT
 201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
 251 CTTCGGGCAA AACGGTGTCG GGCGGGCGCA GCAAAACCAT CCAGCCGCTG
 301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
      ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
      TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
      TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
 501
      TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
 551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
 601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
 651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
 701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTC GGAACATGCG
 751 TTTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAAAG
 801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
 851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
 901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
 951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101
     TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151
     TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
     AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1201
     GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1251
1301
     GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GGCGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG
```

## This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>: m764.pep

```
1 MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEEQAFL PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVKQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVGAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNDLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAEIK
```

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2621>:

```
a764.seq (partial)
         ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
      1
         GCGCAATGTT TGGGCGGTGC GCGACCAGTT GGAACCGCCC AAACGCACGG
    101 CGGAAGAACA GGCGTTTTTG CCCGCGCATT TGGAACTGAC CGATACGCCG
         GTCTCTGCCG CTCCGAAATG GGCGGCGCGT TTTATTATGG CGTTTGCGCT
         TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
    251 CTTCGGGCAA AACGGTGTCG GGCGGGCGCA GCAAAACCAT CCAGCCGCTG
    301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
    351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
    401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
    451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
    501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
    551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
        CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
    651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
```

	•
701·	CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTC GGAACATGCG
751	TTTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801	TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
	AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
851	
901	CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951	GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001	CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051	CAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101	TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151	TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201	AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251	GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301	GCAAA
1501	0.22
Milia a a massa a sa d	s to the amine said assumes SEO ID 2622; ODE 764 s>
	s to the amino acid sequence <seq 2622;="" 764.a="" id="" orf="">:</seq>
a764.pep	(partial)
1	MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEEQAFL PAHLELTDTP
51	VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101	ETVVVKAVHV RDGQHVKQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151	YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201	QLQSALRGHQ AELQSAKAQE QKLVSVGAIE QQKTADYRRL RADNFISEHA
251	FLEQQSKSVS NWNDLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
	LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
301	
351	QKMMVVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401	KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGK
m764 / a764 99	.3% identity in 435 aa overlap
	10 20 30 40 50 60
m764 non	MFFSALKSFLSRYITVWRNVWAVRDQLKPPKRTAEEQAFLPAHLELTDTPVSAAPKWAAR
m764.pep	
a764	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEEQAFLPAHLELTDTPVSAAPKWAAR
	10 20 30 40 50 60
	70 80 90 100 110 120
m764.pep	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDGQHVKQGE
•	
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETVVVKAVHVRDGQHVKQGE
	70 80 90 100 110 120
	130 140 150 160 170 180
m764.pep	TLAELEAVGTDSDVVQSEQALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD
m/o4.pcp	
2764	TLAELEAVGTDSDVVQSEQALQAAQLSKLRYEAVLAALESRTVPHIDMAQARSLGLSDAD
a764	
	130 140 150 160 170 180
	100 000 010 000 000
	190 200 210 220 230 240
m764.pep	VQSAQVLAQHQYQAWAAQDAQLQSALRGHQAELQSAKAQEQKLVSVGAIEQQKTADYRRL
a764	VQSAQVLAQHQYQAWAAQDAQLQSALRGHQAELQSAKAQEQKLVSVGAIEQQKTADYRRL
	<b>19</b> 0 200 210 220 230 240
	<b>250 260 270 280 290 300</b>
m764.pep	RADNFISEHAFLEQQSKSVSNWNDLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA
1 1	
a764	RADNFISEHAFLEQQSKSVSNWNDLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA
4,03	250 260 270 280 290 300
	230 200 270 200 270 300
	210 220 220 240 250 260
5.5.	310 320 330 340 350 360
m764.pep	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVVAPDD
	310 320 330 340 350 360
	370 380 390 400 410 420
m764.pep	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
0	

```
a764
                    DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVSHDAVSHEOLGLVYT
                            370
                                       380
                                                  390
                                                             400
                                                                        410
                                       440
                            430
                                                  450
                                                             460
                                                                        470
                    AVVSLDKHTLNIDGKAVNLTAGMNVTAEIKTGKRRVLDYLLSPLQTKLDESFRERX
      m764.pep
                    a764
                    AVVSLDKHTLNIDGK
                            430
q765.seq not yet found
g765.pep not yet found
The following partial DNA sequence was identified in N. meningitidis <SEO ID 2623>:
         ATGTTAAGAT GCCGTCCGAA ATCCGTTTTG GATTCAGACG GCATTTTTTT
         GAAATTTAAT TTTTTAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
     101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
     151 GCTTGTGCGG TCGTTGCTGA TGTTTACGGT CATGATTCCG CCACAATGAA
     201 CGCTGCGGCT GCCAAAGATT ATATGAAAAC GGTTGAGTTA AACAAGTCTG
     251 CCGGCAATGT CGATACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
     301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
     351 GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
     401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAAACTC
     451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
     501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
     551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
     601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
     651 TCTTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGGG
     701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
         GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
    801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAAC
     851 GGTTGTTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
     901 GGGCGCGTTA ATAAAAAACG TCGGCGTTAA
This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:
m765.pep
         MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
         ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVOAV
     51
    101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
    151 KLTDDEIAAI MGHEMTHALH EHGKNKVGQQ ILTNTAAOIG TOIILDKKPD
    201 TNPELVGLGM DILGTYGLTL PYSRSLEEEA DEGGMMLMAQ AGYHPAAAVR
    251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLLPTVM PVYEQSVRNK
    301 GRVNKKRRR*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2625>:
a765.seq
         ATGTTAAGAT GCCGTCCGAA ATCCGTTTTG GATTCAGACG GCATTTTTTT
      1
         GAAATTTAAT TTTTTAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
     51
    101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
    151 GCTTGTACGG TCGTTGCTGA TGTTTACGGT CAGGATTCCG CCACAATGAA
    201 TGCTGCGGCT GCCGAAGATT ATATGAAAAC GGTTGAGTTG AACAAGTCTG
    251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
    301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
         GTTTGACTGG AAAATGACGG TTTTCAAAAA CGATGAGCTG AACGCGTGGG
    401 CAATGCCCGG CGGGAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
    451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
    501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
    601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
    651 CATTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGGG
    701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTCAGG
    751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAAACGGCT TTATTTATGC
    801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAAC
    851 GGTTGTTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
    901 GGGCGCGTTA ATAAAAACCG TCGGCGTTAA
This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:
a765.pep
```

1 MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG

```
ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
51
    FRRMLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
101
    KLTDGEIAAI MGHEMTHALH EHGKNKVGQK ILTNMAAQIG TQIILDKKPD
151
    TNPELVGLGM DILGMYGITL PYSRSLEEEA DEGGMMLMAQ AGYHPAAAVR
201
    VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLLPTVM PVYEHSVRNK
    GRVNKNRRR*
301
```

Computer analysis of this amino acid sequence gave the following results:

## Homology with a predicted ORF from N meningitidis

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from N. meningitidis:

m765 / a765 96.1% identity in 309 aa overlap

```
10
                        20
                                30
                                       40
          MLRCRPKSVLDSDGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACAVVADVYG
m765.pep
          MLRCRPKSVLDSDGIFLKFNFLRSKPKYEISFLPSFKRILCLSAVISVLGACTVVADVYG
a765
                                       40
                                90
                                       100
                                              110
                                                      120
                        80
          HDSATMNAAAAKDYMKTVELNKSAGNVDTTSRTARRVQAVFRRMLPYADAANNTSHKFDW
m765.pep
          QDSATMNAAAAEDYMKTVELNKSAGNVDTTSKTARRVQAVFRRMLPYADAANNTGHKFDW
a765
                70
                        80
                                90
                                       100
                                              110
                                              170
                                       160
               130
                       140
                               150
          KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKNKVGQQ
m765.pep
          KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKNKVGQK
a765
                                       160
                                              170
                                                      180
                               150
                       140
               130
                                       220
                       200
                               210
               190
          ILTNTAAQIGTQIILDKKPDTNPELVGLGMDILGTYGLTLPYSRSLEEEADEGGMMLMAQ
m765.pep
          {\tt ILTNMAAQIGTQIILDKKPDTNPELVGLGMDILGMYGITLPYSRSLEEEADEGGMMLMAQ}
a765
                       200
                               210
                                       220
               190
               250
                       260
                               270
                                       280
                                              290
                                                      300
          AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPTVMPVYEQSVRNK
m765.pep
          AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPTVMPVYEHSVRNK
a765
                                       280
                                              290
               250
                       260
                               270
               310
          GRVNKKRRRX
m765.pep
          11111:1111
a765
          GRVNKNRRRX
               310
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2627>: g767.seq

```
ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
 1
    GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
51
    CCATTCCTCA AGAACAGCCG GGAAAAATTG AGGTTTTGGA ATTTTTCGGC
101
    TATTTTTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
    CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
201
    GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCG
    GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTTAAAGCAG TTTACGAACA
    AAAAATCCGT TTGGAAAACA GGGCTGTTGC CGGGAAATGG GCTTTATCTC
    AAAAAGGTTT TGACGGCAAA AAACTGATGC GCGCCTATGA TTCCCCCGAA
401
    GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
    TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
    ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTTGCCAAA
    GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG
```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>: g767.pep

- MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
- YFCVHCHHFD PLLLKLGKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS 51

```
101 GLKYQANSAV FKAVYEQKIR LENRAVAGKW ALSQKGFDGK KLMRAYDSPE
151 AAAVALKMQK LTEQYGIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
```

201 VREERKROTP AVQK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2629>:

```
1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AGAACAGTCG GGTAAAATTG AGGTTTTGGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCGT CAATTTGTCG
301 GGTTTGAAAT ATCAGGCAAA CCCTGCTTGT TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGGAAAACA GGTCGGTTGC CGGAAAATGG GCTTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAACTGATGC GCGCCTATGA TTCCCCCGAA
451 GCTGCCGCCG CCGCATTAAA AATGCAGAAA CTGACGGAAC AATACCGCAT
501 CGACAGCACG CCGACCGTTA TTGTCGCGG AAAATACCGC GTTATCTTCA
551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTTGCCCAAA
```

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>: m767.pep

- 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG 51 YFCVHCHHFD PLLLKLGKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
- 101 GLKYQANPAV FKAVYEQKIR LENRSVAGKW ALSQKGFDGK KLMRAYDSPE

601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

- 151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
- 201 VREERKROTP AVQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from N. gonorrhoeae

m767/g767	95.8%	identity	in 214 aa	overlap			
		10	20	30	40	<del>-</del> -	60
g767.pep	MKFKHLL	PLLLSAVLS	AQAYALTEGE	DATATOKAIA	QEQPGKIEVL:	EFFGYFCVHCHHI	FD
	11:111		[1111]	1111111111		,	П
m767	MKLKHLLI		-			EFFGYFCVHCHH	
		10	20	30	40	50	60
		70	80	90	100		20
g767.pep	PLLLKLG	KALPSDTYLI	RTEHVVWRPE	MLGLARMAAA	VKLSGLKYQA:	NSAVFKAVYEQKI	
	111111	111111:11	[]:[[][]:[]		1:1111111		
m767	PLLLKLG					NPAVFKAVYEQK:	
		70	80	90	100	110 12	20
	:	130	140	150	160	170 18	80
g767.pep	LENRAVA	GKWALSQKG	FDGKKLMRAY	DSPEAAAVAL	KMQKLTEQYG	IDSTPTVIVGGK	ΥR
	1111111		111111111	1111111:11			H
m767	LENRSVA	GKWALSQKÇ!	FDGKKLMRAY			IDSTPTVIVGGKY	
	:	130	140	150	160	170 18	80
	:	190	200	210			
g767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX						
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX						
	;	190	200	210			

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2631>: a767.seq

```
1 ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTTGTCCGC
51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCCTCA AAAACAGTCG GGCAAAATTG AGGTTTTGGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAATTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCA
301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGGAAAACA GGTCGGTTGC CGAAAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AAACTGATGC GCGCCTACGA CTCTCCTGCG
```

- 451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT 501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
- 551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTTGCCAAA
- 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>: a767.pep

- 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQKQS GKIEVLEFFG
- 51 YFCVHCHHFD PLLLKLGKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
- 101 GLKYQANPAV FKAVYEQKIR LENRSVAEKW ALSQKGFDGK KLMRAYDSPA
- 151 AAAAASKMQQ LTEQYRIDST PTVVVGGKYR VIFNNGFDGG VHTIKELVAK
- 201 VREERKROTP AVOK*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from N. meningitidis

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from N. meningitidis:

m767/a767	96.7% identity	in 214 aa	a overlap			
	10	20	30	40	50	60
a767.pep	MKLKHLLPLLLSAVL	SAQAYALTI	EGEDYLVLDKP:	I PQKQSGKI E	EVLEFFGYFCV	HCHHFD
		11111111		111:11111	111111111111	
m767	MKLKHLLPLLLSAVL	SAQAYALTI	EGEDYLVLDKP:	IPQEQSGKIE	EVLEFFGYFCV	HCHHFD
	10	20	30	40	50	60
	70	80	90	100	110	120
a767.pep	PLLLKLGKALPSDAY	LRTEHVVW	PEMLGLARMA	AAVKLSGLKY	'QANPAVFKAV	YEOKIR
	1111111111111		1111111111		IIIIIIII	11111
m767	PLLLKLGKALPSDAY	LRTEHVVWQ	PEMLGLARMA	AAVNLSGLKY	QANPAVFKAV	YEOKIR
	70	80	90	100	110	120
	130	140	150	160	170	180
a767.pep	LENRSVAEKWALSQK	GFDGKKLMF	RAYDSPAAAAA	ASKMOOLTEC	YRIDSTPTVV	VGGKYR
	1111111 111111	111111111	THE HILL	111:111	111111111111111111111111111111111111111	
m767	LENRSVAGKWALSQK	GFDGKKLMF	AYDSPEAAAA	LKMQKLTEQ	YRIDSTPTVI	VGGKYR
	130	140	150	160	170	180
	190	200	210			
a767.pep	VIFNNGFDGGVHTIK	ELVAKVREE	RKRQTPAVQKX	3		
- <b>-</b>	311111111111111111111111111111111111111	[]]]]				
m767	VIFNNGFDGGVHTIK	ELVAKVREE	RKRQTPAVQKX			
	190	200	210			

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2633>: g768.seq

- 1 ATGAATATCA AACAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
- 51 TGCCACGCAG GCAGCCCCGC AAAAACCCGT ATCCGCCGCC CAAACCGCGC
- 101 AACATTCAGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
- 151 GGTCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
- 201 CATATACGAA GCCGCCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC
- 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG
- 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>: g768.pep

- 1 MNIKQLITAA LIASAAFATQ AAPQKPVSAA QTAQHSAVWI DVRSEQEFSE
- 51 GHLHNAVNIP VDQIVRRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
- 101 YTNVANHGGY EDLLKKGMK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2635>: m768.seq

- 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
- 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCGT ATCCGCCGCC CAAACCGCGC
- 101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
- 151 GGGCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
- 201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC

- 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
- 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG
- 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>: m768.pep

- 1 MNIKHLITAA LIASAAFAAQ AAPOKPVSAA QTAQHPAVWI DVRSEQEFSE 51 GHLHNAVNIP VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
- 101 YTNVANHGGY EDLLKKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from N. gonorrhoeae

```
m768/g768
          96.6% identity in 119 aa overlap
                        20
                                30
                                       40
a768.pep
          MNIKQLITAALIASAAFATQAAPQKPVSAAQTAQHSAVWIDVRSEQEFSEGHLHNAVNIP
          m768
          MNIKHLITAALIASAAFAAQAAPQKPVSAAQTAQHPAVWIDVRSEQEFSEGHLHNAVNIP
                        20
                                30
                                       40
                70
                        80
                                90
                                       100
                                              110
                                                      120
g768.pep
          VDQIVRRIYEAAPDKDTPVNLYCRSGRRAEAALQELKKAGYTNVANHGGYEDLLKKGMKX
          m768
          VDQIVRRIHEAAPDKDTPVNLYCRSGRRAEAALQELKKAGYTNVANHGGYEDLLKKGMKX
                70
                        80
                                90
                                      100
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2637>: a768.seq

- 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
- 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCGT ATCCGCCGCC CAAACCGCGC
- 101 AACATTCAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
- 151 GGTCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
- 201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC
- 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC 301 TATACGAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAAGG
- 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>: a768.pep

- 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSAA QTAQHSAVWI DVRSEQEFSE
- 51 GHLHNAVNIP VDQIVRRIHE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
- 101 YTNVANHGGY EDLLKKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N meningitidis

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from N. meningitidis:

```
m768/a768
          99.2% identity in 119 aa overlap
                10
                                30
                                       40
                                               50
          MNIKHLITAALIASAAFAAQAAPQKPVSAAQTAQHSAVWIDVRSEQEFSEGHLHNAVNIP
a768.pep
          m768
          MNIKHLITAALIASAAFAAQAAPQKPVSAAQTAQHPAVWIDVRSEQEFSEGHLHNAVNIP
                10
                        20
                                       40
                                               50
                                                       60
                70
                        80
                                90
a768.pep
          VDQIVRRIHEAAPDKDTPVNLYCRSGRRAEAALQELKKAGYTNVANHGGYEDLLKKGMKX
          m768
          VDQIVRRIHEAAPDKDTPVNLYCRSGRRAEAALQELKKAGYTNVANHGGYEDLLKKGMKX
                70
                        80
                               90
                                      100
```

WO 99/57280

1250

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2639>:
q769.seq
          TTGATAATGG TTATTTTTA TTTTTATTTT TGTGGGAAGA CATTTATGCC
       1
      51
          TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
     101 CCGAAqaAAC ACCgtgCGAA CCGGATTTGA GAAGCCGTCC CGAGTTCAGG
     151 CTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
     201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGGCGAA ACCCTGCTGA
     251 AAAATCCCGA ATTGTTGTCG CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
     301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
     351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
     401 AGGGCAGGGT GAAGGAGGCG GTTTCCCATT ACCGGGAATT GATTGCCGCC
     451 CAACCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
     501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
         AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
         TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GGCGGTTTCA GCGTTACCCG
     651 CGAACACAAT ATCAACCAAG CCCCGAAACA GCAGCAGTAC GGCAATTGGA
     701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
     751 GAGAAAAAT GGTCGCTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
     801 CGTGTCCGGC AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
     851 CAGGTGTTTC CGGCGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
         CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
     951 CGCCAACGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
    1001 AAACGCTGTC TTCGGCGGAG TGGGGGCGTT TGAAGAATAC GCGCCGGGCG
    1051 CGTTCCGACA ATACCCATTT GCAAATTTCC AATTCGCTGG TGTTTTACCG
    1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTTAC CGCGAGCGCA
    1151 ACCCCGCCGA CCGTGGCGAC AATTTCAACC GTTACGGCCT GCGCTTTGCC
    1201 TGGGGGCAGG AATGGGGCGG CAGCGGCCTG TCTTCGCTGT TCCGCCTCGG
         CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTTAAAG
    1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
         CGGGCATTGC ATTTCAAAGG CATCACGCCG CGCCTGACGC TGTCGCACCG
    1401
         CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
         TTGTCGAGTT TAACAAAACG TTCTGA
This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:
g769.pep
         LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
      51 LHEAEVKPID REKVPGQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
     101 NIAGIRVILP IYLQQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
         QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPQL MEQVELYRKA
     201 LRERDAWKVN GGFSVTREHN INQAPKQQQY GNWTFPKQVD GTAVNYRFGA
     251 EKKWSLKNGW YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
     301 LAVFHERRTY GNDAYSYANG ARLYFNRWQT PRWQTLSSAE WGRLKNTRRA
         RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
         WGQEWGGSGL SSLFRLGVAK RHYEKPGFFS SFKGERRRDK ESDTSLSLWH
     451 RALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*
The following partial DNA sequence was identified in N. meningitidis <SEO ID 2641>:
m769.seq
         TTGATAATGG TTATTTTTA TTTTTGTGGG AAGACATTTA TGCCTGCACG
      51 AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
    101 AAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
         CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
    201 GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
     251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
     301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
         GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
     401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGGAATTGAT TGCCGCCCAA
     451 CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCAGCAT TGTTTGAAAA
     501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
     551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
     601 CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
     651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
         TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
     751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
     801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
     851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GGCGCAAAGA TGCCGGGCTG
         GCAGTGTTCC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
     951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
    1001 CGTTGTCTTC GGCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
    1051
         TCCGACAATA CCCATTTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
    1101 TGCGCGCCAA TATTGGATGG GCGGTTTGGA TTTTTACCGC GAGCGCAACC
    1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
```

1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC

1251	GGCGAAACGG	CATTATGAAA	AACCCGGCTT	TTTCAGCGGT	TTTAAAGGGG
1301	AAAGGCGCAG	GGATAAAGAA	TTGAACACAT	CCTTGAGCCT	TTGGCACCGG
1351	GCATTGCATT	TCAAAGGCAT	CACGCCGCGC	CTGACGTTGT	CGCACCGCGA
1401	AACGCGGAGT	AACGATGTGT	TCAACGAATA	CGAGAAAAAT	CGGGCGTTTG
1451	TCGAGTTTAA	TAAAACGTTC	TGA		

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>: m769.pep

1 LIMVIFYECG KTFMPARNRW MLLLPLLASA AYAEETPREP DLRSRPEFRL
51 HEAEVKPIDR EKVPGQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKRQQYG KWTFPKQVDG TAVNYRLGAE
251 KKWSLKNGWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGGSGLS SLIRLGAAKR HYEKPGFFSG FKGERRDKE LNTSLSLWHR

ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from N. gonorrhoeae

```
m769
             KRHYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
            420
                                440
                                          450
                                                   460
           480
                     490
             KNRAFVEFNKTFX
g769.pep
             1111111111111
m769
             KNRAFVEFNKTFX
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2643>:
          TTGATAATGG TTATTTTTA TTTTTGTGGG AAGACATTTA TGCCTGCACG
       1
      51
          AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
     101
          AAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
          CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
          GCGGGAAAAA GGAAAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
          ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
     251
     301
          ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
     351
          GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
     401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGGAATTGAT TGTCGCCCAA
          CCCGACGCGC CCGCCGTCCG TATGCGTTTG GCGGCGGCAT TGTTTGAAAA
     501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
          ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
          CGCGAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
     651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
     701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
     751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
          GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
     851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GGCGCAAAGA TGCCGGGCTG
     901 GCAGTGTTCC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
     951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
    1001
          CGTTGTCTTC GGCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
         TCCGACAATA CCCATTTGCA AATTTCCAAT TCGCTGGTGT TTTACCGGAA
    1101 TGCGCGCCAA TATTGGATGG GCGGTTTGGA TTTTTACCGC GAGCGCAACC
    1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
         GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC
    1201
    1251 GGCGAAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTTAAAGGGG
         AAAGGCGCAG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCGG
    1301
          GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
    1351
    1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
    1451 TCGAGTTTAA TAAAACGTTC TGA
This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:
a769.pep
          LIMVIFYFCG KTFMPARNRW MLLLPLLASA AYAEETPREP DLRSRPEFRL
         HEAEVKPIDR EKVPGQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
     101
         IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAO
         PDAPAVRMRL AAALFENRON EAAADQFDRL KAENLPPOLM EQVELYRKAL
         RERDAWKVNG GFSVTREHNI NQAPKRQQYG KWTFPKQVDG TAVNYRLGAE
         KKWSLKNGWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
     251
         AVFHERRTYG NDAYSYTNGA RLYFNRWQTP KWQTLSSAEW GRLKNTRRAR
         SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
         GQEWGGSGLS SLLRLGAAKR HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
         ALHFKGITPR LTLSHRETRS NDVFNEYEKN RAFVEFNKTF *
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. meningitidis
ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from
N. meningitidis:
m769/a769
            99.8% identity in 490 aa overlap
            LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAEETPREPDLRSRPEFRLHEAEVKPIDR
a769.pep
            m769
            LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAEETPREPDLRSRPEFRLHEAEVKPIDR
```

40

80

a769.pep

90

EKVPGQVREKGKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

50

120

m769	!	1
a769.pep m769	130 140 150 160 170 180 LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL	
a769.pep m769	190 200 210 220 230 240 KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQQYGKWTFPKQVDG	
a769.pep m769	250 260 270 280 290 300 TAVNYRLGAEKKWSLKNGWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL	
a769.pep	310 320 330 340 350 360 AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSDNTHLQISN !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	ı
a769.pep m769	370 380 390 400 410 420 SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSGLSSLLRLGAAKR SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSGLSSLLRLGAAKR 370 380 390 400 410 420	t t
a769.pep m769	430 440 450 460 470 480 HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYEKN	1
a769.pep	490 RAFVEFNKTFX            RAFVEFNKTFX 490	

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2645>: g770.seq

```
ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCGG
 51 CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AGCGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTTG GTTTACAGCG
401 ATAAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTTCCTGT
451 TTCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCCGATA AAAAATCCCG
551 ACAAACGCTG A
```

### This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>: g770.pep

- MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDRI EVEGFDDPDV 1
- QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK 51
- 101 EVFKRGTGFA FKSRQIVRYY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
- 151 FGSGIPQTDG VQADTSGKLL AGACIISNPI KNPDKR*

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2647>: m770.seq

- ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
  - 51 CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

```
101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAAATT CCTTAAGCGC GGTTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCTCG
551 ACAAACGCTG
```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>: m770.pep

- 1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDRI EVEGFDDPDV
- 51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
- 101 EVFKHGASFA FKSRQIVRYY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
- 151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDKR*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from N. gonorrhoeae

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from N. gonorrhoeae

```
m770/g770
          93.5% identity in 186 aa overlap
                 10
                         20
                                 30
                                                        60
          MNRLLLLSAAVLPTACGSGETDKIGRASTVFNMLGKNDRIEVEGFDDPDVQGVACYISYA
g770.pep
          m770
          MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
                 10
                         20
                                 30
                                        40
                                                50
                 70
                        80
                                 90
                                       100
                                               110
g770.pep
          KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKRGTGFAFKSRQIVRYY
          m770
          KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRYY
                        80
                                90
                                       100
                                               110
                130
                        140
                                150
                                               170
                                       160
                                                       180
          DPKRKAFAYLVYSDKIVQGSPKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI
g770.pep
          m770
          DPKRKTFAYLVYSDKIIQGSPKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
                130
                        140
                                150
                                       160
                                               170
g770.pep
          KNPDKRX
          : 1 1111
m770
          ENLDKRX
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2649>: a770.seq

```
ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
  1
 51
    CAGCGGCGAA ACCGATAAAA TCGGACGGC AAGTACCGTT TTCAACATAC
    TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTCGACGA TCCCGACGTT
101
    CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
    AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
    CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTTG GTGTACAGCG
351
401
    ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCCCG
551 ACAAACGCTG A
```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>: a770.pep

- 1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDRI EVEGFDDPDV
- 51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
- 101 EVFKHGASFA FKSRQIVRYY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

#### 151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPDKR*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. meningitidis* 

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from N. meningitidis:

```
m770/a770
          99.5% identity in 186 aa overlap
                         20
                                30
                                        40
a770.pep
          MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
          m770
          MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIEVEGFDDPDVQGVACYISYA
                                30
                                        40
                 70
                         80
                                90
                                       100
                                               110
                                                       120
          KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRYY
a770.pep
          m770
          KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKEVFKHGASFAFKSRQIVRYY
                70
                        80
                                90
                                       100
                                               110
                130
                        140
                               150
                                       160
                                               170
a770.pep
          DPKRKTFAYLVYSDKIIQGSPKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
          m770
          DPKRKTFAYLVYSDKIIQGSPKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI
                130
                        140
                               150
                                       160
                                               170
          ENPDKRX
a770.pep
          11 1111
m770
          ENLDKRX
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2651>: g771.seq

```
ATGGATTTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
   1
  51
      GGTGCTGACG ATGCTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
 101
      ATCGCACCTT CACGCCCGAA AACATCCGCA GCCGCCTCCA ACAAAGCATT
 151
      GCCCATACCC ACCGGAAAAT CTCGTTTGAT GCGGATATAC GGCGCAGGCT
      TCTGCCCCGC CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
      ACGGCGGCCG GGTCGCCGTT TCCGTCAAAG AAACCAAAAT CGGATTGAGC
 251
      TGGAAAAACC TGTGGTCGGA TCGGATACAG GTTGAAAAAT GGGTGGTTTC
 301
      GGGTGCGGAT CTTGCCCTGA CGCGCGACAG AAACGGCGCT TGGAACATCC
 351
      AAGACCTGTT CGACGGCGCG AAACACTCCG CCTCAGTCAA CCGCATTATC
 401
      GTCGAAAACA GCACCGTCCG CCTCAATTTC CTGCAGCAAC AGCTTATCCT
 451
 501
     GAAGGAAATC AGCCTCAACC TGCAATCCCC CGATTCGTCG GGGCAGCAGT
      TTGAAAGTTC GGGCATACTG GTTTGGAGAA AGCTGTCCGT CCCGTGGAAA
 601
      AGCAGGGGGC TGTTCCTTTC AGACGGCATC GGCACGCCCG AAATCTCACC
 651
      GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATCACCATTT
 701
      CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
 751
      GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
 801
      CGCGCAAATC CCCGCACTGG CACTCAAAAA CAACAGCATC AAAACCGGCA
 851
     CGGTCAACGG CACGTTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
     TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
 901
 951
      CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCTT CAAACCAATT
1001
      TCTCCCTCGG CTCGCCGTTG GTTTGGAGTC GGGACAACGG GCTGGACGCC
     CCGCGCCTGC ACATATCGAC CCTTCAGGAT ACCGTCGACC GCCTGCCGCA
1051
1101
     ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCATA CCGAATCTGC
      AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA ACCCGTTGCC
1151
1201
      GCAAAATTCA AATATACGCG GGAAGGCGCA CCGCACCTGG AAGCCGCCGC
     CGCGCTGCAA AAATTAAACC TCGCCCCCTA TCTTGACGAA TTTCGGCAAC
1251
     AAAACGGCAA AATATTCCCC GACATCCTCG GCAGGCTGTC CGGCAACGTC
1301
1351
     GAGGCACACC TCAAAATCGG CAGCATCCAA CTCCCCGGCT TGCAACTGGA
1401
     CGATATGGAA ACCTACCTCC ACGCCGACAA AGACCATATC GCGCTCAGCC
1451
     GTTTCAAGTC AGGGCTTTAC GGCGGCCATA CCGAAGGCGG CATCAGCATC
     GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1501
     CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1551
1601
     GCAACGGCGA TGCGGTCATC GACCTGACCG CAAGCGGCGA AAACCGCAAA
     CAGCTTATCC GCTCGCTGCA AGGCAGCCTG TCGCTGAATA TTTCCAACGG
1651
     CGCGTGGCAC GGCATCGATA TGGACAGCAT TTTAAAAAAC GGCCTTTCCG
```

```
1751 GGAAAATCTC GGGCAGCACA CCCTTCTACC GATTCACGCT CAACAGCGAA
1801 ATTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGCCGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
1701 TAA
```

# This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```
MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQQSI
     AHTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
 51
    WKNLWSDRIQ VEKWVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRII
101
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
    AGLGLRADTS FRNLHLTAQI PALALKNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNGLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNWNAEL NGTFDRQPVA
401 AKFKYTREGA PHLEAAAALQ KLNLAPYLDE FRQQNGKIFP DILGRLSGNV
451 EAHLKIGSIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
    AKFKYTREGA PHLEAAAALQ KLNLAPYLDE FRQQNGKIFP DILGRLSGNV
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSGNGDAVI DLTASGENRK
    QLIRSLQGSL SLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDVLIR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGRL TGGINSRKEK QKILEDTLLE QWQWLKPKEP
701
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2653>: m771.seq

```
ATGGATTTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
  51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
 101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAAGCATT
 151 GCACACACA ACCGGAAAAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
 201 CCTGCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
 251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
 301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
 351 GAGTGCGGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
 401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
 451 GTCGAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
 501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCGTCG GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
 601 AGCAGGGGC TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
 651 GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATTACCATTT
 701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
 751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
 801 CGCCCAAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
 851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
 901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
 951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
      CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
      GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCCTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCC GACACCCTCG CCAAGCTGTC CGGCGACATC
     GAGGCGCACC TGAAAATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
     CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
     GTTTCAAGTC AGGGCTTTAC GGCGGCCATA CCGAAGGCGG CATCAGCATC
1451
1501
     GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
     CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1551
1601
     GCAACGGCGA CGCGGTCATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
     GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1651
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
     GCAAAACTGC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTCACG
1801 CTCAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCCTGAA AATCACCGGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCG CGCAAAGAGA
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA
```

WO 99/57280

1257

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>: m771.pep

MDLLSVFHKY RLKYAVAVLT ILLLAAVGLH ASVYRTFTPE NIRSRLQQSI AHTHRKISFD ADIQRRLLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS 101 WKNLWSDQIQ IEKWVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII 151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK 201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA 251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA 401 AKFRYTHEDA PHLEAAVALQ KLNLTPYLDD VRQQNGKIFP DTLAKLSGDI 451 EAHLKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSGNGDAVI DLTAGGETRK ELIRSLQGSL SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTQELSED VLIRNAVHPK 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from N. gonorrhoeae

m771/g771	90.3% identity in 704 aa overlap 10 20 30 40 50 60
g771.pep	10 20 30 40 50 60 MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSIAHTHRKISFD
m771	MDLLSVFHKYRLKYAVAVLTILLLAAVGLHASVYRTFTPENIRSRLQQSIAHTHRKISFD 10 20 30 40 50 60
g771.pep	70 80 90 100 110 120 ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVVSGAD    :
g771.pep m771	130 140 150 160 170 180 LALTRDRNGAWNIQDLFDGAKHSASVNRIIVENSTVRLNFLQQQLILKEISLNLQSPDSS       : :      : :
g771.pep	190 200 210 220 230 240 GQQFESSGILVWRKLSVPWKSRGLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
g771.pep m771	250 260 270 280 290 300  VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG
g771.pep	310 320 330 340 350 360  SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPLVWSRDNGLDAPRLHISTLQD
g771.pep m771	370 380 390 400 410 420 TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFKYTREGAPHLEAAAALQ   :
g771.pep m771	430 440 450 460 470 480 KLNLAPYLDEFRQQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDHI     :   :

```
430
                                450
                                       460
                                               470
                                                        480
                        500
                                510
                                       520
                490
                                               530
          ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI
q771.pep
          ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI
m771
                        500
                               510
                490
                                       520
                                               530
                550
                        560
                               570
                                       580
                                                  590
          DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG----STPFYRFT
q771.pep
          1111:111
m771
          DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT
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                               570
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                           620
                                   630
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g771.pep
          LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG
m771
                610
                        620
                               630
                                       640
                                               650
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                   670
                           680
                                   690
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g771.pep
          m771
          TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
                        680
                               690
                670
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2655>: a771.seq

```
ATGGATTTAT TATCGGTCTT CCACAAATAC CGTCTGAAAT ATGCGGTAGC
   1
     CGTGCTGACG ATACTGCTTT TGGCGGCAAT CGGGCTGCAC GCTTCCGTAT
  51
     ATCGCATCTT CACACCTGAA AACATCCGAA GCCGCCTCCA ACAAAGCATT
 101
      GCCCATACGC ACCGGAAAAT CTCGTTTGAT GCGGATATAC AGCGCAGGCT
     TCTGCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
 201
     GCGGCGACCG GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
 251
     TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
 301
     GAGTGCGGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
 351
     AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
     GTCGAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
 451
     GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCGTCG GGGCAGCCGT
 501
     TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
 551
     AGCAGGGGC TGTTCCTTTC AGACGGCATC GGCACGCCCA AAATCTCACC
     GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATTACCATTT
 651
     CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
 701
     GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
 751
     CGCCCAAATC CCTACGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
 801
     CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCA ATGGGACGGT
 851
     TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
 901
     CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
     TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1001
     CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1051
     ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1101
     AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1151
     GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1201
     CGCACTGCAA AAATTGAACC TGACCCCCTA TCTTGACGAC GTGCGGCAAC
1251
     AAAACGGCAA AATATTTCCC GACACCCTCG CCAAGCTGTC CGGCGACATC
     GAGGCGCACC TGAAAATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1351
1401
     CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
     GTTTCAAGTC AGGGCTTTAC GGCGGCCATA CCGAAGGCGG CATCAGCATC
1451
     GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1501
     CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1551
     GCAACGGCGA CGCGGTCATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
1601
     GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1651
     TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1701
1751
     GCAAAACTGC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTCACG
     CTCAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1801
     CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
     CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1901
     AACAAACCGA TTCCCCTGAA AATCACCGGT ACGGTGGACA AACCGTCCAT
1951
     TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCG CGCAAAGAGA
2001
     AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2051
     CCTAAAGAAC CGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

```
1751 GGAAAATCTC GGGCAGCACA CCCTTCTACC GATTCACGCT CAACAGCGAA
     ATTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
     CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
     CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
     TCGAAGACAC CCTGCTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
2051
3051
```

## This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```
g771.pep
          MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQQSI
          AHTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
      51
     101 WKNLWSDRIQ VEKWVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRII

    VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLSVPWK
    SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA

          VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLSVPWK
     251 AGLGLRADTS FRNLHLTAQI PALALKNNSI KTGTVNGTFT AGGEYARWDG
     301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNGLDA
     351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNWNAEL NGTFDRQPVA
     401 AKFKYTREGA PHLEAAAALQ KLNLAPYLDE FRQQNGKIFP DILGRLSGNV
     451 EAHLKIGSIQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
     501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSGNGDAVI DLTASGENRK
     551 OLIRSLOGSL SLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
     601 ISDGISRHID TELFSDSLYV TSNGYTNLDT QELSEDVLIR NAVHPKNKPI
     651 PLKITGTVDK PSITVDYGRL TGGINSRKEK QKILEDTLLE QWQWLKPKEP
     701
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2653>:

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m771.seq
         ATGGATTTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
      51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
     101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAAGCATT
     151 GCACACACA ACCGGAAAAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
     201 CCTGCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
          GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
     301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
     351 GAGTGCGGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
     401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
         GTCGAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
     451
     501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCGTCG GGGCAGCCGT
     551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
         AGCAGGGGC TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
     651 GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATTACCATTT
     701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
     751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
     801 CGCCCAAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
     851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCG ATGGGACGGT
     901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
    951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
    1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
    1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
         AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
    1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
    1251 CGCACTGCAA AAATTGAACC TGACCCCCTA TCTTGACGAC GTGCGGCAAC
         AAAACGGCAA AATATTTCCC GACACCCTCG CCAAGCTGTC CGGCGACATC
    1351 GAGGCGCACC TGAAAATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
    1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
    1451 GTTTCAAGTC AGGGCTTTAC GGCGGCCATA CCGAAGGCGG CATCAGCATC
         GCCAACACC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
    1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
    1601 GCAACGGCGA CGCGGTCATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
          GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
         TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
    1751 GCAAAACTGC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTCACG
    1801 CTCAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
         CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
          CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
    1901
    1951 AACAAACCGA TTCCCCTGAA AATCACCGGC ACGGTGGACA AACCGTCCAT
    2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCG CGCAAAGAGA
    2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
    2101 CCTAAAGAAC CGTA
```

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

m771.pep MDLLSVFHKY RLKYAVAVLT ILLLAAVGLH ASVYRTFTPE NIRSRLQQSI AHTHRKISFD ADIQRRLLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS 51 WKNLWSDQIQ IEKWVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII 101 151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK 201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA 251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA 401 AKFRYTHEDA PHLEAAVALQ KLNLTPYLDD VRQQNGKIFP DTLAKLSGDI 451 EAHLKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI 501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSGNGDAVI DLTAGGETRK 551 ELIRSLQGSL SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTQELSED VLIRNAVHPK 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from N. gonorrhoeae

m771/g771	90.3% identity				5.0	
g771.pep	10 MDLLSVFHKYRLKYA	20 VAVLTMLLL	30 AAVGLHASVYR'	40 PFTPENIRSF	50 RLQQSIAHTI	60 HRKISFD
g//lipop	11111111111111111	11111:111				[]][]
m771	MDLLSVFHKYRLKYA	VAVLTILLL	AAVGLHASVYR'	<b>TFTPENIRSF</b>	RLQQSIAHTI	HRKISFD
	10	20	30	40	50	60
	70	80	90	100	110	120
g771.pep	ADIRRRLLPRPTVIL					WVVSGAD
g//i.pep	111:31111111111	1111111	1::1111:11	[[]][]]		11111:1:
m771	ADIORRLLPRPTVIL	KNLTITEPG	GDQTAVSVQET	KIGLSWKNLW	SDQIQIEK	WVVSSAE
	70	80	90	100	110	120
	130	140	150	160	170	180
q771.pep	LALTRORNGAWNIQD	LFDGAKHSA	SVNRIIVENST	VRLNFLQQQI	LILKEISLN	LQSPDSS
	111111:1:11111	1:1: 1::1		1111111:11		
m771	LALTROGKGVWNIQD				'ITKEINTN	LQSPDSS
	130	140	150	160	170	180
	190	200	210	220	230	240
g771.pep	GQQFESSGILVWRKL	SVPWKSRGL	FLSDGIGTPEI	SPFHFEASTS	LDGHGITI	STTGSPS
g, i, pep	31 11111111 11	1111111111	111:111 111			[1111]
m771	GQPFESSGILVWGKL	SVPWKSRGL	FLSNGIGPPEI	SPFHFEASTS	LDGHGITI	STTGSPS
	190	200	210	220	230	240
	250	260	270	280	290	300
g771.pep	VRFNAGGADAAGLGI	RADTSFRNL	HLTAQIPALAL	KNNSIKTGTV	/NGTFTAGG	EYARWDG
3	1111111111111111	1111111111	1111111111	:11111 11	HE: HTH.	111111
m771	VRFNAGGADAAGLGI					EYARWDG
	250	260	270	280	290	300
	310	320	330	340	350	360
g771.pep	SFKLDKANLHSGIAN	IIGNAEISGS	FKTPRLQTNFS	LGSPLVWSRI	ONGLDAPRL	HISTLQD
j	1111111111111111111	1111111111		1:11111:::	::1111111	:: [] [] [
m771	SFKLDKANLHSGIAN	IIGNAEISGS	FKTPRHQTNFS	LNSPLVWTE	NKGLDAPRL	YVSTLQD
	310	320	330	340	350	360
	370	380	390	400	410	420
g771.pep	TVDRLPQPRFISRLE	GSLSIPNLQ	NWNAELNGTFD	RQPVAAKFK	YTREGAPHL	EAAAALQ
5 F - F	11:1111111111111	1111:1111	11111111111	11 11111:	11:1 1111	111:111
m771	TVNRLPQPRFISRL					
	370	380	390	400	410	420
	430	440	450	460	470	480
g771.pep	KLNLAPYLDEFRQQN					
	1111:1111: 1111		:111::1111	11::1111	111111111	1111 11
m771	KLNLTPYLDDVRQQN	IGKI FPDTLA	KLSGDIEAHLK	IGKVQLPGL(	<b>QLDDMETYL</b>	HADKGHI

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1258
```

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHT	EGGISIANTRE				
		1111111111				
m771	ALSRFKSGLYGGHT					
	490	500	510	520	530	540
	***	5.60	r 7 0	500	500	
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIF					
	-    :  :					[]:
m771	DLTAGGETRKELIF	RSLQGSLSLNIS				
	550	560	570	580	590	600
	600 610		630	640	650	
g771.pep	LNSEISDGISRHID	TELFSDSLYVI	SNGYTNLDTQ	ELSEDVLIRNA	VHPKNKPI	PLKITG
• •	1111111111111111	3111111111111			411131111	
m771	LNSEISDGISRHIL	TELFSDSLYVI	SNGYTNLDTQ	ELSEDVLIRNA	VHPKNKPI	PLKITG
	610	620	630	640	650	660
	660 <b>6</b> 70	680	690	700		
g771.pep	TVDKPSITVDYGRI	TGGINSRKEKÇ	KILEDTLLEQV	NOWLKPKEPX		
J	1111111111111111	11111111111	11111111111			
m771	TVDKPSITVDYGRI	TGGINSRKEKO	KILEDTLLEOV	OWLKPKEPX		
m / / ±	670	680	690	700		
	0.0	000		. • •		

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2655>: a771.seq

```
ATGGATTTAT TATCGGTCTT CCACAAATAC CGTCTGAAAT ATGCGGTAGC
  51 CGTGCTGACG ATACTGCTTT TGGCGGCAAT CGGGCTGCAC GCTTCCGTAT
101 ATCGCATCTT CACACCTGAA AACATCCGAA GCCGCCTCCA ACAAAGCATT
151 GCCCATACGC ACCGGAAAAT CTCGTTTGAT GCGGATATAC AGCGCAGGCT
     TCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCG GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
 351 GAGTGCGGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTCGTCG GGGCAGCCGT
     TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
 601 AGCAGGGGC TGTTCCTTTC AGACGGCATC GGCACGCCCA AAATCTCACC
 651 GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATTACCATTT
 701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
     GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
 751
801 CGCCCAAATC CCTACGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCA ATGGGACGGT
     TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
 901
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
     TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
     ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1101
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
     CGCACTGCAA AAATTGAACC TGACCCCCTA TCTTGACGAC GTGCGGCAAC
1251
1301 AAAACGGCAA AATATTTCCC GACACCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGAAAATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
     GTTTCAAGTC AGGGCTTTAC GGCGGCCATA CCGAAGGCGG CATCAGCATC
1451
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
     GCAACGGCGA CGCGGTCATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
1601
     GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1651
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
     GCAAAACTGC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTCACG
1751
     CTCAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1801
     CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
1851
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
     AACAAACCGA TTCCCCTGAA AATCACCGGT ACGGTGGACA AACCGTCCAT
1951
     TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCG CGCAAAGAGA
2001
     AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2051
     CCTAAAGAAC CGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

PCT/US99/09346 WO 99/57280

1259

```
a771.pep
            MDLLSVFHKY RLKYAVAVLT ILLLAAIGLH ASVYRIFTPE NIRSRLQQSI
       51 AHTHRKISFD ADIQRRLLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
      101 WKNLWSDQIQ IEKWVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
      151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
      251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
      301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
      351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KLNLTPYLDD VRQQNGKIFP DTLAKLSGDI
      451 EAHLKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI
      501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFSGNGDAVI DLTAGGETRK
551 ELIRSLQGSL SLNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
      601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTQELSED VLIRNAVHPK
      651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
      701
            PKEP*
```

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. meningitidis

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from N. meningitidis

m771/a771	98.9%	identity i	n 704 aa o	verlap			
a771.pep m771	111111	1111111111	111111111	:1111111	111111111	50 QQSIAHTHRK           QQSIAHTHRK 50	1111
a771.pep	HHILL	нини	1111111111	:1111111111	111111111	110 DQIQIEKWVVS            DQIQIEKWVVS 110	$\Pi\Pi$
a771.pep	HILL	ппппін	нійнін	11111111111		170 LKEINLNLQSI !!!!!!!!!!! LKEINLNLQSI 170	1111
a771.pep	111111	111111111	нинын	1:111 1:11		230 DGHGITISTTO            DGHGITISTTO 230	1111
a771.pep	111111		1111111111	1111:1111		290 GAFTAGGEYA(           GAFTAGGEYAF 290	:111
ą771.pep m771	111111	H111111	1111111111	111111111		350 GLDAPRLYVST           GLDAPRLYVST 350	1111
a771.pep	111111	шини	11111111111	1111111111		410 HEDAPHLEAAV           HEDAPHLEAAV 410	1111
a771.pep m771	111111		111111111	швшш		470 DDMETYLHADI           DDMETYLHADI 470	HH

```
510
                                      520
                                             530
               490
         ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI
a771.pep
         ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI
m771
                      500
                              510
                                      520
                                             530
                                                     540
                              570
                                      580
                                             590
               550
                       560
         DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT
a771.pep
         DLTAGGETRKELIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT
m771
                       560
                              570
                                      580
                                             590
                       620
                              630
                                      640
                                             650
         LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG
a771.pep
          LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG
m771
                                      640
                       620
                              630
                       680
                              690
               670
         TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
a771.pep
          TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
m771
               670
                       680
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2657>: g772.seq

```
GTGTTCGGCA CGGTCTTGCG GACTGATGCC GACTGCCTGC AAATCATCGT
    CGTCGGCAAG TTCTTTCAGG TTGTTGCGTA TGGTTTTGCG GCGTTGGCGG
51
    AAGGCGAGTT TCACCAGTTT GGCGAAATGA TCGAAATCGT CCGCCTTGCC
101
    GATACGGTGT TTCACCGGAA TCATGCGCAC CACTGCGGAA TCGATTTTCG
    GCGCGGGATC GAACGATTCG GGCGGCACGT CAATCAGCAG CTCCATATCG
251 AAAAAATATT GCAGCATCAC ACCCAAGCGA CCGTAGTCGT TGCTTTTCGG
    CGCGGCAACC ATGCGCTCGA CCACTTCTTT TTGCAACATA AAGTGCATAT
    CGGCGACATC GTCCGCCACC TCCGCCAGTT TGAACAAAAG CGGCGTGGAG
351
    ATGTTATACG GCAGGTTGCC GACGATTTTC TTTTTGCCTG AGATGCCGTT
401
    GAAATCAAAC TGCAACACGT CGCCTTCGTG AATCACCAGT TTATCCGCAA
451
    ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
    TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATTG CCGCCAAACC
    CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
601
    CAATATCGCC GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC
    TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTCTTCGGT TGAAACCCCG
701
    CCCTTTAGGG CGGCAGGATC AGACTCTGTT TGGGCGGGGC GTAACCCCTT
    CCAAATCAGG ACGACACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
    TGGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA
```

### This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>: g772.pep

- VFGTVLRTDA DCLQIIVVGK FFQVVAYGFA ALAEGEFHQF GEMIEIVRLA DTVFHRNHAH HCGIDFRRGI ERFGRHVNQQ LHIEKILQHH TQATVVVAFR 51 RGNHALDHFF LQHKVHIGDI VRHLRQFEQK RRGDVIRQVA DDFLFA*DAV EIKLOHVAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNCRQT
- RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSSSVETP
- PFRAAGSDSV WAGRNPFQIR TTHRAVLYVS SCVLEHKCVY SIRLMSAL*

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2659>:

```
m772.seq
          ATGTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
          CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTGCG GCGTTGGTGG
      51
          AAGGCGAGTT TCACGAGTTT GGCAAAATGC TCGAAATCGT CCGCCTTGCC
     101
          GATGCGGTGT TTCACCGGAA TCATACGGAC GACGGCGGAA TCCACTTTCG
     151
          GCGCAGGGTC GAACGATTCG GGCGGTACGT CAATCAGCAT TTCCATATCG
          AAAAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
     251.
          CGCGGCAACC ATACGCTCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
          CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGTGTGGAA
          ATGTTGTACG GGAGGTTGCC GACGATTTTC TTTTTGCCTG CGATGCCGTT
     451
          GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
     501
          ACGGCAGCGT TTTCAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
          TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
          CGGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
          CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC
```

```
1261
```

```
TTGCGGGCTT TGTGTTCTTT CATCGTGTTT CCTTTTCGGT TGAAACCCCG
    CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACTCTTT
751
    CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
801
    TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA DAVFHRNHTD DGGIHFRRRV ERFGRYVNQH FHIEKILQHH AQAAVVVAFR

- 51 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV 101 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT 151
- RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
- PFRAVESDSI WEGRNSFQIR MAHRAVLYVS SCVLKHKCVY SIRLMSAL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from N. gonorrhoeae

```
85.2% identity in 298 aa overlap
m772/g772
                                 30
                                         40
                                                 50
                         20
          VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHQFGEMIEIVRLADTVFHRNHAH
g772.pep
          MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD
m772
                                 30
                                                         60
                10
                         20
                                 90
                                        100
                         80
                70
          HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI
g772.pep
            и на эпининания полиции и пойна и
          DGGIHFRRRVERFGRYVNQHFHIEKILQHHAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI
m772
                                        100
                                                110
                                 90
                 70
                                150
                                        160
                                                170
                                                        180
                130
                        140
          VRHLRQFEQKRRGDVIRQVADDFLFAXDAVEIKLQHVAFVNHQFIRKRQRFQTAYDVAVD
q772.pep
          VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD
m772
                                                170
                                        160
                130
                        140
                                150
                                        220
                                                230
                                210
                        200
                190
          FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
q772.pep
          FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
m772
                                                230
                                        220
                                210
                190
                        200
                                270
                                        280
                        260
                250
          HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTTHRAVLYVSSCVLEHKCVYSIRLMSALX
q772.pep
          HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLYVSSCVLKHKCVYSIRLMSALX
m772
                                        280
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2661>: a772.seq

, ~					
1	ATGTTCGGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	
51	CGCCTGCAAG.	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTGCG	GCGTTGGTGG
101	AAGGCGAGTT	TCACGAGTTT	GGCGAAATGC	TCGAAATCGT	CCGCCTTGCC
151	GATACGGTGT	TTCACCGGAA	TCATGCGGAC	GACGGCCGAA	TCCACTTTCG
201	GCGCGGGGTC	GAACGATTCG	GGCGGCACGT	CAATCAGCAT	TTCCATATCG
251	AAGAAATATT	GCAGCATCAC	GCCCAAGCGG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGATCGA	CCACTTCTTT	TTGCAGCATA	AAGTGCATAT
351	CGACGACATC	GTCCGCCACC	TCCGCCAGCT	TGAACAAAAG	CGGCGTGGAA
401	ATGTTGTAGG	GCAGGTTGCC	GACGATTTTC	TTTTTGCCTG	CGATGCCGTT
451	GAAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCGAT	TTCGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATCG	CCGCCAAACC
601	CGGACCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGCTT	TGTGTTCTTT	CATCGTGTTT	CCTTTTCGGT	TGAAACCCCG
751	CCCTTTAGGG	CGGTAGAATC	AGACTCTATT	TGGGAGGGC	GTAACTCCTT
801	CCAAATCAGG	ACGGCACATA	GGGCGGTGCT	TTATGTGTCG	TCCTGTGTGT
851	TGAAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>: a772.pep

- MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GEMLEIVRLA
- 51 DTVFHRNHAD DGRIHFRRGV ERFGRHVNQH FHIEEILQHH AQAAVVVAFR 101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
- EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT 151
- 201 RTDFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
- 251 PFRAVESDSI WEGRNSFQIR TAHRAVLYVS SCVLKHKCVY SIRLMSAL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from N. meningitidis

m772/a772	95.6% identity in 298 aa overlap
	10 20 30 40 50 60
a772.pep	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD 10 20 30 40 50 60
	70 80 90 100 110 120
a772.pep	DGRIHFRRGVERFGRHVNQHFHIEEILQHHAQAAVVVAFRRGNHTIDHFFLQHKVHIDDI
m772	DGGIHFRRRVERFGRYVNQHFHIEKILQHHAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI
10/12	70 80 90 100 110 120
	170 170
	130 140 150 160 170 180 VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD
a772.pep	VRHLRQLEQKRRGNVGQVADDI LIACDAVEIREGITAI VANQI ITAKKQKI QIAIDVAVE
m772	VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD
MI / / L	130 140 150 160 170 180
	190 200 210 220 230 240
	190 200 210 220 230 240 FDNVQAVQLFRQRFGNRQTRTDFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
a772.pep	
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF
.,,	190 200 210 220 230 240
	250 260 270 280 290 299
2772 man	250 260 270 280 290 299 HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRAVLYVSSCVLKHKCVYSIRLMSALX
a772.pep	
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLYVSSCVLKHKCVYSIRLMSALX
	250 260 270 280 290

q773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2663>: m773.seq

J. 5C4					
1	ATGGGATTGG	GTGCAACGAC			
51		ACCGGGATTG		CGGTGGACTT	
101	CAGGTATGAC	CGGTGGTTAT	ACACAGGCCT	CAGAAGGAAG	CCGGCAATTG
151	TTTGGCACTT	ACCAGTCCGA	TTTTGGTAAA	AAAGTTGTCC	TATCTTTGGG
201	TACACCAATA	GAATACGAAT	CGCCGTTAGT	ATCTGATGCG	AAAAATCTAG
251	CCGTATGGGG	ATTGGAAACG	CTGATTACGC	GCAAATTGGG	AAACTTGGCA
301	ACGGGTGTGA	AAACTTCCTT	GACTCCGAAA	ACTGCTGACG	TACAGCGAAA
351	TATCCTGTCC	CAATCCGAAG	TCGGTATCAA	GTGGGGCAAG	GGGATTGAAG
401	GACAGGGAAT	GCCTTGGGAG	GATTATGTCG	GTAAGGGCTT	GTCTGCCAAT
451	GCAAGGTTAC	CTAAAAATTT	TAAAACATTT	GATTATTTTG	ATCGTGGTAC
501	AGGCACGGCA	ATCAGTGCCA	AAACTCTGGA	TACGCAAACT	ACGGCACGCC
551	TGTCCAAACC	CGAACAGCTT	TACAGTACCA	TGAAAGGGTA	CATCGATAAG
601	ACGGCAAATT	TCAAAAGTTA	TGAATTATCA	GAAGTACCGT	TAAGGGCAGA
651	CATGATCAAA	CAGCGCGAAA	TCCATCTGGC	CATACCCGCA	CAAACTAATA
701		ATTGCAGTTG		TAGAGTATGG	CAAAAGTCAA
751		TCAAAATTAC	GGAGATCGAA	TAA	

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This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>: m773.pep MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL 51 FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA 101 TGVKTSLTPK TADVQRNILS QSEVGIKWGK GIEGQGMPWE DYVGKGLSAN ARLPKNFKTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKGYIDK 201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEYGKSQ 251 NITVKITEIE * a773.seq not found yet a773.pep not found yet The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2665>: q774.seq ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC 51 CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA 101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA 151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT 201 GGAAATGTTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC 251 CTTCCGGCAG GACATACGTC CAAAAACTCG ACGACCGCAA ATTGAAAGAG 301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC 351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT 401 TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC 451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT 501 GGGGAACTGT GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT 551 TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAAT CGGCGAATGC 601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT 651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG 701 TACGCAAACG ATAG This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>: q774.pep MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRTYV QKLDDRKLKE 101 HYLNTEGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG 151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC 201 QYRLQQKDIA RATWRSLIQT YPGSPAAKRA AAAVRKR* The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2667>: m774.seq ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC 51 CTGTGCTTCC GTTTCACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA 101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA 151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT 201 GGAAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT 251 CTTCCGGCAG GGCATACGTC CAAAAACTCG ACGACCGCAA GTTGAAAGAG 301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC CGCACAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT 351 CGCACAAAAC CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401 TTTCTGCCGC TGCCTCCTG TTGAAAGGCG CGGACGGAGG CGACGGCGGC 451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT 501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT 551 TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC 601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCGCAGCCT 651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG TGCGCAAACG ATAG This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>: m774.pep MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE 51 101 HYLNTEGGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG

Computer analysis of this amino acid sequence gave the following results:

SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC

QYRLQQKDIA RATWRSLIQT YPGSPAAKRA AAAVRKR*

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### Homology with a predicted ORF from N. gonorrhoeae

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from N. gonorrhoeae

```
92.8% identity in 237 aa overlap
m774/g774
                                       40
                                               50
                               30
                        20
          MKTKLPLFIIWLSVSASCASVLPVPEGSRTEMPTQENASDGIPYPVPTLQDRLDYLEGKI
q774.pep
          MKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGKI
m774
                                30
                        20
                10
                                      100
                                              110
                        80
                                90
                70
          VRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDDRKLKEHYLNTEGGSASAHTVETAQN
g774.pep
          VRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDDRKLKEHYLNTEGGSASAHTVETAQN
m774
                                90
                                      100
                                              110
                70
                                              170
                                      160
                       140
                               150
          LYNQALKHYQNGRFSAAAALLKGADGGDGGSIAQRSMYLLLQSRARMGNCESVIEIGGRY
g774.pep
          LYNQALKHYKSGKFSAAASLLKGADGGDGGSIAQRSMYLLLQSRARMGNCESVIEIGGRY
m774
                                      160
               130
                       140
                               150
               190
                       200
                               210
                                      220
                                              230
          ANRFKDSPTAPEVIFKIGECQYRLQQKDIARATWRSLIQTYPGSPAAKRAAAAVRKRX
g774.pep
          ANRFKDSPTAPEAMFKIGECQYRLQQKDIARATWRSLIQTYPGSPAAKRAAAAVRKRX
m774
                                      220
                                              230
                       200
                               210
               190
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2669>:

```
ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCCG TATCCGCCGC
 1
    CTGTTCTTCC CCTGTTTCCC GCAATATTCA GGATATGCGG CTCGAACCGC
51
    AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACTCTG
101
    CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
    AGTGGAAACC TTAAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAAACAC
201
251
    ACCCTTCCAG CAGGGCATAC GTCCAAAAAC TCGACGACCG CAAGTTGAAA
    GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
    AACCGCACAA AACCTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
351
    GGTTTTCTGC CGCTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
    GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGGCGCG
451
    TATGGGCAAC TGCGAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAACC
    GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
551
    TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGGCGA CTTGGCGCAG
601
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCCGCCGCAG
701 CCGTGCGCAA ACGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>: a774.pep

- MKTKLPLFII WLSVSAACSS PVSRNIQDMR LEPQAEAGSS DAIPYPVPTL QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKLDDRKLK 51
- 101 EHYLNTEGGS ASAHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
- 151 GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
- CQYRLQQKDI ARATWRSLIQ TYPGSPAAKR AAAAVRKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from N. meningitidis

```
89.5% identity in 238 aa overlap
m774/a774
                         20
                                 30
                                         40
          MKTKLPLFIIWLSVSAACSSPVSRNIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEGT
a774.pep
                                  MKIKLPLFIIWLSVSASCAS-VSPVPAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK
m774
                                                  50
                         20
                                  30
                                          40
```

```
90
                                               100
                                                         110
                                                                  120
                             80
                    70
            LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLDDRKLKEHYLNTEGGSASAHTVETAQ
a774.pep
            IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDDRKLKEHYLNTEGGSASAHTVETAQ
m774
                                                100
                                                          110
                              80
                                        90
                                      150
                                               160
                   130
                            140
            NLYNQALKHYKSGRFSAAASLLKGADGGDGGSIAQRSMYLLLQSRARMGNCESVIEIGGR
a774.pep
            NLYNQALKHYKSGKFSAAASLLKGADGGDGGSIAQRSMYLLLQSRARMGNCESVIEIGGR
m774
                                                160
                                                          170
                                       150
                             140
          120
                    130
                             200
                                      210
                                               220
                                                         230
                                                                 239
                   190
            YANRFKDSPTAPEAMFKIGECQYRLQQKDIARATWRSLIQTYPGSPAAKRAAAAVRKRX
a774.pep
            YANRFKDSPTAPEAMFKIGECQYRLQQKDIARATWRSLIQTYPGSPAAKRAAAAVRKRX
m774
                                                220
                             200
                                       210
q790.seq not found yet
q790.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2671>:
m790.seq
         ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
         ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
      51
         AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTCGAGG
     101
         TACTCCAATA TGTTCATAGG AAGTAGCTGG GGTTGCCCCT CTTGTGGTAA
     151
         TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
         CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
         ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
     301
         CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACAACCATC
     401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
         AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
     451
         CCGTACAGGC AAACTCACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
         CCCCCTCGCA GTACACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCG
     551
         CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
         TGCGGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCG
         TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
         GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
         TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
         GCGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
         TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
     951 CGTATGCTTT CTTCGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
    1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA
This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:
m790.pep
          MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCSR
          YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
         ITTQAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTHNH SDADGKALSM
     101
         RLTPRPLLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
     151
          PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
          GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
          SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NA*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2673>:
          ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
       1
          ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
     101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTCGAGG
     151 TACTCCAATA TGTTCATAGG AAGTAGCTGG GGTTGCCCCT CTTGTGGTAA
     201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
          CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
     301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
      351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAACCATC
          ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
          AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
      501 CCGTACAGGC AAACTCACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
          CCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCG
          CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
          TGCGGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCG
      651
          TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
```

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1266
```

```
751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
 801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
 951 CGTATGCTTT CTTCGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT
```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>: a790.pep

- MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCSR
- 51 YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
- 101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTHNH SDADGKALSM
- RLTPRPLLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
  PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
- 251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
- 301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAC

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from N. meningitidis

a790/m790	98.2%	identity	in 342	aa overlap			
a790.pep m790	111111	111111111	1111111	30 GIKLVEFEGTAK            GIKLVEFEGTAK 30	11111111		
a790.pep m790	11111	111111111	1111111	90 IALEMLKQAVTG             IALEMLKQAVTG  90	111111111	1111111111111	
a790.pep m790	11111	111111111	1111111	150 ADGKALSMRLTP           ADGKALSMRLTP 150		1111111111	111111
a790.pep	111111	111111111		210 IEKGDLLVVEPR             EKGDLLVVEPR 210	1 11 11 11:	11111111111	111111
a790.pep m790	111111	11111111	11:1111	270 SVILGVVLESKN  :          STILGVVLESKN 270	11111111		
a790.pep m790	11111		111111	330 FWQATRGIPKTR            FWQATRGIPKTR 330	11111111		

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2675>: q791.seq

```
ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTACTTGTTT
  1
     TGGTTTGTTT TTTGGTTTTT GTGTATTTGG AGTGGGTCTG GTTGCCATTG
TGGTTTGTTT TTTGGTTTTT GTGTAILIGG AGGGGTT TTTGCAGCAT

101 CTATTTTGGT AACGTATCCG AAACTGCCGT CTTTGGATTC TTTGCAGCAT

GACTATTTAT TCGGCGGATG GAGAAGTCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GAGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GGCGCGAATT TACAAAAATC GGCGATTTCC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG
```

WO 99/57280

1267

```
401 TGGCGAAAAA TTTTTATTTG AGCAGTGAAA AAACGTTCAC ACGCAAATTC
 451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
       AATCCTTGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
 551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
 601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
       CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
       TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
 701
 751 CAGGCATTGA ATGAGGAACT GCATTATGAG CGGTTTGTTC GGAAAATCGA
 801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
 851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
 901 CGCACCGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
 951 GAATTTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT
      TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCGCTTG
1151 ACAGGCGCC CTTGGGTTTT GCGGCCCGAG CGGTCGATAA TGAGAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GGCGGAGGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTTCTTCGC ACGTGATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCAGGGCA
1851 ANATOGGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT 2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTCAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGATGAAGC 2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA
```

#### This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>: g791.pep

```
MVNYYSAMIK KILTTCFGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
     YOPKMPLTIY SADGEVIGMY GEORREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 OALNEELHYE REVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFKVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRAGYGGTI
     AVPVWVDYMR FALKGKQGKG MKMPEGVVSS NGEYYMKERM VTDPGLMLDN
     SGIAPQPSRR AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
751
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2677>:

```
m791.seq
         ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
     51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
     101 CTATTTTGGT AACGTATCCG AAACTGCCGT CTTTGGATTC TTTGCAGCAT
     151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGGAAGTCAT
     201 CGGTATGTAT GGGGAGCAGC GGCGCGAATT TACAAAAATC GGCGATTTCC
     251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
     301 CGGCATTGGG GGGTGGATGT TTGGGGTGTT GCCCGCGCTG CCGTCGGCAA
     351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
     401 TGGCGAAAAA TTTTTATTTG AGCAGTGAAA AAACGTTCAC ACGCAAATTC
```

m79

451	AATGAGGTGT	TGCTTGCCTA	TAAAATCGAG	CAGTCTTTAA	GCAAAGACAA
501	AATCCTCGAG	TTGTATTTCA	ATCAGATTTA	CCTCGGTCAG	CGCGCCTATG
551	GTTTTGCATC	TGCCGCGCAA	ATCTATTTCA	ATAAGAATGT	CCGAGATTTG
601	ACTTTGGCGG	AAGCCGCCAT	GCTTGCGGGA	CTGCCCAAGG	CTCCGTCTGC
651	CTATAATCCG	ATTGTTAATC	CAGAACGTGC	CAAGTTGCGC	CAGAAGTATA
701	TTTTGAACAA	TATGCTCGAG	GAGAAGATGA	TTACCGTGCA	ACAGCGCGAT
751	CAGGCGTTGA	ATGAGGAACT	GCATTACGAG	CGGTTTGTTC	GGAAAATCGA
801	TCAGAGTGCG	TTATATGTGG	CGGAAATGGT	GCGTCAGGAA	CTGTATGAGA
851	AATACGGTGA	AGATGCCTAT	ACGCAGGGTT	TTAAGGTTTA	TACCACGGTC
901	CGCGCCGATC	ATCAGAAGGT	GGCAACCGAG	GCATTGCGCA	AGGCTCTACG
951	GAATTTCGAT	CGCGGCAGCA	GCTACCGCGG	TGCGGAAAAC	TATATCGATT
1001	TGAGTAAGAG	TGAAGATGTC	GAGGAGACTG	TCAGCCAGTA	TCTGTCGGGA
1051	CTCTATACCG	TCGATAAAAT	GGTTCCCGCC	GTTGTGTTGG	ATGTGACTAA
1101	AAAGAAAAAT	GTCGTCATAC	AGCTGCCCGG	CGGCAGGCGG	GTTACGCTTG
1151	ACAGGCGCGC	CTTGGGTTTT	GCGGCCCGCG	CGGTCAATAA	TGAAAAAATG
1201	GGGGAGGACC	GTATCCGCAG	GGGCGCGGTC	ATCCGTGTCA	AAAACAACGG
1251	CGGGCGTTGG	GCGGTGGTTC	AAGAGCCGTT	GCTGCAGGGG	GCTTTGGGTT
1301	CGCTGGATGC	AAAAACCGGA	GCTGTGCGCG	CGCTGGTCGG	CGGTTATGAT
1351	TTTCACAGCA	AAACATTCAA	TCGTGCCGTT	CAGGCAATGC	GGCAGCCGGG
1401.	TTCGACCTTT	AAGCCGTTTG	TCTATTCGGC	GGCATTATCT	AAGGGGATGA
1451	CCGCGTCCAC	AGTGGTTAAC	GATGCGCCGA	TTTCCCTGCC	GGGGAAAGGG
1501	CCGAACGGTT	CGGTTTGGAC	ACCTAAAAAT	TCAGACGGCA	GATATTCCGG
1551	CTACATTACT	TTGAGACAGG	CTCTGACGGC	TTCCAAGAAT	ATGGTTTCCA
1601	TCCGTATTTT	GATGTCTATC	GGTGTCGGTT	ACGCGCAACA	GTATATCCGG
1651	CGTTTCGGCT	TCAGGTCGTC	CGAGCTGCCG	GCAAGCCTGT	CTATGGCTTT
1701	AGGTACGGGC	GAGACAACGC	CGTTGAAAGT	GGCGGAGGCA	TATAGCGTAT
1751	TTGCGAACGG	CGGATATAGG	GTTTCTTCGC	ACGTAATCGA	TAAGATTTAT
1801	GACAGAGACG	GCAGGTTGCG	CGCCCAAATG	CAACCTTTGG	TGGCTGGGCA
1851	AAATGCGCCT	CAGGCAATCG	ATCCGCGCAA	TGCCTATATT	ATGTATAAGA
1901	TTATGCAGGA	TGTGGTCCGT	GTTGGTACGG	CAAGGGGGC	AGCTGCGTTG
1951	GGAAGAACGG	ATATTGCCGG	TAAAACGGGT	ACGACCAATG	ACAATAAGGA
2001	TGCGTGGTTT	GTCGGTTTTA	ACCCTGATGT	GGTTACTGCC	GTATATATCG
2051	GCTTCGACAA	ACCTAAGAGT	ATGGGGCGTG	TCGGCTACGG	CGGTACGATT
2101	GCGGTGCCGG	TTTGGGTGGA	CTATATGCGT	TTTGCGTTGA	AAGGAAAGCA
2151	GGGCAAGGGG	ATGAAAATGC	CTGAAGGTGT	GGTCAGCAGC	AATGGCGAAT
2201	ACTATATGAA	GGAACGTATG	GTAACCGATC	CGGGCTTGAC	GCTGGACAAC
2251	AGCGGTATTG	CGCCGCAACC	TTCCCGACGG	GCAAAAGAAG	ATGACGGGG
2301	CGCGGCAGAA	GGCGGACGGC	AGGCGGCGGA	TGACGAAGTC	CGCCAAGATA
2351	TGCAGGAAAC	GCCGGTGCTT	CCGAGTAATA	CTGGTTCCAA	ACAGCAGCAG
2401	TTGGATTCTC	TGTTTTAA			
is corr	esponds to	the amino a	icid sequen	ce <seq ii<="" td=""><td>D 2678; OR</td></seq>	D 2678; OR
1.pep	•		-	•	
1	MVNYYSAMIK	KILTTCFGLV	FGFCVFGVGL	VAIAILVTYP	KLPSLDSLQH
_					~

#### RF 791>: Thi

```
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
     NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
151
     TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
     QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFKVYTTV
251
     RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
     GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALGSLDAKTG AVRALVGGYD
     FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
451
     PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
501
     RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
551
    DRDGRLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
601
651
701 AVPVWVDYMR FALKGKQGKG MKMPEGVVSS NGEYYMKERM VTDPGLTLDN
     SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
751
801 LDSLF*
```

```
q791/m791
            97.3% identity in 805 aa overlap
```

<b>3</b> · • - / - · · · · ·		•	•			
	. 10	20	30	40	50	60
g791.pep	MVNYYSAMIKKI	LTTCFGLFFGFC	VFGVGLVAIA	ILVTYPKLPS	LDSLQHYQPK	MPLTIY
	1111111111111	111111111111	111111111	1111111111	1111111111	111111
m791	MVNYYSAMIKKI	LTTCFGLVFGFC	VFGVGLVAIA	ILVTYPKLPS	LDSLQHYQPK	MPLTIY
	10	20	30	40	50	60
	70	80	90	100	110	120
g791.pep	SADGEVIGMYGE	QRREFTKIGDFP	EVLRNAVIAA	EDKRFYRHWG	VDVWGVARAA	VGNVVS
	1111111111111	111111111111	1111111111	111111111	3   1   1   1   1   1   1	11111
m791	SADGEVIGMYGE	QRREFTKIGDFP	EVLRNAVIAA	EDKRFYRHWG	VDVWGVARAA	VGNVVS
	70	80	90	100	110	120

g791.pep	130 140 150 160 170 180 GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ 130 140 150 160 170 180
g791.pep m791	190 200 210 220 230 240 RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE
g791.pep m791	250 260 270 280 290 300  EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFKVYTTV
g791.pep m791	310 320 330 340 350 360 RTDHQKAATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA  :   :   :
g791.pep m791	370 380 390 400 410 420  VVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRRGAVIRVKNNGGRW
g791.pep m791	430 440 450 460 470 480 AVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
g791.pep m791	490 500 510 520 530 540 KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
g791.pep m791	550 560 570 580 590 600  GVGYAQQYIRRFGFRPSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
g791.pep m791	610 620 630 640 650 660  DRDGRLRAQMQPLVAGQNAPQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
g791.pep m791	670 680 690 700 710 720 TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKQGKG
g791.pep m791	730 740 750 760 770 780 MKMPEGVVSSNGEYYMKERMVTDPGLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET
g791.pep m791	790 800  RQDVQETPVLPSNTDSKQQQLDSLFX    :

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2679>:

PCT/US99/09346 WO 99/57280

1270

a791.seq ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG CTATTTTGGT AACGTATCCG AAACTGCCGT CTTTGGATTC TTTGCAGCAT TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGGAAGTCAT 151 201 CGGTATGTAT GGGGAGCAGC GGCGCGAATT TACAAAAATC GGCGATTTCC 251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC CGGCATTGGG GGGTGGATGT TTGGGGTGTT GCCCGCGCTG CCGTCGGCAA TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG 351 TGGCGAAAAA TTTTTATTTG AGCAGTGAAA AAACGTTCAC ACGCAAATTC 451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG 551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTC GGAAAATCGA TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA 801 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG 901 GAATTTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAAC TATATCGATT TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA 1001 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTTGG ATGTGACTAA 1051 AAAGAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG 1101 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG 1151 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT 1251 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG 1351 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA 1401 1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG 1501 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG 1601 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCGGAGGCA TATAGCGTAT TTGCGAACGG CGGATATAGG GTTTCTTCGC ACGTAATCGA TAAGATTTAT GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCCGGGCA 1801 1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAATG ACAATAAGGA TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTTACTGCC GTATATATCG 2001 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT 2051 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA 2101 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTCAGCAGC AATGGCGAAT 2151 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG CGCGGCAGAA GGCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG 2351 TTGGATTCTC TGTTTTAA

### This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>: a791.pep

MVNYYSAMIK KILTTCFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY 51 101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF 151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFKVYTTV RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG LYTVDKMVPA VVLDVTKKKN VVIOLPGGRR VTLDRRALGF AARAVNNEKM GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD 451 FHSKTFNRAV OAMROPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY 551 DRDGRLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI AVPVWVDYMR FALKGKQGKG MKMPEGVVSS NGEYYMKERM VTDPGLTLDN SGIAPOPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ 751 LDSLF* 801

a791/m791 99.9% identity in 805 aa overlap

a791.pep	MVNYYSAMIKKILTTC	1111111111	1111111111	1111111111	пінішин
m791	MVNYYSAMIKKILTTC 10	FGLVFGFCVF 20	GVGLVAIAIL 30	VTYPKLPSLE 40	SLQHYQPKMPLTIY 50 60
a791.pep	70 SADGEVIGMYGEQRRE				
m791	SADGEVIGMYGEQRRE				
a791.pep	130 GSVQSGASTITQQVAK	140 NFYLSSEKTF	150 TRKFNEVLLA	160 YKIEQSLSKD	170 180 KILELYFNQIYLGQ
m791	GSVQSGASTITQQVAK				
a791.pep	190 RAYGFASAAQIYFNKN	200 VRDLTLAEAA	210 MLAGLPKAPS	220 AYNPIVNPER	230 240 AKLRQKYILNNMLE
m791					
a791.pep	250 EKMITVQQRDQALNEE	260 LHYERFVRKI	270 DQSALYVAEM	280 VRQELYEKYG	290 300 EDAYTQGFKVYTTV
m791		LHYERFVRKI			
a791.pep	310 RADHOKVATEALRKALI	320 RNFDRGSSYR	330 GAENYIDLSK	340 SEDVEETVSO	350 360 YLSGLYTVDKMVPA
m791		1111111111	111111111		11111111111111
-701	370 VVLDVTKKKNVVIQLPO	380	390	400	410 420
a791.pep m791		111111111	111111111		1111111111111
a791.pep	430 AVVQEPLLQGALVSLDA	440	450	460	470 480
m791		111111111			
a791.pep	490 KGMTASTVVNDAPISLI	500	510	520 SVITI. BOALT	530 540
m791			 TPKNSDGRYSO	 GYITLRQALT.	
	490 550	560	510 570	520 580	<ul><li>530</li><li>540</li><li>590</li><li>600</li></ul>
a791.pep	GVGYAQQYIRRFGFRSS	SELPASLSMA	LGTGETTPLK	/AEAYSVFAN	GGYRVSSHVIDKIY
m791	GVGYAQQYIRRFGFRSS 550	SELPASLSMA: 560	LGTGETTPLK 570	JAEAYSVFAN 580	GGYRVSSHVIDKIY 590 600
a791.pep	610 DRDGRLRAQMQPLVAG	620 QNAPQAIDPRI	630 NAYIMYKIMQI	640 OVVRVGTARG	650 660 AAALGRTDIAGKTG
m791		нини	11111111111		
a791.pep	670 TTNDNKDAWFVGFNPDV	680 JVTAVYIGFD	690 KPKSMGRVGYO	700 GGTIAVPVWV	710 720 DYMRFALKGKOGKG
m791	TTNDNKDAWFVGFNPDV 670			11111111	
a791.pep	730 MKMPEGVVSSNGEYYMI	740	750	760 PSRRAKEDDG	770 780
m791	MKMPEGVVSSNGETIME MKMPEGVVSSNGEYYMI		{	11111111	ШШЙШЕ

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740
                                       750
                                                 760
                                                          770
                                                                    780
                   730
                             800
                   790
            RQDMQETPVLPSNTGSKQQQLDSLFX
a791.pep
             RQDMQETPVLPSNTGSKQQQLDSLFX
m791
                   790
                             800
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2681>:
         ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
         CTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
      51
         CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
    101
         GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
    151
    201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTTG
    251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
         AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
    351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
         GGGAAGAGGC GGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
         AGGATTTTCG AACTGTATTT AAACTCAATC GAATGGCACT ACGGCGTTTT
         CGGCGCGGAA GCTGCGTCCC GGtatTttTA TAAAAAACCG GCCGCaGACC
    551 TGACCAAACA GCAggcggcG aaactgacgg tactcgtccc cgccccgttt
     601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
         cgtgctcaga cgcatgggtt cggcaaatta ccccaaagcg aaacggactg
         attgttccag atatggaaat gccgcctgaa ctggggttcg aacggcatat
         gttttctggg acttataa
This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:
g792.pep
         MFRIVKWLIA LPVGIFIFFN AYVYGNIITY RAVAPHRTAF MSMRMKQFEQ
         EGRDVALDYR WVPYNRISTN LKKALIASED VRFAGHGGFD GDGIQNAIRR
      51
         NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
         RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTKQQAA KLTVLVPAPF
         YYSDHPKSKR LRNKTNIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
     201
         VEWDI.*
     251
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2683>:
m792.seq
         ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
      1
         CTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
      51
         CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
     101
         GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAACGCAT
         TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
         CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
     251
         AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
         GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
     351
         GCGAAGAAGC GGCGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
         AGGATTTTTG AACTGTATTT AAACTCAATC GAATGGCACT ACGGCGTTTT
     451
         CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAATACCC GCCGCCAAGC
     501
         TGACCAAACA GCAGGCGGCA AAACTGACGG CGCGCGTCCC CGCCCCGCTC
         TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
         CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
     651
This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:
m792.pep
         MFRIIKWLIA LPVGIFIFFN AYVYGNIITY RAVAPHRTAF MSMRMKQFEQ
         EGRDVALDYR WMPYKRISTN LKKALIASED ARFAGHGGFD WGGIQNAIRR
      51
         NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
         RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTKQQAA KLTARVPAPL
         YYADHPKSKR LRNKTNIVLK RMGSAELPES DTD*
g792 / m792 90.4% identity in 230 aa overlap
                                        30
                                                  40
                                                           50
                              20
             MFRIVKWLIALPVGIFIFFNAYVYGNIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
a792.pep
             {\tt MFRIIKWLIALPVGIFIFFNAYVYGNIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR}
m792
                              20
                                        30
                                                  40
                                                           50
                    10
                                        90
                                                 100
            WVPYNRISTNLKKALIASEDVRFAGHGGFDGDGIQNAIRRNRNSGEVKAGGSTISQQLAK
g792.pep
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WO 99/57280

1273

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WMPYKRISTNLKKALIASEDARFAGHGGFDWGGIQNAIRRNRNSGKVKAGGSTISQQLAK
m792
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                                    90
                                            100
                                                     110
                  130
                           140
                                    150
                                            160
                                                     170
                                                              180
g792.pep
           NLFLNESRNYLRKGEEAAITAMMEAVTDKNRIFELYLNSIEWHYGVFGAEAASRYFYKKP
            \verb| NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAASRYFYQIP| \\
m792
                  130
                           140
                                    150
                                            160
                  190
                           200
                                    210
                                            220
                                                     230
                                                              240
            AADLTKQQAAKLTVLVPAPFYYSDHPKSKRLRNKTNIVLRRMGSANYPKAKRTDCSRYGN
g792.pep
            AAKLTKQQAAKLTARVPAPLYYADHPKSKRLRNKTNIVLKRMGSAELPESDTDX
m792
                  190
                           200
                                   210
                                            220
                                                     230
                  250
            AAXTGVRTAYVFWDLX
g792.pep
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2685>:
a792.seq
         ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
      1
         CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
     51
         CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
         GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAACGCAT
    151
    201
         TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
         CCGGGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
    251
        AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
    301
    351
         GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
         GCGAAGAAGC GGCGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
    401
         AGGATTTTTG AACTGTATTT AAACTCAATC GAATGGCACT ACGGCGTTTT
         CGGCGCGAA GCCGCGTCCC GGTATTTTTA TCAAATACCC GCCGCCAAGC
    501
         TGACCAAACA GCAGGCGGCA AAACTGACGG CGCGCGTCCC CGCCCCGCTC
    551
         TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
    601
         CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
    651
    701
This corresponds to the amino acid sequence <SEQ ID 2686; ORF 792.a>:
a792.pep
         MFRIIKWLIA LPVGIFIFFN AYVYGNIITY RAVAPHRTAF MSMRMKQFEQ
        EGRDVALDYR WMPYKRISTN LKKALIASED ARFAGHGGFD WGGIQNAIRR
     51
    101
        NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
    151
         RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTKQQAA KLTARVPAPL
         YYADHPKSKR LRNKTNIVLR RMGSAELPES DTD*
    201
m792/a792
           99.6% identity in 233 aa overlap
                           20
                                    30
                                             40
           MFRIIKWLIALPVGIFIFFNAYVYGNIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
a792.pep
           m792
           MFRIIKWLIALPVGIFIFFNAYVYGNIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
                           20
                                    30
                                             40
                                                     50
                                                              60
                           80
                                    90
                                           100
                                                    110
                                                             120
           WMPYKRISTNLKKALIASEDARFAGHGGFDWGGIQNAIRRNRNSGKVKAGGSTISQQLAK
a792.pep
           m792
           WMPYKRISTNLKKALIASEDARFAGHGGFDWGGIQNAIRRNRNSGKVKAGGSTISQQLAK
                  70
                           80
                                    90
                                           100
                 130
                          140
                                   150
                                           160
                                                    170
a792.pep
           NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAASRYFYQIP
           m792
           NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNSIEWHYGVFGAEAASRYFYQIP
                 130
                          140
                                   150
                                           160
                                                    170
                                                             180
                          200
                 190
                                   210
                                           220
           AAKLTKQQAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESDTDX
a792.pep
           m792
           AAKLTKQQAAKLTARVPAPLYYADHPKSKRLRNKTNIVLKRMGSAELPESDTDX
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2687>: g793.seq

220

210

200

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1 ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
  51 GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
 101 CAATGGCGGT CTTGTTTGCC TGTCTGATTG CCCGCGGGCT GTATCTGCAG
 151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GGCGACAACC GGATTGTGCG
 201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTTCGGAC CGGAACGGTG
 251 CGGTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
     GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
 351 TGTCGATGTG CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
 401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
      GTCAAAGCCT TGGGTTTGGA AAACTTTGTA TTTGAAAAAG AATTAAAACG
 501 CCATTACCCG ATGGGCAACC TGTTTGCACA CGTCATCGGA TTTACCGATA
 551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTCGCTTGA AGACAGCCTG
 601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCGCAA AACGGCAAAG
 701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
 751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
      TTTGGATGCC CGCACGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
 851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
 901 GCCGTAACCG ATATGATCGA ACCTGGTTCG GCAATCAAAC CGTTCGTGAT
 951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
      CGCAGCCTTA TAAAATCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGTCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
     ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1151
1201 ACTGCAGGTT TGTTGAGAAA TTGGCGCAGG TGGCGGCCCA TCGAACAGGC
      GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
      GAGAAGCAGG CGGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
     CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1401
      CCGGTACGGC GGGTGCGGTG GACGGTTTCG ATGTCGGCGC TAAAACCGGC
      ACGGCGCGCA AGTTCGTCAA CGGGCGTTAT GCCGACAACA AACACGTCGC
      TACCTTTATC GGTTTTGCCC CCGCCAAAAA CCCCCGTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCCACGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCCGACC AAGCCACTGA CCGCCGCAGC CGTCAAAACA CCGTCTTAA
```

### This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>: q793.pep

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1 MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
 51 TVTYNFLKEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYP MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
     YPSLDVRGIM QKSSNVGTSK LSARFGAEEM YDFYHELGIG VRMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSLL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQGK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFDVGAKTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVA
551 GPPFKKIMGG SLNILGISPT KPLTAAAVKT PS*
     TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYYGGVVA
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### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2689>: m793.seq

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1 ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
 51 GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
    CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GGCGACAACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTG CGGGACCGGC AGGGCAATAT
     TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTCG GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
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1001	CGCAGCCTTA '	TAAAATCGGA	CCGTCTCCCG	TGCGCGATAC	CCATGTTTAC	
	CCCTCTTTGG	ATCTCCCCGG	CATCATCCAC	AAATCGTCCA	ACGTCGGCAC	
1051	AAGCAAACTG	MCMCCCCCCTT	TECETECECA	ACANATOTAT	CACTTCTATC	
1101	ATGAGTTGGG	1C1GCGCGT1	CCMAMCCACM	AGAMATGIAI	CCCCCAAACT	
1151	ATGAGTTGGG	CATCGGIGIG	CGIAIGCACI	CGGGCTTTCC	DACACCCAC	
1201	GCAGGTTTGT	TGAGAAATTG	GCGCAGGIGG	CGGCCTATCG	MACAGGGGAC	
1251	GATGTCTTTC	GGTTACGGCC	TGCAATTGAG	CCTGCTGCAA	TTGGCGCGCG	
1301	CCTATACCGC	ACTGACGCAC	GACGGCGTTT	TACTGCCGGT	CAGCTTTGAA	
1351	AAACAGGCGG '	TTGCGCCGCA	AGGCAAACGC	ATATTCAAAG	AATCGACCGC	
1401	GCGCGAGGTA	CGCAATCTGA	TGGTTTCCGT	AACCGAGCCG	GGCGGCACCG	
1451	GTACGGCGGG '	TGCGGTGGAC	GGTTTCGATG	TCGGCGCGAA	AACCGGCACG	
1501	GCGCGCAAGT '	TCGTCAACGG	GCGTTATGCC	GACAACAAAC	ACATCGCTAC	
1551	CTTTATCGGT '	TTTGCCCCCG	CCAAAAATCC	CCGTGTGATT	GTGGCGGTAA	
	CCATTGACGA	ACCCACTCCC	CACCCTTATT	ACGCCGCCGT	ACTGGCAGGG	
1601	CCGCCCTTCA	ACCUACIGCC	CACGGIIAII	CTCAACATCT	TCCCCATTTC	
1651	CCGCCCTTCA	AAAAAATTAT	GGGCGGCAGC	CIGAACAICI	TOGGCA111C	
1701	CCCGACCAAG	CCACTGACCG	CCGCAGCCGT	CAAAACACCG	TUTTAA	
mı :	4 - 4 - 4'	h - amaim a a	aid acauca	oo <ceo ii<="" td=""><td>D 2600: OI</td><td>E 702\.</td></ceo>	D 2600: OI	E 702\.
This corr	esponds to t	ne amino a	icia sequen	ice /SEQ II	D 2090; Or	Cr 193/.
m793.pep			•			
1	MLIKSEYKPR I	MLPKEEQVKK	PMTSNGRISF	VLMAIAVLFA	GLIARGLYLQ	
51	TVTYNFLKEQ	GDNRIVRTQT	LPATRGTVSD	RNGAVLALSA	PTESLFAVPK	
101	EMKEMPSAAQ	LERLSELVDV	PVDVLRNKLE	OKGKSFIWIK	ROLDPKVAEE	
	VKALGLENEV	EEKELKDHAD	MONIFAHUTG	FTDIDGKGOE	GLEUSLEDSL	
151	HGEDGAEVVL	PPROCNITIE	TOCODYNADA	NCUDITICID	ODDEDEDEDE	
201	HGEDGAEVVL	KDKOGNI VDS	LUSPKNKAPK	MOVDIITOTO	OVIGITATES	
251	LNKAVEYHQA	KAGTVVVLDA	RTGEILALAN	TPAYDPNRPG	RADSEQRENE	
301	AVTDMIEPGS 2					
351	PSLDVRGIMQ 1	KSSNVGTSKL	SARFGAEEMY	DFYHELGIGV	RMHSGFPGET	
401	AGLLRNWRRW	RPIEOATMSF	GYGLQLSLLQ	LARAYTALTH	DGVLLPVSFE	
451	KQAVAPQGKR					
	ARKEVNGRYA	DNEHLYMETC	ENDARNDDUT	UNUTTOFOTA	HCAACCAAV	
501					ngridgvvno	
551	PPFKKIMGGS	LNILGISPTK	PLTAAAVKTP	5.		
g793/m793	98.5% ident:	ity in 582	aa overlap			
			20 30		50	60
g793.pep	MLTKSEYK	PRMLPKEEOVE	KEMTSNGRIS	FVLMAMAVLFA	CLIARGLYLQT	TYNFLKEQ
g.55.pcp	1111111				1111111111	11111111
-703	MITUCEVE	DDMIDEFOUR	KEDMTSNGRTSI	FVI.MATAVI.FA(	GLIARGLYLQT	TYNFI.KEO
m793		_	_		50	
			3N 31			
		10 2	20 30	0 40	50	60
				-		
		70 8	30 90	100	110	120
g793.pep	GDNRIVRT	70 E	30 90 SDRNGAVLALS	) 100 APTESLFAVPKI	110 OMKEMPSAAQLE	120 ERLSELVDV
g793.pep	GDNRIVRTO	70 & QALPATRGTVS	30 90 SDRNGAVLALS	) 100 APTESLFAVPKI	110 DMKEMPSAAQLE	120 ERLSELVDV
	GDNRIVRTO	70 & QALPATRGTVS	30 90 SDRNGAVLALS	) 100 APTESLFAVPKI	110 DMKEMPSAAQLE	120 ERLSELVDV
g793.pep m793	GDNRIVRT          GDNRIVRT	70 E QALPATRGTVS  :         QTLPATRGTVS	30 96 SDRNGAVLALS            SDRNGAVLALS	D 100 APTESLFAVPKI           APTESLFAVPKI	110 OMKEMPSAAQLE	120 ERLSELVDV
	GDNRIVRT          GDNRIVRT	70 E QALPATRGTVS  :         QTLPATRGTVS	30 90 SDRNGAVLALS	D 100 APTESLFAVPKI           APTESLFAVPKI	110 DMKEMPSAAQLE :         EMKEMPSAAQLE	120 ERLSELVDV
	GDNRIVRT         GDNRIVRT	70 & QALPATRGTVS  ::	30 90 SDRNGAVLALSA              SDRNGAVLALSA   90	D 100 APTESLFAVPKI                APTESLFAVPKI D 100	110 DMKEMPSAAQLE :         EMKEMPSAAQLE 110	120 ERLSELVDV          ERLSELVDV 120
m793	GDNRIVRTO	70 & QALPATRGTVS  ::           CTLPATRGTVS  70 & 8	30 90 SDRNGAVLALS:                SDRNGAVLALS: 30 90	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :         EMKEMPSAAQLE 110	120 ERLSELVDV          ERLSELVDV 120
	GDNRIVRTO	70 E QALPATRGTVS  :        QTLPATRGTVS 70 E 30 14 LEQKGKSFIWJ	30 90 SDRNGAVLALS             SDRNGAVLALS 30 90 40 150 IKRQLDPKVAE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :         EMKEMPSAAQLE 110 170 FEKELKRHYPMO	120 ERLSELVDV          ERLSELVDV 120 180 GNLFAHVIG
m793	GDNRIVRTO	70	30 90 SDRNGAVLALS            SDRNGAVLALS 30 90 40 150   KRQLDPKVAE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110 170 FEKELKRHYPMC	120 ERLSELVDV          ERLSELVDV  120  180 GNLFAHVIG
m793	GDNRIVRTO	70	30 90 SDRNGAVLALS            SDRNGAVLALS 30 90 40 150   KRQLDPKVAE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMO	120 ERLSELVDV          ERLSELVDV 120 180 GNLFAHVIG
m793 g793.pep	GDNRIVRTO	70	30 90 SDRNGAVLALS STRINGAVLALS SDRNGAVLALS 30 90 40 150 KKQLDPKVAE STRINGAVLALS	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110 170 FEKELKRHYPMC	120 ERLSELVDV          ERLSELVDV  120  180 GNLFAHVIG
m793 g793.pep	GDNRIVRTO	70 E QALPATRGTVS  :        QTLPATRGTVS 70 E 30 14 LEQKGKSFIWI	30 90 SDRNGAVLALS STRINGAVLALS SDRNGAVLALS 30 90 40 150 KKQLDPKVAE STRINGAVLALS	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMO	120 ERLSELVDV          ERLSELVDV 120 180 GNLFAHVIG
m793 g793.pep	GDNRIVRTO	70 E QALPATRGTVS  :        QTLPATRGTVS 70 E 30 14 LEQKGKSFIWI	30 90 SDRNGAVLALS             SDRNGAVLALS            SDRNGAVLALS	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMO	120 ERLSELVDV          ERLSELVDV 120 180 GNLFAHVIG
m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS             SDRNGAVLALS            SDRNGAVLALS	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC           FEKELKRHYPMC 170  230	120 ERLSELVDV          ERLSELVDV   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   100   1
m793 g793.pep	GDNRIVRTO	70 & QALPATRGTVS  :	30 90 SDRNGAVLALS             SDRNGAVLALS            SDRNGAVLALS	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC           FEKELKRHYPMC 170  230 LDSPRNKAPQNC	120 ERLSELVDV          ERLSELVDV     180 GNLFAHVIG          SNLFAHVIG 180 240 GKDIILSLD
m793 g793.pep m793 g793.pep	GDNRIVRTO	70 E QALPATRGTVS [:         QTLPATRGTVS 70 E 30 14 LEQKGKSFIWI           LEQKGKSFIWI 30 14 90 20 QEGLELSLEDS	30 90 SDRNGAVLALS             SDRNGAVLALS            SDRNGAVLALS             SDRNGAVLALS              SDRNGAVLALS              STRONGAVLALS               STRONGAVLALS               STRONGAVLA	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC            FEKELKRHYPMC 230 LDSPRNKAPQNC	120 ERLSELVDV          ERLSELVDV            180 ENLFAHVIG          180 240 EKDIILSLD
m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS             SDRNGAVLALS             SDRNGAVLALS	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC            FEKELKRHYPMC 230 LDSPRNKAPQNC	120 ERLSELVDV          ERLSELVDV   120  180 ENLFAHVIG          ENLFAHVIG          ENLFAHVIG
m793 g793.pep m793 g793.pep	GDNRIVRTO	70 E QALPATRGTVS [:         QTLPATRGTVS 70 E 30 14 LEQKGKSFIWI           LEQKGKSFIWI 30 14 90 20 QEGLELSLEDS	30 90 SDRNGAVLALS             SDRNGAVLALS             SDRNGAVLALS	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC            FEKELKRHYPMC 230 LDSPRNKAPQNC	120 ERLSELVDV          ERLSELVDV            180 ENLFAHVIG          180 240 EKDIILSLD
m793 g793.pep m793 g793.pep	GDNRIVRTO	70 & QALPATRGTVS   :	30 90 SDRNGAVLALS SITTE STRINGAVLALS 30 90 40 150 KKRQLDPKVAEI STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGAVLALS STRRNGA	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC            FEKELKRHYPMC 230 LDSPRNKAPQNC	120 CRLSELVDV          CRLSELVDV   20  180 CNLFAHVIG          CNLFAHVIG           SKDIILSLD           SKDIILSLD
m793 g793.pep m793 g793.pep	GDNRIVRTO	70	30 90 SDRNGAVLALS	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171 FEKELKRHYPMC 170  230 LDSPRNKAPQNC            LDSPRNKAPKNC 230  290	120 ERLSELVDV          ERLSELVDV   20  180 SNLFAHVIG          SNLFAHVIG           SKDIILSLD   240   300
m793 g793.pep m793 g793.pep	GDNRIVRTO	70	30 90 SDRNGAVLALS	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC            FEKELKRHYPMC 230 LDSPRNKAPQNC	120 ERLSELVDV          ERLSELVDV   20  180 SNLFAHVIG          SNLFAHVIG           SKDIILSLD   240   300
m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171 FEKELKRHYPMC 170  230 LDSPRNKAPQNC            LDSPRNKAPKNC 230  290 FPAYDPNRPGRA	120 ERLSELVDV          ERLSELVDV   20  180 SNLFAHVIG          SNLFAHVIG   SNLFAHVIG   SNLFAHVIG   240             300 ADSEQRRNR
m793 g793.pep m793 g793.pep m793 g793.pep	GDNRIVRTO	70	30 90 SDRNGAVLALS	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171  230 LDSPRNKAPQNC             LDSPRNKAPKNC 230  290 TPAYDPNRPGR	120 ERLSELVDV          ERLSELVDV   20   80 GNLFAHVIG           SKDIILSLD   1       GKDIILSLD   00   00   00   00   00   00   00
m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171  230 LDSPRNKAPQNC            LDSPRNKAPKNC 230  290 TPAYDPNRPGRA	120 ERLSELVDV          ERLSELVDV   20   80 ENLFAHVIG   1      ENLFAHVIG   50 EKDIILSLD   1       EKDIILSLD   1      ADSEQRRNR
m793 g793.pep m793 g793.pep m793 g793.pep	GDNRIVRTO	70	30 90 SDRNGAVLALS	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171  230 LDSPRNKAPQNC             LDSPRNKAPKNC 230  290 TPAYDPNRPGR	120 ERLSELVDV          ERLSELVDV   20   80 GNLFAHVIG           SKDIILSLD   1       GKDIILSLD   00   00   00   00   00   00   00
m793 g793.pep m793 g793.pep m793 g793.pep	GDNRIVRTO	70	30 96 SDRNGAVLALS             SDRNGAVLALS            SDRNGAVLALS             SCRRGLDPKVAE             IKRQLDPKVAE            IKRQLDPKVAE            SLYGEDGAEVVI    :        SLHGEDGAEVVI 00 216 SQAKAGTVVULD            QAKAGTVVVLD	D 100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171 FEKELKRHYPMC 170  230 LDSPRNKAPQNC             LDSPRNKAPKNC 230  290 FPAYDPNRPGRA             FPAYDPNRPGRA 290	120 CRLSELVDV          CRLSELVDV   20  180 GNLFAHVIG          GNLFAHVIG 180  240 SKDILLSLD           GKDILLSLD           GKDILLSLD 240  ADSEQRRNR
m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171 FEKELKRHYPMC 170  230 LDSPRNKAPQNC (           LDSPRNKAPKNC 230 290 FPAYDPNRPGR/	120 CRLSELVDV          CRLSELVDV           CRLSELVDV   180  SMLFAHVIG           SKDIILSLD            SKDIILSLD            CRLSEQRENR            ADSEQRENR 300 360
m793 g793.pep m793 g793.pep m793 g793.pep	GDNRIVRTO	70 & E QALPATRGTVS  :          CTLPATRGTVS 70 & E  30	30 90 SDRNGAVLALS SITTE STRINGAVLALS 30 90 40 150 KRQLDPKVAE STRINGAVLALS STRINGAVLALS STRINGAVLALS STRINGAVLALS STRINGAVLALS STRINGAVLALS STRINGAVLALS STRINGAVLA STRINGAVLA STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171 FEKELKRHYPMC 230 LDSPRNKAPQNC !          LDSPRNKAPKNC 230 PPAYDPNRPGRA 290 350 PSPVRDDTHVYP	120 CRLSELVDV          CRLSELVDV          CRLSELVDV            SNLFAHVIG              SKDIILSLD            KDIILSLD            ADSEQRRNR            ADSEQRRNR 300 360 PSLDVRGIM
m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS SITTE STRINGAVLALS 30 90 40 150 KRQLDPKVAE SITTE STRINGAVLALS 30 90 40 150 KRQLDPKVAE STRINGAVLALS 50 210 STRINGAVLALS 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVLD	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC             FEKELKRHYPMC 230 LDSPRNKAPQNC              LDSPRNKAPKNC 230  290 FPAYDPNRPGRI            FPAYDPNRPGRI 290 350 PSPVRDDTHVYI	120 CRLSELVDV          CRLSELVDV           CRLSELVDV            180 CSNLFAHVIG              CSKDIILSLD              CKDIILSLD             ADSEQRRNR             ADSEQRRNR               CRLSEDVRGIM
m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS SITTE STRINGAVLALS 30 90 40 150 KRQLDPKVAE SITTE STRINGAVLALS 30 90 40 150 KRQLDPKVAE STRINGAVLALS 50 210 STRINGAVLALS 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVVLD 50 270 DAKAGTVLD	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC 171 FEKELKRHYPMC 230 LDSPRNKAPQNC !          LDSPRNKAPKNC 230 PPAYDPNRPGRA 290 350 PSPVRDDTHVYP	120 CRLSELVDV          CRLSELVDV           CRLSELVDV            180 CSNLFAHVIG              CSKDIILSLD              CKDIILSLD             ADSEQRRNR             ADSEQRRNR               CRLSEDVRGIM
m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS SITTE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC             FEKELKRHYPMC 230 LDSPRNKAPQNC              LDSPRNKAPKNC 230  290 FPAYDPNRPGRI            FPAYDPNRPGRI 290 350 PSPVRDDTHVYI	120 CRLSELVDV          CRLSELVDV           CRLSELVDV            180 CSNLFAHVIG              CSKDIILSLD              CKDIILSLD             ADSEQRRNR             ADSEQRRNR               CRLSEDVRGIM
m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS SITTE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMG             FEKELKRHYPMG 230 LDSPRNKAPQNG              LDSPRNKAPKNG 230  290 FPAYDPNRPGR/            FPAYDPNRPGR/ 290  350 PSPVRDDTHVYI	120 CRLSELVDV          CRLSELVDV           CRLSELVDV            180 CSNLFAHVIG              CSKDIILSLD              CKDIILSLD             ADSEQRRNR             ADSEQRRNR               CRLSEDVRGIM
m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS SITTE STRINGAVLALS 30 90 40 150 KRQLDPKVAEI STRINGAVLALS 30 90 40 150 KRQLDPKVAEI STRINGAVLALS 30 210 SLYGEDGAEVV STRINGAVLALS 30 210 SLYGEDGAEVV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV STRINGAV S	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC            FEKELKRHYPMC 170  230 LDSPRNKAPQNC             LDSPRNKAPKNC 230  290 FPAYDPNRPGRA             FPAYDPNRPGRA 290  350 PSPVRDDTHVYI            PSPVRD-THVYI 350	120 CRLSELVDV          CRLSELVDV   20  180 CNLFAHVIG           CRLSELVDV  180  SMLFAHVIG           CRLSELVDV  240  300 ADSEQRENR           ADSEQRENR           ADSEQRENR           SSLDVRGIM
m793 g793.pep m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS SITTE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC            FEKELKRHYPMC 170  230 LDSPRNKAPQNC             LDSPRNKAPKNC 230  290 FPAYDPNRPGR/             FPAYDPNRPGR/ 290  350 PSPVRDDTHVYI             PSPVRD-THVYI             PSPVRD-THVYI	120 ERLSELVDV          ERLSELVDV   20   80 SNLFAHVIG   1       SNLFAHVIG   50 LIVINIA SKDIILSLD   240   300 ADSEQRRNR           ADSEQRRNR   1        ADSEQRRNR   1        SSLDVRGIM
m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 96 SDRNGAVLALS SDRNGAVLALS SDRNGAVLALS 30 96 40 156 EKRQLDPKVAE SITTE STREET EKRQLDPKVAE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET S	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC 170  230 LDSPRNKAPQNC !          LDSPRNKAPKNC 230  290 FPAYDPNRPGRA            FPAYDPNRPGRA            FPAYDPNRPGRA            FPAYDPNRPGRA 290  350 PSPVRDTHVYE	120 ERLSELVDV          ERLSELVDV           ERLSELVDV
m793 g793.pep m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS SITTE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :           EMKEMPSAAQLE 110  170 FEKELKRHYPMC 170  230 LDSPRNKAPONC (            LDSPRNKAPKNC 230  290 FPAYDPNRPGR/ 290  FPAYDPNRPGR/ 290  S50 PSPVRDDTHVYI             PSPVRD-THVYI 350  410 FAGLLRNWRRWI	120 CRLSELVDV          CRLSELVDV           CRLSELVDV   20  180 CNLFAHVIG           CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD              CKDIILSLD              CKDIILSLD              CKDIILSLD
m793 g793.pep m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70	30 90 SDRNGAVLALS SITTE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE :            EMKEMPSAAQLE 110  170 FEKELKRHYPMC 170  230 LDSPRNKAPQNC !          LDSPRNKAPKNC 230  290 FPAYDPNRPGRA            FPAYDPNRPGRA            FPAYDPNRPGRA            FPAYDPNRPGRA 290  350 PSPVRDTHVYE	120 CRLSELVDV          CRLSELVDV           CRLSELVDV   20  180 CNLFAHVIG           CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD              CKDIILSLD              CKDIILSLD              CKDIILSLD
m793 g793.pep m793 g793.pep m793 g793.pep m793 g793.pep m793	GDNRIVRTO	70 & EQALPATRGTVS  :	30 90 SDRNGAVLALS SITTE	100 APTESLFAVPKI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	110 DMKEMPSAAQLE HIIIIIIIIII EMKEMPSAAQLE 110  170 FEKELKRHYPMC 170  230 LDSPRNKAPQNC (               LDSPRNKAPKNC 230  290 FPAYDPNRPGRY 290  350 PSPVRDDTHVYI HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	120 CRLSELVDV          CRLSELVDV           CRLSELVDV   20  180 CNLFAHVIG           CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD             CKDIILSLD              CKDIILSLD              CKDIILSLD              CKDIILSLD

```
450
                                               460
                            440
                   430
            FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
a793.pep
            {\tt FGYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE}
m793
                                       450
                                                460
                                                         470
                             440
                    430
          420
                            500
                                      510
                                               520
                                                         530
                                                                  540
                   490
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q793.pep
            PGGTGTAGAVDGFDVGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPT
m793
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                                                520
          480
                    490
                             500
                                      570
                            560
                   550
            AHGYYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX
g793.pep
            AHGYYGGVVAGPPFKKIMGGSLNILGISPTKPLTAAAVKTPSX
m793
                             560
                                       570
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2691>:
a793.seq
         ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
         GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
     51
         CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
     101
    151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GGCGACAACC GGATTGTGCG
    201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTTCGGAC CGGAACGGTG
         CGGTTTTGGC GTTGAGTGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
     251
         GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
     301
         TGTCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
     351
         AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
     401
         GTCAAAGCCT TGGGTTTGGA AAACTTTGTA TTTGAAAAAG AATTAAAACG
     451
         CCATTACCCG ATGGGCAACC TGTTTGCACA CGTCATCGGA TTTACCGATA
     501
         TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTCGCTTGA AGACAGCCTG
     551
         CATGGCGAAG ACGGCGCGGA AGTCGTTTTG CGGGACCGGC AGGGCAATAT
     601
         TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
     651
     701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
         TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
    751
     801
         TTTGGATGCC CGCACGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
    851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
     901 GCCGTAACCG ATATGATCGA ACCCGGTTCG GCAATCAAAC CGTTTGTGAT
         TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
     951
         CGCAGCCTTA TAAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
    1001
         CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
   1051
         AAGCAAACTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
    1101
         ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
    1151
         GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
   1201
         GATGTCTTTC GGTTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
   1251
         CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
   1301
         AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
   1351
         GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GGCGGCACCG
   1401
         GTACGGCGGG TGCGGTGGAC GGTTTCGATG TCGGCGCGAA AACCGGCACG
   1451
         GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
   1501
         CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
   1551
         CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
         CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
         CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```
a793.pep
         MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
      1
         TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
    101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIWIK RQLDPKVAEE
         VKALGLENFV FEKELKRHYP MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
    151
         HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
    201
    251
         LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRRNR
         AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
     301
         PSLDVRGIMO KSSNVGTSKL SARFGAEEMY DFYHELGIGV RMHSGFPGET
     351
         AGLLRNWRRW RPIEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPVSFE
     401
         KQAVAPQGKR IFKESTAREV RNLMVSVTEP GGTGTAGAVD GFDVGAKTGT
         ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYYGGVVAG
     501
         PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*
     551
```

	10	20	30	40	50	60
a793.pep	MLIKSEYKPR	MLPKEEQVKK	PMTSNGRISFV	LMAIAVLFAG	LIARGLYLQT	VTYNFLKEQ
m793		ALPKEEÖVKK:		'LMAIAVLFAG	!              LIARGLYLQT	VTYNFLKEQ
111755	10	20	30	40	50	60
	70	80	90	100	110	120
a793.pep	GDNRIVRTQT	1111111111	1111111111111	1111111111	[1][1][1][]	11111111
m793	GDNRIVRTQT	LPATRGTVSDI 80	RNGAVLALSAF 90	TESLFAVPKE	MKEMPSAAQL 110	ERLSELVDV 120
a793.pep	130 PVDVLRNKLE	140 OKGKSFIWIK	150 RQLDPKVAEEV	160 KALGLENFVF	170 EKELKRHYPM	180 GNLFAHVIG
		1111111111		11111111111	11111111111	11111111
m793	130	140	150	160	170	180
	190	200	210	220	230	240
a793.pep	FTDIDGKGQE	GLELSLEDSL	HGEDGAEVVLF	RDRQGNIVDSL	DSPRNKAPKN	GKDIILSLD
m793	FTDIDGKGQE	GLELSLEDSL	HGEDGAEVVLF	RDRQGNIVDSL	DSPRNKAPKN	GKDIILSLD
	190	200	210	220	230	240
	250	260	270	280	290	300
a793.pep	QRIQTLAYEE		1111111111	1111111111	111111111	
m793	QRIQTLAYEE	LNKAVEYHQA 260	KAGTVVVLDAF 270	RTGEILALANT 280	PAYDPNRPGR 290	ADSEQRRNR 300
a793.pep	310 AVTDMIEPGS	320 AIKPFVIAKA	330 LDAGKTDLNEF	340 RLNTQPYKIGP:	350 SPVRDTHVYP	360 SLDVRGIMQ
		11111111	[11111111111			111111111
m793	310	320	330	340	350	360
	370	380	390	400	410	420
a793.pep	KSSNVGTSKL	SARFGAEEMY	DFYHELGIGVE	MHSGFPGETA	GLLRNWRRWR	PIEQATMSF
m793	KSSNVGTSKL		DFYHELGIGVF	RMHSGFPGETA	GLLRNWRRWR	PIEQATMSF
	370	380	390	400	410	420
	430 GYGLQLSLLQ	440	450	460	470	480
a793.pep	1111111111	111111111		1111111111	11111111111	111111111
m793	GYGLQLSLLQ	LARAYTALTH 440	DGVLLPVSFEF 450	QAVAPQGKRI 460	FKESTAREVR 470	NLMVSVTEP 480
				500	520	5.40
a793.pep	490 GGTGTAGAVD	500 GFDVGAKTGT.	ARKFVNGRYAL	520 ONKHIATFIGF	530 APAKNPRVIV	540 AVTIDEPTA
• •		111111111	11111111111		11111111111	1111111111
m793	GGTGTAGAVD	500 S	510	520	530	540
	. 550	560		580		
a793.pep	550 HGYYGGVVAG	PPFKKIMGGS	LNILGISPTKI	PLTAAAVKTPS	X	
a793.pep m793	. 550	PPFKKIMGGS	LNILGISPTKI          LNILGISPTKI	PLTAAAVKTPS	1	

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2693>: g794.seq

1	gtgcgtttca	ATCATTTCAT	AATGGTAACG	ATTATTATAT	ATGTGATTTC
51	CCCTGCAAAC	AAGCCGGTCC	GCCGCCCGG	CGTTCCCACT	TATCCGGCTT
101	TGCCTTATAA	TTGCTTTTTT	TATGTAACAG	ATTCACCTAT	GAATTTCCCC
151	AAAACAGCGG	CCTCCCTGCT	GCTGCTTCTC	GCCTCCCTCG	CCGCACACGC
201	GCTCGATACC	GGCCGCATTC	CGCAAAACGA	AATCGCTGTA	TATGTCCAAG
251	AGCTTGACAG	CGGAAAAGTC	ATCATTGACC	ACCGTGCCGG	CATACCCGTC
301	AATCCCGCGT	CCACGATGAA	GCTCGTTACC	GCGTTTGCCG	CCTTCAAAAC
351	CTTCGGCAGC	AATTACCGCT	GGGCGACCGA	GTTTAAAAGC	AACGGTACGG
401	TAAACGACGG	CACGCTTGAC	GGAAACCTGT	ATTGGGCGGG	CAGCGGCGAC
451	CCCGTTTTCA	ATCAGGAAAA	CCTGCTTGCC	GTCCAACGCC	AGTTGCGCGA
501	CAAAGGCATC	CGCAATATCA	CGGGGCGCCT	GATGCTCGAC	CACAGCCTGT

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1278
```

```
551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTCGCCG
     TTTATGACGC CCCCAAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
     GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
 701 CTTTGCCGCA TATTTTTGCC CAAAACAACT TGAAAATTAC CGCCTCCCAA
 751 GCTGCCTGCC CTTCGGTCAA AAAACTGATG CGCGCATCTT TTTCGGGCAA
     TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
     TCGGTGTCCG GATGTTCGCG CTTGACGAAC TGATCCGCCA AAGTTTTACC
 851
 901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
     CGACACCCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
951
     TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1001
     CGTTCCGTCT TCCTCAAACT CGGCGGCGAC GGCAAACTGC CCGCCGTTTC
1051
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151
     ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCGCAAATG TTGGAAACGG CTTATTTCAG
     CCCGTTTGCA CAAGATTTCA TCGACACGCT GCCCATCGCC GGCACAGACG
     GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1301
     ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1351
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
     TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGGC
1451
     GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA
```

#### This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>: g794.pep

```
VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNFP
 51 KTAASLLLLL ASLAAHALDT GRIPQNEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
    PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVGSP DHFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
    NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILTD MNKRSDNLIA
    RSVFLKLGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDAKLMC KERRA*
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2695>: m794.seq

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GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
  51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
 101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
     AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
 201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
 251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC
 301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
     CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
     TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGGCGAC
 451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAAC AGTTGCGCGA
     ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
     GGGGCGAAGT CGGCAGCCCC GACGATTTCG AAGCCGACAG CGGTTCGCCG
 601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
     GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
 651
 701 CTTTGCCGCA TATTTTCGCC CAAAACAACT TGAAAATTAC CGCCTCCCAA
     GCTGCCTGCC CTTCGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
 801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
     TCGGTGTCCG GATGTTCGCG CTTGACGAAC TGATCCGGCA AAGTTTTACC
 901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
     CGACACGCCG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
     TGAAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1001
     CGTTCCGTCT TCCTCAAACT CGGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CGGGCCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCGCAAATG TTGGAAACGG CTTATTTCAG
     CCCGTTTGCA CAAGATTTCA TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401
     CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>: m794.pep

- 1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
- 51 KTAASLLLLL ASLAAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV

101 151 201 251 301 351 401 451 501	NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD PVFNQENLLD AQKQLREQGI LNITGHLMLD HSLWGEVGSP DDFEADSGSP FMTPPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSDNLIA RSVFLKLGGD GKLPAVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE RVTARMMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLLRLK TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG DGWLDAKLMC KERRA*
g794/m794	95.5% identity in 515 aa overlap
g794.pep m794	10 20 30 40 50 60  VRFNHFIMVTIIIYVISPANKPVRRPGVPTYPALPYNCFFYVTDSPMNFPKTAASLLLLL    :    ::
g794.pep m794	70 80 90 100 110 120 ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS
g794.pep m794	130 140 150 160 170 180 NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRLMLD
g794.pep m794	190 200 210 220 230 240 HSLWGEVGSPDHFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
g794.pep m794	250 260 270 280 290 300 QNNLKITASQAACPSVKKLMRASFSGNTLKLRGNIPESCLGKPVGVRMFALDELIRQSFT
g794.pep m794	310 320 330 340 350 360 NRWLLGGGRISDGIGIADTPEGAQTLAVAHSKPMKEILTDMNKRSDNLIARSVFLKLGGD  :
g794.pep m794	370 380 390 400 410 420 GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVTARMMAQMLETAYFSPFA
g794.pep m794	430 440 450 460 470 480 QDFIDTLPIAGTDGTLRNRFKQSGGLLRLKTGTLNNVRALAGYWLGDKPMAVVVIINSGR
g794.pep m794	490 500 510 AVSLLPDLDNFVAKNIISGGDGWLDAKLMCKERRAX
The follo	wing partial DNA sequence was identified in N meningitidis <s< td=""></s<>

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2697>: a794.seq

- 1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
- 51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT
  101 TGCCTTATAA TTGCTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
- 151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
- 201 GCTCGATACA GGTCGCATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
- 251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC

a794.pep

	•
301	AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351	CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401	TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
	CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
451	ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
501	GGGGCGAAGT CGCCAGCCCC GACGATTCG AAGCCGACAG CGGTTCGCCG
551	TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
601	GCGCGCCGAA CGCAATGCC CCGACAGTAC CGACATCCTC ACCGATCCGC
651	CTTTGCCGCA TATTTTCGCC CAAAACAACT TGAAAATTAC CGCCTCCCAA
701	GCTGCCTGCC CTTCGATCAA AAAACTGATG CGTGCATCTT TTTCGGACAA
751	TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
801	TACGCTGAAA TTGCGCGGCA ATATICCCGA GAGCIGITIG GGCAAGGCIG TCGGTGTCCG GATGTTCGCG CTTGACGAAC TGATCCGGCA AAGTTTTACC
851	TCGGTGTCCG GATGTTCGCG CTTGACGAAC TGACCGCGA TCCCCATATC
901	AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951	CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAAGCCGA
1001	TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051	CGTTCCGTCT TCCTCAAACT CGGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101	CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151	ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CAGGTCTGTC CAGAAAAGAA
1201	AGGGTAACGG CGAGAATGAT GGCGCAAATG TTGGAAACGG CTTATTTCAG
1251	CCCGTTTGCA CAAGATTTCA TCGATACGCT GCCCATCGCC GGCACAGACG
1301	GGACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351	ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401	CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451	TGCTGCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501	GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA
This corr	esponds to the amino acid sequence <seq 2698;="" 794.a="" id="" orf="">:</seq>
	esponds to the animo acid sequence 522 12 2000, 522
a794.pep	WIND DAYS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
1	VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
5 <b>1</b>	KTAASLLLLL ASLAAHALDT GRIPQNEIAV YVQELDSGKV IIDHRSDVPV
101	NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151	PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGSP DDFEADSGSP
201	FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251	AACDSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301	NHWLLGGGRI SDGIGISDTP EGAOTLAVAH SKPMKEILTD MNKRSDNLIA
351	RSVELKLGGD GKLPAVSEOA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401	PUTARMMAOM LETAYESPFA ODFIDTLPIA GTDGTLRNRF KQSGGLLRLK
451	TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
501	DGWLDAKLMC KERRA*
301	2011.22.11.12.12
a794/m794	98.6% identity in 515 aa overlap
Q134/11/34	30.00 200020, 200
	10 20 30 40 50 60
2704 pap	VRLNHFIMIAIIIYVISPANKPARRHSVPTYPALPYNCFFYVTDLPMNFPKTAASLLLLL
a794.pep	
704	VRLNHFIMIAIIIYVISPANKPARRHSVPTYPALPYNCFFYVTDLPMNFPKTAASLLLLL
m794	10 20 30 40 50 60
	10 20 30 10 30
	70 80 90 100 110 120
	70 80 90 100 110 120 ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
a794.pep	ASLAAHALDTGKIPQNEIAVIVQEBDSGKVIIDIKSDVFVKIAGIKKDVIATIKA KIIGG
	ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
m794	
	70 80 90 100 110 120
	170 170
	130 140 150 160 170 180
a794.pep	NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLREQGIRNITGHLMLD
	MINMISTROMOTAMO
m794	
m794	
m794	
m794	
m794 a794.pep	
a794.pep	
a794.pep	
a794.pep	
a794.pep m794	
a794.pep	
a794.pep m794 a794.pep	
a794.pep m794	
a794.pep m794 a794.pep	
a794.pep m794 a794.pep	

NHWLLGGGRISDGIGISDTPEGAQTLAVAHSKPMKEILTDMNKRSDNLIARSVFLKLGGD

```
NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDMNKRSDNLIARSVFLKLGGD
m794
                 310
                          320
                                  330
                                           340
                 370
                          380
                                  390
                                           400
                                                   410
                                                            420
           GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVTARMMAQMLETAYFSPFA
a794.pep
           GKLPAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVTARMMAQMLETAYFSPFA
m794
                          380
                                  390
                                           400
                 430
                          440
                                  450
                                           460
                                                   470
           ODFIDTLPIAGTDGTLRNRFKQSGGLLRLKTGTLNNVRALAGYWLGDKPMAVVVIINSGR
a794.pep
           QDFIDTLPIAGTDGTLRNRFKQSGGLLRLKTGTLNNVRALAGYWLGDKPMAVVVIINSGR
m794
                 430
                          440
                                  450
                                           460
                                                   470
                          500
                 490
                                  510
          AVSLLPDLDNFVANNIISGGDGWLDAKLMCKERRAX
a794, pep
           AVSLLPDLDNFVANNIISGGDGWLDAKLMCKERRAX
m794
                 490
                          500
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2699>:
    g900.seq
              ATGCCGTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
           1
              ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
              AACAATTCGC GCGCTTCTTT GCGCGCTTTT TGCGCGCCCtq cctGCAAAAT
              CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TGCGTTGTAG CGTTCGCGCA
              GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCGCCTCG
              CCCCAAGCCA AGCCGTCGGC AAGCATTTGC GTAAATTCCG CCGTTTCAGA
         251
              CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
         301
              GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
         351
              TTTTGGGTTT TTTTGTCGTT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
         401
              TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCGT
         451
         501
              CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtqaag
              cggccggcAa tgtcgcgcgc cATTTcgacg tgttgGATTT GGTCGCGCCC
              GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGGCA GTCATCAGAA
         651
              TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
         701
              CCGTTTTCCG CATTGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
              CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
         751
              CTTCGGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCGCTC GGGGTCGAGT
         801
         851
              CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tqGGTGGATT GGTGAATCAT
              CTCCTGCTCG TGGCATTTGA TGATGCCGTG GTAATCGGCG AGGAAGAGGA
         901
              AGGATTCGGT ATCGGGGTTT TGCGCCGCG GGACGCGGG GCGGATGGCG
         951
              CCGACGTAGT TGCCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
              AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
        1051
              AAGGGAAAa. qatqcqCCGA TTATACCCGA TTTGCCACAT ACATCCAGCC
              GacaACagaC TTTTCCATAT TAA
        1151
This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:
    q900.pep
              MPSEMPSETW QAEVRTALGL FQRADADRIA YFIQQFARFF ARFLRACLQN
              LFDLRRIRGO CVVAFAQFCO FGVDFRRRKF FRLAPSQAVG KHLRKFRRFR
              RRGEGFIDFK QRAFVGLFRL ARLFHVGNDF VDRFLGFFVV FPKRNGIAVG
         101
              FGHFASVQTD QEFDVFVDFH FGQGEEFLET VGEAAGNVAR HFDVLDLVAP
         151
              DGDFVGVEHQ NVGSHQNRIT EQTHFHTEIG VFLPVFRIGL NGGFVGVGAV
         201
              HQTLGGDAGQ NPVQLHHFGN VALAVEGGAL GVESAGKPSG GNGLGGLVNH
         251
              LLLVAFDDAV VIGEEEEGFG IGVLRRADGG ADGADVVAQM RGAGGGYAGQ
         301
              NSFFAHKNVL TAAMPSEREK DAPIIPDLPH TSSRQQTFPY *
The following partial DNA sequence was identified in N. meningitidis <SEO ID 2701>:
     m900.seg
```

ATGCCGTCTG AAACGCGGCA GGCGGAGGTT CGGACGGCAT CGGGTTCATT 1 TCAACGGGCG GATGCCGACC GCATCGG.TA CTTTGTCCAA TAATTCGCGT 51 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTTG

```
CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
      CGGCGTTGAT TTTCGCCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
201
     CCGTCGCCAA GCATTTTCGT AAATTCCACC GTTTCAGACG GCGTGGAGAA
251
      GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
301
      CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATTT TTGGGTTTTT
      tTGTCGTTTT CCCAAAGCGG AATGGTGTTG CCGTAGGATT TGGACATTTT
401
      GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
      CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTTGAAGCG GCCGGCGATG
      TCGCGCGCCA TTTCGACGTG TTGGATTTGG TCGCGCCCGA CQGGCaCTTC
 551
      GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
601
651
      ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCCTGCCC GTTTTCTGCA
      TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCCTT
 701
      GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCGGGAGTGT
751
      CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTCGAGTCC GCAGGCAAGC
801
     CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
851
     GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCGGTAT
901
      CGAGGTTTTG CGCCGCGCG ACGCCGGGC GGATGGCGCC GACGTAGTTG
951
     CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
      GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
      TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1101
      TTCCATATTA A
1151
```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

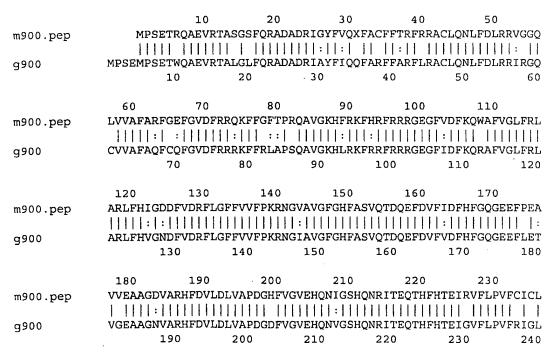
- 1 MPSETRQAEV RTASGSFQRA DADRIXYFVQ *FACFFTRFR RACLQNLFDL 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE 01 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVFPKR NGVAVGFGHF 51 ASVQTDQEFD VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
- 201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAVHQTL 251 GSDAGONPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHLRLV
- 301 AFDDTVVIGE EEEGFGIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
- 351 AHKNVLAASM PSEREKDVPI IPDLPPTSSR QQTFPY*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from N. gonorrhoeae:

m900/g900



	•					
	240	250	260	270	280 290	
m900.pep					EVESAGKPSGGNGL	GGLVNH
dad.pell				:		
~0.00					GVESAGKPSGGNGL	GGLVNH
g900		50 26			290	300
	-,	20			2,0	
	300	310	320	330	340 350	
m900.pep					RDAGGGYAGQNSFF.	AHKNVL
dad.ooelli		:				
g900					RGAGGGYAGQNSFF.	AHKNVL
9900		10 32			350	360
	360	370	380			
m900.pep	AASMPSER	EKDVPIIPDLE	PTSSRQQTFP	YX		
,00.12-1	:1:1111	111:111111		11		
g900			HTSSROOTFP	ΥX		
9200		70 38				
The following p	artial DNA se	auence was	identified in	n <i>N. meningi</i>	tidis <seo 2<="" id="" td=""><td>2703&gt;:</td></seo>	2703>:
a900.seq	(partial)	4				
a900.seq	GAGGTTCGGA	CGGCATTGGG	тттатттсаа	CGGGCGGATA	CCGACCGCAT	
51	CACGTACTTT					
101	CCTGCCTGCA					
151	GTAGCGTTCG					
201	GTTTTTTTGC					
251	TCTGCCGTTT	CAGACGGCGT	GGAGAAAGCT	TTGTAGATTT	CAAACAGAGG	
301	GCTTTCGTCG	GGCTTCTTCG	GCTCGCCCGG	CTCTTTCATA	TTGGTGATGA	
351	TTTTGTTGAC					
401	GTGTTGCCGT					
451	TTCGACGTTT					
501	AGCGGTGGTT					
551	ATTTGGTCGC					
601	GGCAGTCATG .					
651	CGGGGTCTTC					
701	GCGTGGGCGC GTTCAATTCC					
751 801	GCTCGGGGTC					
851	GATTGGTGAA					
901	GGCGAGGAAG					
951	CGGGGCGGAT					
1001	GTTACGCCGG					
1051	TCAATGCCGT					
1101	ACCTACATCC	AGCCGACAAC	AGACTTTTCC	ATATTAA		
This correspond	ls to the amino	acid seque	nce <seq i<="" td=""><td>D 2704; ORI</td><td>7 900.a&gt;:</td><td></td></seq>	D 2704; ORI	7 900.a>:	
a900.pep	(partial)	-	-			
1	EVRTALGLFQ	RADTDRITYF	AQ*FACFFTR	FLRACLQNLF	DLRRVGGQLV	
51	VAFARFGEFG					
101	AFVGLLRLAR					
151						
201						
251	VQFHHFGNVA					
301				AGGGYAGQNS	FFAHKNVLAA	
351	SMPSEREKDA	PITEDLPPTS	2KÖÖT.F.P.A.*			
000/000 00		:- 270 00 01	rowlow			
m900/a900 88	8.4% identity		-			
				0 40	50	60
m900.pep	MPSETRQA				RACLQNLFDLRRVG	
- 000						
a900		EVRTALGLEQ.	KADTURITYFA 20	QXFACFFTRFL 30	RACLONLE DLRRVG 40	.GQLVVA 50
		10	20	30	-1 U	30
		70	80 9	0 100	110	120

m900.pep	FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEGFVDFKQWAFVGLFRLARLE
a900	FARFGEFGVDFRRQKFFCLAPSQAVGKHFRKFCRFRRRGESFVDFKQRAFVGLLRLARLE 60 70 80 90 100 110
000	130 140 150 160 170 180 HIGDDFVDRFLGFFVVFPKRNGVAVGFGHFASVOTDQEFDVFIDFHFGOGEEFPEAVVE
m900.pep	
a900	HIGDDFVDRFLGFFVVFPKRNGVAVGFGHFASVQTNQEFDVFVDFHFGQCEEFPEAVVEA
	120 130 140 150 160 170
	190 200 210 220 230 240
m900.pep	AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICLHGGF
1 1	
a900	AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFHAEIGVFLPVFRICLHGGE
	180 190 200 210 220 230
	<b>250 260 270 280 290 300</b>
m900.pep	VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNHLRLV
a900	VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSGGNGLGGLVNHLRLV
	<b>240 250 260 270 280 290</b>
•	310 320 330 340 350 360
m900.pep	AFDDTVVIGEEEEGFGIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
a900	AFDDTVVIGEEEEGFGIRVLRRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
	<b>300 310 320 330 340 350</b>
	370 380
m900.pep	PSEREKDVPIIPDLPPTSSRQQTFPYX
a900	PSEREKDAPIIPDLPPTSSRQQTFPYX
	360 370

g901.seq not found yet not found yet g901.pep

801 CCATTTTAA

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2705>: m901.seq

ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATCACATT 1 51 GGCTGCCGGT TTGTTTACCG TATTAKGYAG TGGCTTGGTG ATGTTTTCCA 101 AAACGCCCAA TCCGCGTGTG TTGTCGTTTG GTTTGGCGTT TGCCGGCGGT 151 GCGATGGTAT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG CATTTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG 301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG 401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTTGCCAC ATTGGAAAAT 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGCCACC CGCAGCCGTA 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG 601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTTGTCGC CTGCCGTGTT 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTT TTGGCGTTGG 701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT 751 TACGGCCTGA CAACGGGTAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>: m901.pep

- MPDFSMSNLA VAFSITLAAG LFTVLXSGLV MFSKTPNPRV LSFGLAFAGG
- 51 AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP

- 101 NPHETLDAOD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
- 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTVWAC LLSGLAEPLG
- 201 AALGYLVLQP FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV
- 251 YGLTTGMAVI AVSLVLFHF*

## The following partial DNA sequence was identified in N. meningitidis <SEO ID 2707>:

a901.seq 1 ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATTACGTT GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCA AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGGCGGT GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG 251 CATTTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG 301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG 401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTTGCCAC ATTGGAAAAT 451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC 501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGCCACC CGCAGCCGTA 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG 601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTTGTCGC CTGCCGTGTT 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGTTT TTGGCGTTGG 701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT TACGGCCTGA CAATGGGCAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT

## This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

- 1 MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG
  - 51 AMVYVSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRLVP
  - 101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
  - 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTVWAC LLSGLAEPLG
  - 201 AALGYLVLQP FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
  - 251 YGLTMGMAVI AVSLVLFHF*

### m901/a901 98.9% identity in 269 aa overlap

a901

CCATTTTTAA

1/4/01 /0.	70 radinary m 203	aa o . orrap				
	10	20	30	40	50	60
m901.pep	MPDFSMSNLAVAFS	ITLAAGLFTV	/LXSGLVMFSF	(TPNPRVLSF	SLAFAGGAMV	VSLTEI
	11111111111111	111111111111		111111111	HIIIIIIIII	
a901	MPDFSMSNLAVAFS	I <b>T</b> LAAGLFTV	/LGSGLVMFSk	TPNPRVLSF	GLAFAGGAMVY	VSLTEI
	10	20	30	40	50	60
	70	80	90	100	110	120
m901.pep	FSKSSEAFAEIYDK	DHAFAAATMA	AFLAGMGGIAI	JIDRLVPNPHE	CTLDAQDPSFQ	)ESKRRH
a901	FSKSSEAFAEIYDK	DHAFAAATMA	AFLAGMGGIAI	IDRLVPNPH	ETLDAQDPSFQ	DESKRRH
	70	80	90	100	110	120
	130	140	150	160	170	180
m901.pep	IARVGMMAAFAITA	HNFPEGLATE	FFATLENPAVO	MPLALAIAI	HNIPEGISIAA	APVYFAT
		111111111				
a901	IARVGMMAAFAITA					APVYFAT
	130	140	150	160	170	180
	190	200	210	220	230	240
m901.pep	RSRKKTVWACLLSG					
a901	RSRKKTVWACLLSG					
	190	2.00	210	220	230	240
	0.50	0.60	000			
004	250	260	270			
m901.pep	KRYSDGHETVYGLT	TGMAVIAVSI	JVLFHFX			

KRYSDGHETVYGLTMGMAVIAVSLVLFHFX

PCT/US99/09346 WO 99/57280 1286

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2709>: q902.seq ATGCCGTCCG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC 51 GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA 101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTTGATTTC 151 ACGCCGCGC TGTTCGCCGT CGGGCATTTC GCCGATGTAC CAGCCTATGT 201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG 251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC 301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC 351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT TGTTTGAGGA cggCGGCGGC TTTTTgcggc GAagtGATGT CGCCGTTGac 451 cCaggCCGGG ATGTTCAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC qcGCCTCGCC TTTGTACATT TGCGTGcgcG CGcgcccgtg aacggcaaGg gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg 601 atcgtcgtcg tgccaaccca AacggGTTTT GaggGTAACG GGTAcgcCCG 651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTCGTCCTGC ATCAGCGCGC TACCGGCTTG GACGTTGCAC ACTTTCttgg cqqqGCAGCC CATALLEGATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgccg catCCGCCAT CtgttcggGG TCGCTGCCGG CAATCTGCAC GGCAACGATG CCGccttcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCCT 901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCAA CCTGCGCCAA 951 ACGCCCGACA GAGGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC 1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG CCCGCGTTTC AAAAAGTGC GCCATTGTAC ATTTTTTAA This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>: q902.pep 1 MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF 51 TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVVQN GGSAFCQTQG 101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD 151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAAIF GDFGDGGQVL 201 IVVVPTQTGF EGNGYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA 251 HIDVDDLRPE SDVVTRRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP 301 ERRIAGOHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG 351 PAFQKSAPLY IF* The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2711>: m902.seq TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG 1 51 CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA 101 AGCATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG 151 TGTCTGTTCG CCGTcGGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC 201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG 251 ATGTGGTTCA AAATAGCGGC GGCGCATTCT GCCAAACTCA AGGCAGGCGG 301 CAAAACACCG TGTTCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC 351 TGCCTTGCGC GCCGCGCCT ATCATAATGC CGTCGGCGGC GGTTTGTTTG 401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCCGT TGACCCAGAC 451 CGGGATGTTC AGACGGCATT TGGTTTCGGC GATGAGTTCG TAACGCGCTT 501 CGCCTTTGTA CATTTGCGTA CGCGTGCGTC CGTGGACGGC AAGGGCGGCG 551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC 701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT 751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG 801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT 851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT 901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAAATCTC 951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGcGCAAGT 1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG 1051 TTTCAAAAAA GTACGCCATT GTACATTTTT TAA This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

PCT/US99/09346 WO 99/57280 1287

m902.pep 1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT 51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVVQNSG GAFCQTQGRR 101 QNTVFGIMFQ IAEEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD 151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAAIFGD FGDDGOVLMV 201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV 251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER 301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRKCDGVVDK IAADVHNGSA 351 FQKSTPLYIF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

		10	20	30	40	50	
m902.pep	LHFQ		WAVGARPTVG	FFGKSFKITC			AVGHF
~000	MDCEDE	מ. ז משתאשמם	  FPIAARPTVG				
g902	MESEPEI	10	20	30	40	QAVDETPRLE 50	AVGHF 60
m902.pep	60 1/01/DAVI	70 /FACDAHTG	80 GVAVKRVYGAJ	90 วงกงกระสภาย	100 СОТОСТВОМТ	110	ממחחם:
msoz.pep	:		:::   :			:	:
g902		/FACDAHTD	GLTI KRVHGA	OVVQNGGSAF	COTOGRRXNA	VFGIMLQIAE	
		70	80	90	100	110	120
	120	130	140	150	160	170	
m902.pep			EDGLGFLRRS				
g902		:        !DAVGGGLF!	 EDGGGFLRRSI			:	
9702	Didn'i II	130	140	150	160	170	180
m902.pep	180	190 ATEGDEGDI	200 DGQVLMVVVP'	210 TOTGEFGNGV	220 acptniceon	230	א שיביד
mooz.pep	:   :						
g902	NGKGGN		GGQVLIVVVP'				
		190	200	210	220	230	240
	240	250	260	270	280	290	
m902.pep			KLRPKADVVTI				
g902		:   :     :       GAAHTDVDI	::     DLRPESDVVTI		:	FIGKITAVOG	:  :FSGTD
9202	21.2.2	250	260	270	280	290	300
	200	310	320	220	240	350	
m902.pep	300 ERRVAGO		320 AKISAKSAERI	330 FVGNARHRRK	340 CDGVVDKIAA	350 DVHNGSAFOK	STPLY
				HIPHIP			1:11
g902	ERRIAG(	OHFAHRPTCA 310	AKRPTEAAEGI			<del>-</del>	
		210	320	330	340	350	360
	360						
m902.pep	IFX						
g902	 IFX						
J: ++							

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2713>: a902.seq

- TTGCACTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
- 51 CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA

101 151 201 251 301 351 401 451 501 551 601 651 701 751 801 851 901 951 1001	AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG TGTCTGTTCG CCGTCGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAAACTCA AGGCAGGCGG TAAAACACCG TGTTCGGCGT AATGTTTCAA ATCGCGGAA AACCACGGTC TGCCTTGCGC GCCGCCCCT ATCATAATGC CGTCTGCGGC GGTTTGTTTG AGGACGGCTT GGGCTTTTTG CGGCGAGGTA ATTGTCGCCGT TGACCCAGAC CGGGATGTTC AGACGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT CGCCTTTGTA CATTTGCGTG CGCGTGCGTC CGTGGACGGC AAGGGCGGCA ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC GTCGTGCCAA CCCAAACGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT TGACCACCGC CTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC GCGCTACCGG CTTGGACATT GCAGACTTT TTAGCGGGAC AGCCCATGTT GATGTCGATA AGCTGCGCC CAAGGCTGAC GTTGTAACGC GCGCATCCG CCATCTGCTG CGGATCGCT CCGGCAACCT GCACGGCAAC AATGCCGCCT TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAAGTAT TTCTGAGCGT CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAAATCTC GGCAAAGTCG GCGGAACGGT TTTGTCGGTAA TGCCCGCCAT CGGCTCGCTG TCTCGACATTT CGCACACCGC CCAACCTGCG CCAAAATCTC GGCAAAGTCG GCGGAACGGT TTTGTCGGTAA TGCCCGCCAT TTTCAAAAAAA GTACGCCCATT GTACATTTTT TAA	
	ds to the amino acid sequence <seq 2714;="" 902.a="" id="" orf="">:</seq>	
a902.pep	THE PARTY OF THE PROPERTY OF T	
1	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR	
51 101	*NTVFGVMFQ IAEEPRSALR AAPYHNAVCG GLFEDGLGFL RRGNVAVDPD	
151	RDVOTAFGFG NQVVSRFAFV HLRARASVDG KGGNAAIFGD FGDDGQVLMV	
201	VVPTOTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV	
251	DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER	
301	RVAGQHFAHR PTCAKISAKS AERFVGNARH RRKCDGVVDK IAADVHNGSA	
351	FQKSTPLYIF *	
m902/a902 94	4.7% identity in 360 aa overlap	
m902/a902 94	10 20 30 40 50 LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	
m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD
•	10 20 30 40 50 LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD
m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD
m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60
m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60 120 RPALR
m902.pep a902 m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60 120 RPALR
m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60 120 RPALR 
m902.pep a902 m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60 120 RPALR
m902.pep a902 m902.pep	10 20 30 40 50  LHFQRIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60 120 RPALR       RSALR 120
m902.pep a902 m902.pep a902	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD        GHFVD 60 120 RPALR       RSALR 120
m902.pep a902 m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60  120 RPALR      RSALR 120  180 ASVDG
m902.pep a902 m902.pep a902	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60  120 RPALR      RSALR 120  180 ASVDG
m902.pep a902 m902.pep a902	10 20 30 40 50  LHFQRIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60  120 RPALR      RSALR 120  180 ASVDG
m902.pep a902 m902.pep a902 m902.pep	10 20 30 40 50  LHFQRIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD       GHFVD 60  120 RPALR      RSALR 120  180 ASVDG       ASVDG 180
m902.pep a902.pep a902 m902.pep a902.pep	10 20 30 40 50  LHFQRIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD             GHFVD   60  120 RPALR           RSALR   120  180 ASVDG           ASVDG 180  240
m902.pep a902 m902.pep a902 m902.pep	10 20 30 40 50  LHFQRIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD             GHFVD   60  120 RPALR           RSALR   120  180 ASVDG             ASVDG 180  240 TGLDI
m902.pep a902.pep a902.pep a902.pep a902.pep	10 20 30 40 50  LHFQRIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD             GHFVD   60  120 RPALR           RSALR   120  180 ASVDG             ASVDG 180  240 TGLDI
m902.pep a902.pep a902 m902.pep a902.pep	10 20 30 40 50  LHFQRIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD             GHFVD   60  120 RPALR           RSALR   120  180 ASVDG             ASVDG 180  240 TGLDI
m902.pep a902.pep a902.pep a902.pep a902.pep	10 20 30 40 50  LHFQRIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD             GHFVD   60  120 RPALR           RSALR   120  180 ASVDG           ASVDG   180  240 TGLDI           TGLDI
m902.pep a902.pep a902.pep a902.pep a902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD             GHFVD   60  120 RPALR           RSALR   120  180 ASVDG             ASVDG   180  TGLDI           TGLDI 240 300
m902.pep a902.pep a902.pep a902.pep a902.pep	10	GHFVD               GHFVD   60  120   RPALR             RSALR   120  180   ASVDG               ASVDG   180  TGLDI               TGLDI   240  300   SISER
m902.pep a902 m902.pep a902 m902.pep a902 m902.pep	10 20 30 40 50  LHFQRIIKCSEGIWAVGARPTVGFFGKSFKITCKHVVLRRRTVQAVDFTTCLFAV	GHFVD             GHFVD   60  120 RPALR           RSALR   120  180 ASVDG             ASVDG   180  TGLDI           TGLDI   1       TGLDI   300 SISER
m902.pep a902 m902.pep a902 m902.pep a902	10	GHFVD             GHFVD   60  120 RPALR           RSALR   120  180 ASVDG             ASVDG   180  TGLDI           TGLDI   1       TGLDI   300 SISER

m902.pep

RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF

1289

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a902
                 RVAGOHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFOKSTPLYIF
                                            330
     m902.pep
                 Х
                  1
                 Х
     a902
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2715>:
     q903.seq
              ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
           1
              TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCCGqt
          51
          101 tTGCGCTcaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
              CTGCATGCGG GCGaCatTAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
              GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG CCACAGGATT
              TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TCtgcgctcC
              ATAcgaATCG atcggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
              AGCATTCCAA AACAAATTTC CCACCCGCTC GAACGATCTG TTGAATCTGC
              GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
              GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACCAAACC AAAGTGATGT
          451
              CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
             TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
              TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
              TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAAATTTT GACGGCCATC
          701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
          751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
         801 GGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
          851 CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
         901 TATCTCAGTG TAAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
         951 TGCCGAACTG ACTGTACAAC GGCGTAAAAC CACAGGTTGG TTGGCAGAAC
        1001 TTTCCCACAA AGGATATATC GGTCGCAGTA CGGCAGATTT TAAGTTGAAA
        1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
        1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
        1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
        1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
              TATCGGCGGA CACCACACC TACGTGGCTT CGACGGTGAA ATGAGTTTGC
              CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
        1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
        1401 ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
        1451 TACGCGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA TATATTTACC
        1501 GGCCGTGCAT TGAAAAAGCC cgaatatttt cAGACGAAGA Aatgggtaac
              ggggtTTCAG gtgggttatt cgTTTTGA
This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:
     q903.pep
              MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
              LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
          51
              IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL LNLRDLEQGL ENLKCLPTAE
          101
              ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYOGNIT
              FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHRKEGGSN NYAVHYSAPF
          201
              GKWTWAFNHN GYRYHQAVSG LSEVYDYNGK SYNTDFGFNR LLYRDAKRKT
          301 YLSVKLWTRE TKSYIDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
          351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFOI GKOLFAYDTS
          401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGWY WRNDLSWOFK
              PGHQLYLGAD VGHVSGQSAK WLSGQTLAGT AIGIRGOIKL GGNLHYDIFT
              GRALKKPEYF QTKKWVTGFQ VGYSF*
     m903.seq
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2717>:

- ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTTAACTG ATGCAAATGT
- 51 CCGTTTCGAG CAACCATTGG AGAAGAACAA TTATGTCCTG AGTGAAGATG
- 101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

```
CGCAAATTTT CTTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
               AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
               CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
          301 CAaCCACAGA ATATGGATTC GGGAATTCTG AAATTACGGG TATCAGCAGG
          351 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
          401 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
              ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAAACC TGCGTCGTTT
               GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
              AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTCAGT
              ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
               TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTLTATG
          651
               TTTCATATGG ACGCGGTTTG GCGCACAAAA CGGACTTGAC TGATGCCACC
          701
               GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
               GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
              ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAACAA
          851
               TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
          901
               TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
              TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
         1001
              GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
         1051
              GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
         1101
              AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
         1151
         1201 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AYTTTAGGCA AACAGCAGTT
         1251 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
         1301 CCCAAGATAA ATTGTCAATC GGCAGCCGCT ACACCGTTCG CGGATTTGAT
         1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
         1401 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
         1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
              GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
         1551
              TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
              CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA
This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:
     m903.pep
              MORQOHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
              RKFSFLPSVL MKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAII
              QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNKFPLYRNK
          151 ILNLRDVEQG LENLRRLPSV KTDIQIIPSE EEGKSDLQIK WQQNKPIRFS
          201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
          251 GTETESGSRS YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNGKO
          301 YQSSLAAERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
          351 AELRHRAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGGDI LPGTSRMKII
              TASLDAAAPF XLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
          401
              GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
             GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng)
from N. gonorrhoeae:
    m903/g903
                                   20
                                                       40
                                                                 50
                                                                           60
                 MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL
    m903.pep
                                               1:::[]
                                                       -::: | :: | | |
                                      MATQVGGANSDEASPCFPISEVELVGEETAKFRFALNHA
     g903
                                              10
                                                        20
                                                                  30
                          70
                                    80
                                             90
                                                      100
                                                                          120
                 MKETAFKTGMCLGSNNLSRLQKAAQQILIVRGYLTSQAIIQPQNMDSGILKLRVSAGEIG
    m903.pep
                 LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKLQLTLMPGYLR
    g903
                          50
                                    60
                                              70
                                                        ឧក
                                                                  90
```

m903.pep	130 DIRYEEKRDGKSAEGS :     :::   ::   SIRIDRSNDDQTHAGI 100 110	:  :	1:1111	:                   :	11::::1:11	1:11
m903.pep	190 EE-GKSDLQIKWQQNI : ::  ::: : REPNQSDVVVQWRXRI 160 170	:   :	:: :::	111:::1		:111
m903.pep	240 250 GLAHKTDLTDATGTET :::	1:11:11	11:1 11:	:           :	:1: 1 1	1111
m903.pep	300 310  KQYQSSLAAERMLWRN  : ::::: : : : :  KSYNTDFGFNRLLYRI 280 290	: :   :::	1111:1:11	1111: 1111	:::	1::1
m903.pep	360 370 LNRWQLDGKLSYKRGT ::      :  :   IGRSTADFKLKYKHGT 340 350	::::	1 1: 11		1: :     :	1 1
m903.pep	420 430 YATAIQAQWNKTPLVA    :::       :: YDTSVHAQWNKTPLTS 400 410	:     : : :		1:11:11:	1 1:1 1:1:	11:1
m903.pep	480 490 LGADYGRVSGESAQYV       :  :  ::: LGADVGHVSGQSAKWI 460 470	:    :::	1:11 1:11	:   : : :	1:11:111	:
m903.pep g903	540 YGFNLNYSFX   :::     TGFQVGYSFX 520					

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2719>: a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAACTG	ATGCAAATGT	
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG	
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG	
151	CGCAAATTTT	CTTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA	
201	AACTGGGATG	TGTTTAGGTT	CCAATAATTT	GAGCAGGCTA	CAAAAAGCCG	
251	ÇGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTTCCCA	AGCTATTATC	
301	CAACCACAGA	ATATGGATTC	GGGAATTCTG	AAATTACGGG	TATCAGCAGG	
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG	
401	AGGGCAGTAT	TAGTGCATTC	AATAACAAAT	TTCCCTTATA	TAGGAACAAA	
451	ATTCTCAATC	TTCGCGATGT	AGAGCAGGGC	TTGGAAAACC	TGCGTCGTTT	
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA	
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTCAGT	

601 651 701 751 801 851 901 951 1001	ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG TTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAACAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGC GCCGCTCTGC AGGCTGGGAA GCCCGAATTGC GCCCCGTGC TTACCTCAAC CGTTGGCGCA  CCCCGATTGCCGCAACC TTGACCGCAA	
1101 1151	GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA	
1201	ACCGCCGGAT TGGATGCAGC GGCCCCGTTT ATGTTGGGCA AACAGCAGTT	
1251 1301	TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT ACACCGTTNG CGGATTTGAT	
1351	GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT	
1401	AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG	
1451	GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG	
1501	GGTGCAGTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC	
1551 1601	TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA	
1001	CGACCAACAC CGITTACGGC TICAACITGA ATTACAGITT CTAA	
This correspond	ds to the amino acid sequence <seq 2720;="" 903.a="" id="" orf="">:</seq>	
a903.pep		
1	MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA	
51 101	RKFSFLPSVL MKETAFKTGM CLGSNNLSRL QKAAQQILIV RGYLTSQAII QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNKFPLYRNK	
151	ILNLRDVEQG LENLRRLPSV KTDIQIIPSE EEGKSDLQIK WQQNKPIRFS	
201	IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL VHKTDLTDAT	
251	GTETESGSRS YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNGKQ	
301 351	YQSSLAAERM LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE	
401	AELRHRAYLN RWQLDGKLSY KRGTGMRQSM PAPEENGGGT IPGTSRMKII TAGLDAAAPF MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD	
451	GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM	
451 501	GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLN <u>YSF</u> *	
501	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*	
501	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap	
501	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLN <u>YSF</u> *  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLN <u>YSF</u> *  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903	GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*  8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903	8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903 m903.pep a903 m903.pep	8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903 m903.pep a903	8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903 m903.pep a903 m903.pep	8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903 m903.pep a903 m903.pep a903	8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903 m903.pep a903 m903.pep	8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	
m903/a903 98 m903.pep a903 m903.pep a903 m903.pep a903 m903.pep a903	8.4% identity in 547 aa overlap  10 20 30 40 50 60  MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL	

1293

	250	260	270	280	290	300
m903.pep	310 YQSSLAAERMLWRNF					
a903	YQSSLAAERMLWRNF 310	RFHKTSVGMK 320	LWTRQTYKYI 330	DDAEIEVQRR 340	RSAGWEAELI 350	RHRAYLN 360
m903.pep	370 RWQLDGKLSYKRGTO	нінш	1111 : 111	11111111:1	11111 11	111111
	370 430	380 440	390 450	460	410 470	420
m903.pep	TAIQAQWNKTPLVAÇ            TAIQAQWNKTPLVAÇ 430		н ний	311111111		HĪIII
	490 ADYGRVSGESAQYVS	500	510	520	530	540
m903.pep		111111111	11111111111	1111111111		
m903.pep	FNLNYSFX         FNLNYSFX					·

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2721>: g904.seq

```
ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTq qaGACGATGG
  1
     CGACCGCCG GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101
     TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151
     GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTTCCACC GCATCCGAAC
201
     CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
     CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
251
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAGCC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAATT CGGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTTGTTTT
651 TTTCGTTCAA CACGCgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
     GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGCCATCCA
     GTTTTTCACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
801
 851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
     GCCGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
 901
     TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
     TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGq gaaacgAcaa cGCCCGAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGGAAGC GCACGacGct
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
     ATCGatatTA A
```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>: g904.pep

MMOHNRFFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```
51 AGHGFVNRFA GFHRIRTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
               HTGNAVDLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
          101
               RARTDARGIG FDDAQNIIQH LRTYARACRS RAGETVGRGN EGVSAVVDVO
               QRTLRAFKQQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRSG
               VMQVLELDVV IGKDGIQFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
          301 ADFAFAARCF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVOLVDFAOO
               GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDOGMAR IVAALEAHDA
          401 AGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITYRY*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2723>:
     m904.seq
               ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGqTG GAGACGATGG
            1
           51
               CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
               TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTCGCGCCA
          101
               GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTTCCACC GCATCGGAAC
          151
               CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
          201
               CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
          251
               CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGCCGGCAT
          301
          351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
          401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAATT CGGTCGGGAA
               CGGGCCCGAA CCGACGCGC TGGTATAGGC TTTGACGATG CCCAAAACAT
          451
          501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC TGCGCCCGCC
          551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
               CAACGCACCT TGCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTTGTTTT
          601
               TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGCGGC
          651
               GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGCTCGGC
          701
               ATTGTGCAGA TGTTGCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
               GTTTTTCACG CAGTTTYTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
               CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
               GCCGATTTTG CCTTTGCCGC GCG.ATCTTC GCGGGCTTGG TCGAGCGCGA
               TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
               TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
         1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAAACTTT
         1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
         1151 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGGAAGC GCACCACGCC
         1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
         1251 CCCACTGTGC GCCGATTAST ACAACATTTT TAGCCATAGC CATATAACCT
         1301 ATCGATATTA A
This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:
     m904.pep
              MMQHNRFFSV GAGGDDGDRR AADFFNPFQI CFGVFGQCAV VLHAESGFAP
            1
           51 AGHGFVNRLA GFHRIGTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
          101 HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTY AYFVEQFGRE
          151 RARTDARGIG FDDAQNIIQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
          201 ORTLRAFKQQ FFAVFVFLVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRLG
          251 IVQMLQLDIV IGKDGIQFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
          301 ADFAFAAXIF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
          351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMAR IVAALEAHHA
          401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITYRY*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng)
from N. gonorrhoeae:
     m904/g904
                                    20
                                             30
                  {\tt MMQHNRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA}
     m904.pep
                  {\tt MMQHNRFFAVGAGGDDGDRRAADFFNPFQICFGIGRQCVVAFHADSRFAPAGHGFVNRFA}
     q904
                          10
                                    20
                                             30
                                                       40
                                                                 50
                                                                           60
```

70

80

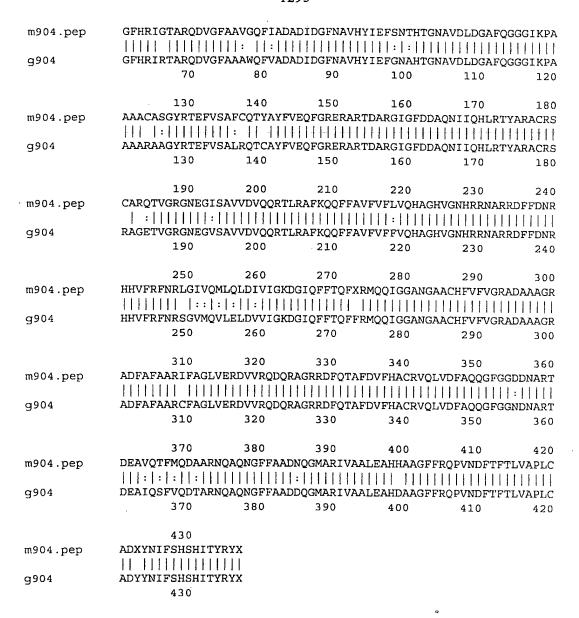
90

1.00

110

PCT/US99/09346

1295



### The following partial DNA sequence was identified in N. meningitidis <SEO ID 2725>: a904.seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTCGCTCCA
151	ACCGGGCATG	GTTTCGTAAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACCAGCC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGGCCT	ACGCCCGCGC	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAAACAGCAG	TTTTTCGCCG	TTTTTGTTTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGT	AATGCGCGGC
701	GCGACTTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

951 1001 1051 1101 1151 1201 1251 1301	TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGGAAGC GCACCACGCC TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT .TCGATATTA A
This correspond	Is to the amino acid sequence <seq 2726;="" 904.a="" id="" orf="">:</seq>
1	MMQHNRFFAV GAGGDDGDRR TADFFNPFQI CFGIGR*CVV AFHAESGFAP
51	TGHGFVNRLA GFYRIRAARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101	HTGNAVDLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTC SDFVEQFGRE
151	RARTDARGIG FDDAQNIIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201	QRTLRAFKQQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFHRLG
251	IVQMLQLDVV ISKDGIQFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
301	ADFAFAARCF SGLVERDVIR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351	GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNOGMTR IVAALEAHHA
401	SGFFRQPVND FTFTLVAPLC ADYYNIFSHS HITXRY*
<b>m904/a904</b> 91	.3% identity in 436 aa overlap
	10 20 30 40 50 60
m904.pep	MMQHNRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA
• •	
a904	MMQHNRFFAVGAGGDDGDRRTADFFNPFQICFGIGRXCVVAFHAESGFAPTGHGFVNRLA
	10 20 30 40 50 60
	70 80 90 100 110 120
m904.pep	GFHRIGTARQDVGFAAVGQFIADADIDGFNAVHYIEFSNTHTGNAVDLDGAFOGGGIKPA
	11:11:11:11:11:11:11:11:11:11:11:11:11:
a904	GFYRIRAARQDVGFAAVGQFVADADIDGFNAVHYIEFGNTHTGNAVDLDGAFQGGGIKPA
	70 80 90 100 110 120
	130 140 150 160 170 180
m904.pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNIIQHLRTYARACRS
a904	AAACASGYRTEFVSAFCQTCSDFVEQFGRERARTDARGIGFDDAQNIIQHLRAYARACRS
	130 140 150 160 170 180
	190 200 210 220 230 240
m904.pep	CARQTVGRGNEGISAVVDVQQRTLRAFKQQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
	1::111:111:1111111111111111111111111111
a904	RAGEAVGRSNEGVSAVVDVQQRTLRAFKQQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR
	190 200 210 220 230 240
	250 260 270 280 290 300
m904.pep	$\verb HHVFRFNRLGIVQMLQLDIVIGKDGIQFFTQFXRMQQIGGANGAACHFVFVGRADAAAGR $
224	
a904	HHVFRFHRLGIVQMLQLDVVISKDGIQFFTQFFRMQQIGGANGAACHFVFVGRADAAAGR
	250 260 270 280 290 300
	210 220 220 220
m004	310 320 330 340 350 360
m904.pep	ADFAFAAXIFAGLVERDVVRQDQRAGRRDFQTAFDVFHACRVQLVDFAQQGFGGDDNART
.004	ADEAEAR CECULE PRODUCE CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF
a904	ADFAFAARCFSGLVERDVIRQDQRAGRRDFQTAFDVFHACRVQLVDFAQQGFGGDDNART
	310 320 330 340 350 360
	370 380 390 400 410 420
m904.pep	
mJO4.pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAALEAHHAAGFFRQPVNDFTFTLVAPLC
a904	DE AVOTEMODA A PRODOCE E A A DROCCHED TARA LA PARTICIO DE LA COLOR DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE LA CALLER DE
аэсч	DEAVQTFMQDAARNQAQNGFFAADNQGMTRIVAALEAHHASGFFRQPVNDFTFTLVAPLC
	370 380 390 400 410 420

```
1297
                  ADXYNIFSHSHITYRYX
     m904.pep
                  41 11111111 111
     a904
                  ADYYNIFSHSHITXRYX
                         430
          not found yet
q906.seq
           not found yet
q906.pep
The following partial DNA sequence was identified in N. meningitidis <SEO ID 2727>:
m906.seq
          ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
      51 GTTTGGGGGA TTTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
     101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACTTGAC
     151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
     201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
     251 GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAACAAA
     301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA
This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:
m906.pep
       1 MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
      51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPYPENK
     101 KYEWPREEGK TK*
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2729>:
     g907.seq (partial)
            1 ATGAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT
           51 GCTGTGTGCC GCCGGCGCG TGTTGATCAG CCCGCTGGCG CACGCCGGCG
          101 CGCAACGTGA AGAAACGCtt gCCGACGATG TGGCTTCCGT GATGAGGAGT
          151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTCGACA ATCCGAAAGA
          201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTCGTCC
          251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
          301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
          351 aagcgggtac cgagctcgaa tcatatca..
This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:
     q907.pep (partial)
               MKKPTDTLPV NLQRRRLLCA AGALLISPLA HAGAQREETL ADDVASVMRS
           51 SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
          101 SRAGLDTQIV LGLIEVESGY RARIIS...
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2731>:
     m907.seq
            1 ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
              GTTGTGTGCC GCCGGTGCGT TGTTGCTCAG TCCTCTGGCG CACGCCGGCG
          101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
               TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
          151
          201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTCGTCC
          251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
          301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
          351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
          401 TGCAGGTTAT GCCGTTkTGG AAAAACTACA TCGGCAAACC GGCGCACAAC
          451 CTGTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
          501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
          551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGGCGCGTGG
          601 CGCAACCGCT GGCAGTGGCG TTGA
```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>: m907.pep

- 1 MRKPTDTLPV NLQRRRLLCA AGALLLSPLA HAGAQREETL ADDVASVMRS 51 SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
- 101 SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPXW KNYIGKPAHN

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW RNRWQWR* Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from N. gonorrhoeae: g907/m907 10 40 50 MKKPTDTLPVNLQRRRLLCAAGALLISPLAHAGAQREETLADDVASVMRSSVGSVNPPRL q907.pep MRKPTDTLPVNLQRRRLLCAAGALLLSPLAHAGAQREETLADDVASVMRSSVGSVNPPRL m907 100 20 30 40 50 70 90 80 100 110 120 VFDNPKEGERWLSAMSARLARFVPDEGERRRLLVNIQYESSRAGLDTQIVLGLIEVESGY q907.pep VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF m907 90 100 110 120 RARIIS q907.pep 11 RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL m907 130 140 150 160 170 180 The following partial DNA sequence was identified in N. meningitidis <SEO ID 2733>: a907.seq ATGAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCCT ATTGTGTGCT GCCGGCGCG TGTTGCTCAG CCCGCTGGCA CAAGCCGGCG 51 CGCAACGTGA AGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC 101 TCTGTCGGCA GCATAAATCC GCCGAGGCTG GTGTTCGACA ATCCGAAAGA GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCGTCC CCGATGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA TGCAGGTTAT GCCGTTTTGG AAAAACTACA TCGGCAAACC GGCGCACAAC 451 CTGTTCGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCCGTTTTA 501 ACGGTAGCCT CGGCAGCAAT AAATATCCGA ACGCCGTTTT GGGCGCGTGG 551 CGCAACCGCT GGCAGTGGCG TTGA This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>: a907.pep MKKPTDTLPV NLQRRRLLCA AGALLLSPLA QAGAQREETL ADDVASVMRS SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPFW KNYIGKPAHN LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW 151 201 RNRWQWR* m907/a907 97.6% identity in 207 aa overlap 10 20 30 40 50 60 m907.pep MRKPTDTLPVNLQRRRLLCAAGALLLSPLAHAGAOREETLADDVASVMRSSVGSVNPPRL MKKPTDTLPVNLQRRRLLCAAGALLLSPLAQAGAQREETLADDVASVMRSSVGSINPPRL a907 10 20 40 50 60 70 80 90 100

VFDNPKEGERWLSAMSARLARFVPEEEERRRLLVNIQYESSRAGLDTQIVLGLIEVESAF

m907.pep

a907

		70	80	90	100	110	120
		130	140	150	160	170	180
m907.pep		VGARGLMQVMI					
		1111111111					
_, a 9 0 7		VGARGLMQVMI					
		130	140	150	160	170	180
		190 2	200				
m907.pep		GSNKYPNAVLO	_			•	
a907		GSNKYPNAVLO 190 2	300 300	Х			
The following p	artial DNA s	sequence wa	s identified	d in N. goi	norrhoeae	<seq id<="" td=""><td>2735&gt;:</td></seq>	2735>:
g908.seq		•		J			
. 1	ATGAG.AAAA						
51	ATTTGTCGCA						
101	ATAAAAATAC						
151	CAAAACGGTC AAGTTATTTT						
201 251	GTAAAGTCGC						
301	GTTACAGTAC						
351	acaagtgaaa						
401	ATGTATTAGA				_		
451		AATCACAGCA					
501	A						
This correspond	ls to the amin	io acid sequ	ence <seq< td=""><td>) ID 2736;</td><td>ORF 908.</td><td>ng&gt;:</td><td></td></seq<>	) ID 2736;	ORF 908.	ng>:	
g908.pep						_	
1	MXKSRLSRYK						
51		GEVEADESY					
101	VTVPNTQTAT		C PDSIVYTD	CY RSYDVL	DVSE FSHF	SFAETS	
151	FSYQSQHTFC			1: 37		א ספס	07275
The following p	artiai DNA s	sequence wa	is identified	in IV. me	ningitiais <	SEQ ID	2/3/>:
m908.seq	, , , , , , , , , , , , , , , , , , ,	<u>ርጥሮርጥርጥ</u> ል እር	י ככזכייז ייז	አአ ሮአአአቊጥ	מאס מאס	DC 3 3 CM	
1 51	GTTTGTCACA	GTCGTCTAAC					
101	ATAAAAATAC						
151		CGCATTTGGA					
201		GGCGGACAAC					
251	GTAAAGTCGC	CGTATTCGGT	CTTTTGAA	GC GAAATG	GTAA GGTT	TATACG	
301	GTTACAGTAC	CGAATACTCA	A AACCGCTA	CT TTATTT	CCTA TTAT	CCGTGA	
351	ACAAGTGAAA						
401							
451		AATCACAGCA	A CACATTTT	GC CGAACG	ACAA AACC	ATATTA	
501	A 	oaid aaan	<cec< td=""><td>117 2720.</td><td>ODE OOD</td><td></td><td></td></cec<>	117 2720.	ODE OOD		
This correspond	is to the amin	io acid sequ	ence <sec< td=""><td>بابر کریں پ</td><td>ORF 908-</td><td>&gt;:</td><td></td></sec<>	بابر کریں پ	ORF 908-	>:	
m908.pep	MDVCDI COVV	OVELTELEVI	ቦ <i>ርህ</i> ምአውሞአአ	ביז זוריז וואזעראו	יתאאע עבוום	DITTY	
1 51	MRKSRLSQYK QNSPHLEMFD						
101	VTVPNTOTAT						
151	FSYQSQHTFC	<del></del>					
Computer analy	sis of this an	nino acid se	quence gav	e the follo	wing resul	ts:	
Homology with			-				
ORF 908 shows					predicted (	JDE (OD)	E 000 22/
		ity over a 1	ou aa uvell	ah wini g	breatetea (	MU) TAC	r. 200'lik)
from N. gonorri							
g908/m908	i						
		10	20	30	40	50	60

10 20 30 40 50 MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRXLIYQNGPHLEMFD g908.pep

m908	:        MRKSRLSQYKQXKLI 10		:  RTAAELVGVN 30			
g908.pep	70 GEVEADESYFGGQRK            GEVEADESYFGGQRK 70		11111111			11111
g908.pep	130 PDSIVYTDCYRSYDV              PDSIFYTDCYRSYDV 130				111	•
a908.seq  1 51 101 151 201 251 301 351 401 451 501  This correspond a908.pep  1 51 101 151	ATGAGAAAAA GTCGTCT ATTTGTCGCA GGTGTAA ATAAAAATAC CGCAGCC CAAAACAGTC CGCATTT AAGTTATTTT GGCGGAC GTAAAGTCC CGTATTC GTAAAGTCGC CGTATTC GTAAAGTGAAA CCTGACA ACAAGTGAAA CCTGACA ATGTATTAGA TGTGCGC TTTTCGTATC AATCACA A  Is to the amino acid so  MRKSRLSQYK QNKLIEL QNSPHLEMFD GEVEADE VTVPNTQTAT LFPLIRE FSYQSQHTFC RTTKPY*	PAAG CCAGTA CTG CAAGAA CTAT TATTT GGA AATGTT CAAC GCAAAC CGCA TTGTT CGAA TTTAG CGCA CACAT CGCA CACAT CGCA GCAAC CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACAT CGCA CACA	ATAAA CAAAACGGC AGCAFCATC GTTT TTGAT GGCG GGCAA ACGC GAAGC GAAACTATAT TATAC GGAT TATAC GGAT TATAC CGAA	AATAAAC TCA AGAGTTA GTA CACGATT ACT GAAGTAG AAG CGGTCGC GGT ATGGTAA GGT CTTCCTA TTA CTTCTAT CGT CCTTCGC TGA ACCACAA AAC  40; ORF 900  KNTAAY YFH KNTAAY YFH	TTGAGCT GGCGTTA TATTTAT CAGATGA GCTGCCG TTATACG TCCGTGA AGCTATG AACTTCG CATATTA  8.a>:  RLRLLIY RNGKVYT	739>:
m908/a908 98 m908.pep a908 m908.pep a908 m908.pep a908	3.2% identity in 166 a  10  MRKSRLSQYKQXKLI                 MRKSRLSQYKQNKLI  10  70  GEVEADESYFGGORK                GEVEADESYFGGORK 70  130  PDSIFYTDCYRSYDV               PDSIVYTDCYRSYDV 130	20 ELFVTGVTAN           :         ELFVAGVTAN 20 80 GKRGRGAAGN                     GKRGRGAAGN 80 140 VLDVREFSHFS		IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		LEMFD 60 120 REQVK

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2741>: g909.seq (partial)

- 1 atgcgtaaaa ccgtacttat cCTgaccatc tccgccgccc ttttgtcggg
  51 ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
  101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg

```
151 aaaaaqqtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
    201 caaccaaaaq cqqqqqaaqc ccgcgacgag gagagccgca acgctgggga
    251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
    301 acgggggagg ggaagcgatc ggcgagg..
This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:
g909.pep (partial)
         MRKTVLILTI SAALLSGCTW ETYQDGSGKT AVRAKCSTGT PLCWQDGRGS
      1
         KKVDCDEYGG ERRAVLRNOK RGKPATRRAA TLGKPSFRAR DGGGRVNRAE
    101 TGEGKRSAR..
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2743>:
m909.seg
      1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCCC TTTTGTCGGG
     51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
    101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
    151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
    201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
    251 AACCAAAGTT TCAAAACCGA TAA
This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:
m909.pep
         MRKTFLFLTA AAALLSGCAW ETYQDGNGKT AVRQKYPAGT PVYYQDGSYS
         KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng)
from N. gonorrhoeae:
m909/g909
                                                 40
                                                           50
                                                                     60
                              20
                                       30
            MRKTFLFLTAAAALLSGCAWETYQDGNGKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP
m909.pep
            MRKTVLILTISAALLSGCTWETYQDGSGKTAVRAKCSTGTPLCWQDGRGSKKVDCDEYGG
q909
                                        30
                                                 40
                    10
                              20
                    70
                              80
            ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
m909.pep
             11:111 11 ::
                            ::
                                   11:1: 1
            ERRAVLRNQKRGKPATRRAATLGKPSFRARDGGGRVNRAETGEGKRSAR
q909
                                                100
                              80
                                        90
                    70
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2745>:
     a909.seq
              ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCCC TTTTGTCGGG
            1
              CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
           51
          101 AAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
          151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
          201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
          251 AGCCCAAATT TCAAAACCGA TAA
This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:
     a909.pep
               MRKTFLILMT AAALLSGCAW ETYQDGNGKT AVRQKYPAGT PVYYQDGSYS
           51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQKPKFQNR *
           96.7% identity in 90 aa overlap
m909/a909
                          10
                                   20
                                             30
                                                       40
                                                                50
                  MRKTFLFLTAAAALLSGCAWETYQDGNGKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP
     m909.pep
                  MRKTFLILMTAAALLSGCAWETYQDGNGKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP
     a909
                          10
                                   20
                                             30
                                                       40
                                                                50
```

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80
                 ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
     m909.pep
                 ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX
     a909
                                   80
                         70
The following partial DNA sequence was identified in N. gonorrhoeae <SEO ID 2747>:
     q910.seq
              ATGAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
          51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
         101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
         151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
              GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTTG TCTTACCCCG
              ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA
This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:
     g910.pep
              MKKLLLAAVV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
           1.
              VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*
          51
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2749>:
     m910.seq
              ATGAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
           1
          51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
         101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
         151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
         201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTTG TCTTACCCCG
         251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA
This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:
     m910.pep
              MKKLLLAAVV SLSAAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
              VYDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng)
from N. gonorrhoeae:
     g910/m910
                                   20
                                            30
                                                      40
                                                                50
                                                                          60
                         10
                 MKKLLLAAVVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW
     q910.pep
                 MKKLLLAAVVSLSAAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDHW
     m910
                                   20
                                                                50
                         10
                                            30
                                                      40
                                   80
                                             90
                         70
                 GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
     q910.pep
                  GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
     m910
                         70
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2751>:
     a910.seq
           1 ATGAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
           51 ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
          101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
          151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGAAGT
              GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTTG TCTTACCCCG
```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>: a910.pep

ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA

1303

```
MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
              VHDVDADDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*
          95.7% identity in 94 aa overlap
                                   20
                                             30
                                                       40
                         10
                 MKKLLLAAVVSLSAAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDHW
     m910.pep
                  MKKLLLVAVVSLSAATAFAGDSAERQIYGDPYFEQNRTKAVKMLEQRGYQVHDVDADDHW
     a910
                                   20
                                             30
                                                       40
                                                                 50
                          10
                                   80
                 GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
     m910.pep
                  GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
     a910
                          70
                                   80
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2753>:
     q911.seq
              ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCTTGATCGG
            1
               CGCGGCGGCG GTTGCCTTTC TCGCTTTCCG CGTGGCGGCC GGCGCGGCGT
           51
               TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
               GGCGGTTTGA AGGTCAATGC CCCCGTCAAA TCCGCAGGCG TATTGGTCGG
          151
               GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
          201
          251
               GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
               ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
               CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT
          351
          401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
          451 GAGAAAACG CTGAGGGCGG CAATGCGGAA AAAGCCGcag aAtaa
This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:
     g911.pep
               MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
              GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLDGK YQFSSDVSAQ
               ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
               EKNAEGGNAE KAAE*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2755>:
     m911.seq
               ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
               CGCGGCGGCG GTTGCCTTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
               TCGGCGGTTC GGACAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
          101
               GGCGGTTTGA AGGTCAATGC CCCCGTCAAA TCCGCAGGCG TATTGGTCGG
               GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
               GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
          251
               ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
          301
          351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT
          401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTTGCC
               GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA
          451
This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:
     m911.pep
               MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
               GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLDGK YQFSSDVSAQ
           51
               ILTSGLLGEO YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
          151 EKNADGGNAE KAAE*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng)
from N. gonorrhoeae:
     q911/m911
                          10
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ANNOTED BEING BUT TO A AVABLA BEDVACOA A BOOCK DVTVAVVA DECDITORI VINIA DVV

g911.pep	MKKNILEFWVGLFVLIGAAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
m911	10 20 30 40 50 60
	70 80 90 100 110 120
g911.pep	${\tt SAGVLVGRVGAIGLDPKSYQARVRLDLDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT}$
m911	SAGVLVGRVGAIGLDPKSYQARVRLDLDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT 70 80 90 100 110 120
	70 00 50 100 110 120
	130 140 150 160
g911.pep	ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEGGNAEKAAEX
_	
m911	ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAEX
	130 140 150 160
The following n	partial DNA sequence was identified in N. meningitidis <seq 2757="" id="">:</seq>
	Januar DIVA sequence was identified in 14. meningulais (SEQ 1D 2757).
a911.seq 1	ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51	CGCGGCGGCG GTTGCCTTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101	TCGGCGGTTC GGACAAAACT TACGCCGTTT ATGCCGATTT CGGCGACATC
151	GGCGGTTTGA AGGTCAATGC CCCCGTCAAA TCCGCAGGCG TATTGGTCGG
201	GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
251 301	ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351	CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT
401	CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTTGCC
451	GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA
rot *	to the amine acid convenes < SEO ID 2758: OPE 011 a>:
	ds to the amino acid sequence <seq 2758;="" 911.a="" id="" orf="">:</seq>
a911 pep	MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
· 1	TO THE PARTY OF THE PROPERTY OF THE PARTY OF
101	
151	EKNADGGNAE KAAE*
011/.011 1/	00 00/ identity in 164 on overlan
m911/a911 1	00.0% identity in 164 aa overlap  10 20 30 40 50 60
m911.pep	
mair.pep	
a911	MKKNILEFWVGLFVLIGAAAVAFLAFRVAGGAAFGGSDKTYAVYADFGDIGGLKVNAPVK
	10 20 30 40 50 60
	70 80 90 100 110 120
m911.pep	
moii.pep	
a911	SAGVLVGRVGAIGLDPKSYQARVRLDLDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
	70 80 90 100 110 120
m911.pep	130 140 150 160
m911.pep	130 140 150 160 ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAEX
m911.pep a911	130 140 150 160 ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAEX
-	130 140 150 160 ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAEX
-	130 140 150 160 ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAEX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2759>: g912.seq

- 1 gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
  - 51 CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
  - 101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```
151 CGCCCAAAAG CCGAAGCCTA TGCGGTTCCC TATTTCGATT TCCAACGTAT
              GACCGCATTG GCGGTCGGCA ACCCTTGGCG TACCGCGTCC GACGCGCAAA
         201
              AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
         251
              GGCACGATGC TGAAATTCAA AAACGCGACC GTCAACGTCA AAGACAATCC
         301
              CATCGTCAAT AAGGGCGGCA AGGAAATCGT CGTCCGTGCC GAAGTCGGCA
         351
              TCCCCGGTCA GAAGCCCGTC AATATGGACT TTACCACCTA CCAAAGCGGC
              GGCAAATACC GTACCTACAA CGTCGCCATC GAAGGCACGA GCCTGGTTAC
              CGTGTACCGC AACCAATTCG GCGAAATCAT CAAAGCCAAA GGCATCGACG
              GGCTGATTGC CGAGTTGAAA GCCAAAAACG GCGGCAAATA A
This corresponds to the amino acid sequence <SEQ ID 2760; ORF 912.ng>:
     g912.pep
              VKKSSFISAL GIGILSIGMA FASPADAVGQ IRQNATQVLT ILKSGDAASA
              RPKAEAYAVP YFDFQRMTAL AVGNPWRTAS DAQKQALAKE FQTLLIRTYS
          51.
              GTMLKFKNAT VNVKDNPIVN KGGKEIVVRA EVGIPGQKPV NMDFTTYQSG
          101
              GKYRTYNVAI EGTSLVTVYR NQFGEIIKAK GIDGLIAELK AKNGGK*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2761>:
              ATGAAAAAT CCTCCCTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
              CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAGCCAA ATCCGTCAAA
          51
          101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA ACGGCGATGC CAACACCGCT
              CGCCAAAAAG CCGAAGCCTA TGCGATTCCC TATTTCGATT TCCAACGTAT
          151
              GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
          201
              AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
          251
              GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
          301
              CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
              TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
              GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
              CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCGTGGACG
              GACTGATTGC CGAGTTGAAA GCCAAAAACG GCGGCAAATA A
This corresponds to the amino acid sequence <SEQ ID 2762; ORF 912>:
     m912.pep
              MKKSSLISAL GIGILSIGMA FAAPADAVSQ IRQNATQVLS ILKNGDANTA
              ROKAEAYAIP YFDFQRMTAL AVGNPWRTAS DAQKQALAKE FQTLLIRTYS
              GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
              GKYRTYNVAI EGASLVTVYR NQFGEIIKAK GVDGLIAELK AKNGGK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng)
from N. gonorrhoeae:
     g912/m912
                                                                         60
                                   20
                                             30
                                                      40
                                                                50
                  VKKSSFISALGIGILSIGMAFASPADAVGQIRQNATQVLTILKSGDAASARPKAEAYAVP
     q912.pep
                  MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
     m912
                                   20
                                             30
                                                      40
                                                                50
                         10
                                             90
                                                     100
                                                               110
                                   80
                  YFDFQRMTALAVGNPWRTASDAQKQALAKEFQTLLIRTYSGTMLKFKNATVNVKDNPIVN
     q912.pep
                  YFDFQRMTALAVGNPWRTASDAQKQALAKEFQTLLIRTYSGTMLKLKNANVNVKDNPIVN
     m912
                                                               110
                                                                        120
                                             90
                                                     100
                          70
                                   80
                                                     160
                                                               170
                                            150
                         130
                                  140
                  KGGKEIVVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEIIKAK
      g912.pep
                  KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEIIKAK
      m912
                                            150
                                                     160
                                                               170
                                  140
                         130
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190 q912.pep GIDGLIAELKAKNGGKX

GVDGLIAELKAKNGGKX m912 190

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The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2763>:
     a912.seq
               ATGAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
           51 CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAAACCAA ATCCGTCAAA
          101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
          151 CGCCAAAAAG CCGAAGCCTA TGCGATTCCC TATTTCGATT TCCAACGTAT
          201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAAA
          251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
               GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
          351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
          401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
          451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
          501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCGTGGACG
          551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A
This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:
     a912.pep
               MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
               RQKAEAYAIP YFDFQRMTAL AVGNPWRTAS DAQKQALAKE FQTLLIRTYS
          101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
          151 GKYRTYNVAI EGASLVTVYR NQFGEIIKAK GVDGLIAELK AKNGSK*
m912/a912 98.0% identity in 196 aa overlap
```

a912

Z/a912 90.0	776 luchuty III 190	aa o voi iap				
	10	20	30	40	50	60
m912.pep	MKKSSLISALGIGI	LSIGMAFAAP	ADAVSQIRQN	NATQVLSILKN	GDANTARQKA	EAYAIP
• •	[[]]	1111111111	1111:1111	13   1   1   1   1   1   1   1   1   1	1111111111	
a912	MKKSSFISALGIGI	LSIGMAFAAP	ADAVNQIRQN	NATQVLSILKS	GDANTARQKA	MEAYAIP
	10	20	30	40	50	60
	70	80	90	100	110	120
m912.pep	YFDFQRMTALAVGN	PWRTASDAQN	QALAKEFQII	TELETISCIME	KTWIMMINAILA	DNETAN
		1111111111			11111111	11111
a912	YFDFQRMTALAVGN	IPWRTASDAQK	QALAKEFQTI	LLIRTYSGTML	KLKNANVNV	KDNPIVN
	70	80	90	100	110	120
					•	
	130	140	150	160	170	180
m912.pep	KGGKEIIVRAEVGV	PGQKPVNMDF	TTYQSGGKYI	RTYNVAIEGAS	LVTVYRNQFO	SEIIKAK
	111111111111111	1111111111		[]]]]]		
a912	KGGKEIIVRAEVGV	PGQKPVNMDE	TTYQSGGKYI	RTYNVAIEGAS	LVTVYRNQFO	SEIIKAK
	130	140	150	160	170	180
	100					
	190			•		
m912.pep	GVDGLIAELKAKNO	GKX				
		:11				

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2765>: g913.seq

GVDGLIAELKAKNGSKX 190

```
1 atGAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51 CCCTGCATTT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCT
151 GCCGCGCGC GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGCGCGACGT GGTCAGTTTC GGCAGCAATA
251 TCTTGCGTTT GGAcatCAAA cgcgcAAGcg aAGACCtcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGgcqGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctqGAAAaa cagcaATTAT TTCGTqttqc CCGtcttagg cccgtccacc
```

```
451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
                501 tategtttte catacecetg eeggaegetg GGgcaegaet gCCGCTGCCG
                551 CCGTcaqtac gcgcqaaggc ctcctcgatt tgaccgacag TCtggacgaa
                601 qccqccatCG ACAAATACAG CTACACGCGc gacctctata tqAAAGTCCG
                651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
                701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
                        CCCGCCGTTC ACGAAGATTC CGTATCCGAA ACACAGGCAG AAGCAGCAGG
                751
                        GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA
                801
This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:
        g913.pep
                        MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
                  51 AARGYRKVTP KPVRAGVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
                101 INTTFGLGGL IDIAGAGGVP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
                151 VRDALGTGIT SVYPPKNIVF HTPAGRWGTT AAAAVSTREG LLDLTDSLDE
                201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
                251 PAVHEDSVSE TQAEAAGEAE TQPGTQP*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2767>:
        m913.seq
                        ATGAAAAAA CCGCCTATGC CTTCCTCCTG CTGATCGGGT TCGCTTCCGC
                   1
                  51 CCCTGCATTT GCCGAAACCC GCCCCGCCGA CCCTTATGAA GGCTACAACC
                101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCT
                        GCCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
                        GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCAGCTTC GGCAGCAATA
                        TCTTGCGCTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
                301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
                351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCCTCGTGGG
                401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
                451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
                        TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
                501
                        CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
                        GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
                601
                        TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
                        ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGC GGAAACTGCC
                 701
                        GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
                751
                 801 CGAAACGCAA CCTGGAACAC AACCTTAA
This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:
        m913.pep
                        MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
                        AARGYRKVAP KPVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
                         INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLGPST
                        VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
                        AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
                        VQEDSVSETQ AEAAGEAETQ PGTQP*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 913 shows 94.9% identity over a 277 as overlap with a predicted ORF (ORF 913.ng)
from N. gonorrhoeae:
        g913/m913
                                           10
                                                           20
                                                                            30
                                                                                            40
                                                                                                             50
                                                                                                                             60
                              MKKTAYAILLLIGFASAPAFAETRPADPYEGYNRAVSKFNDQADRYIFAPAARGYRKVTP
        g913.pep
                              MKKTAYAFLLLIGFASAPAFAETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP
        m913
                                           10
                                                            20
                                                                            30
                                                                                            40
                                                                                                             50
                                            70
                                                            80
                                                                            90
                                                                                          100
                                                                                                           110
                                                                                                                            120
                              {\tt KPVRAGVSNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVPAGGGVPAGGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVPAGGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVPAGGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVPAGGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVPAGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVPAGGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVPAGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGVPAGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGGVPAGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGGVPAGGNFFNNLRDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGGVPAGGNFFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLRDVFNNLR
        g913.pep
                              m913
                              KPVRAGVSNFFNNLCDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGIP
                                                            80
                                                                            90
                                                                                                           110
                                                                                                                            120
                                                                                          100
```

g913.pep m913	130 140 150 160 170 180 DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT
g913.pep m913	190 200 210 220 230 240  AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL  ::
g913.pep m913	250 260 270  VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX
a913.seq  1 51 101 151 201 251 301 351 401 451 501 551 601 651 701 751	ATGAAAAAA CCGCCTATGC CTTCCTCCTG CTGATCGGT TCGCTTCCGC CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC GCCCGCCGC ACCGTACAT TTTCGCCCCT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCT GCGCGCGCGG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGCGG GCTACCAAACC TGTGCGACGT GGTCAATTT TTTAACAACC TGTGCGACGT GGTCAGCTTC GGCAGCAATA ACACCTTGGT GGCGGCGAATA ACACCTTGG CCGCACCGC GACAATAAAA ACACCTTGGG CGAACCGTTC CGGCACGGG GATGGAAAAA ACACCTTGGG CGACACGTTT GCTCGCGGG GATGGAAAAA ACACCTTGGG CGACACGTTT GCTCGCGGG GGTCGGCC GGCCGCGAAGC ACGCTTTAGG GCCGCCAAGC ACCCTCTAGG GCCGCAACG CGCCCAAGAA ACACCTTGGC CGGCACGGC CGCTCGCCA GGCACACGTTT CCGCCAAGAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC GCCCCACCAC GGCTCACCC GCCCCAAGAA CAGCAAATACAA CAGCAATTACC TCCGTTTATT CGCCCAAGAA CCCGCCAACCAC CTCGCCGA ACCCTCACC GACCACCTT TGACAGACT GCCGTATCCG CCGCCAACAA ACAAATACAG CTACAACGCC GACCTCTATA TGAAAGTCCG CTCGCCGA ACCCTGCCGA CCCTGCCGA ACCCTGCCGA ACCCTCTATA   Is to the amino acid sequence <seq 2770;="" 913.a="" id="" orf="">:   MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP AARGYRKVAP KPVRAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG INTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWNSNY FVLPVLGPST VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA</seq>
251 m913/a913 10 m913.pep a913	VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*  00.0% identity in 275 aa overlap  10 20 30 40 50 60  MKKTAYAFLLLIGFASAPAFAETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP
m913.pep a913	70 80 90 100 110 120 KPVRAGVSNFFNNLCDVVSFGSNILRLDIKRASEDLVRVGINTTFGLGGLIDIAGAGGIP
m913.pep a913	130 140 150 160 170 180  DNKNTLGDTFASWGWKNSNYFVLPVLGPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT

```
170
                                                       180
                       140
                               150
                                       160
               130
                               210
                                       220
                                               230
                                                       240
                       200
               190
          AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE
m913.pep
          AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDELVE
a913
                                       220
                               210
                       200
               190
                       260
                250
          SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX
m913.pep
          SAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPGTQPX
a913
                               270
                        260
                250
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2771>:

```
q914.seq
         ATGAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
      1
         ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
      51
     101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
         TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
         GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
     201
         GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
     251
         ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC
     301
         GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
         GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTC TGCCGATTCG
          taggetTCGA CGATTTTTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
         GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
         CGTCTTTCAA TCCCGATTTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
         TCGCCGGTAA TGACGGCTTT CGCgccgaag ccGATGCGGG TCAGGAACAT
          TTTCATTTGT TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
          CGCCGTTGAG CGTCCTGCCG CGCATATAG
```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>: q914.pep

- MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
- FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA 51
- IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS 101
- *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
- SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

The following partial DNA sequence was identified in N. meningitidis <SEO ID 2773>:

m914.seq ATGAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC 1 ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC 51 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT 101 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC 351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT 401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC

- 451 GATTCGTAGG CTTCGACGAT TTTTTGCACC AAAGGATGCC GGACAACGTC
- 501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
- 551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTTGG
- 601 CTGGTGTCGC CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TGCGGGTCAG GAACATTTTC ATTTGTTCGG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
- TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>: m914.pep

- MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
- FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA 51
- 101 IRCRKFDXCI GWTDKETDTD TELGFRICFS LPDFPCIGFQ TALECQSCSA

151 DSXASTIFCT KGCRTTSSPV KVWKYSPSTL CSFSRASFNP DLMFLGRSIW

201 LVSPVMTAFA PKPMRVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from N. gonorrhoeae:

g914/m914

g914.pep				111111111	40 AVLESGGNTV          AVLESGGNTV 40	1111111111	
g914.pep		111111111		111111111	100 GDEAIRCRKF          EDEAIRCRKF 100	1111111111	
g914.pep	:		1111111111	1111111111	160 IFCTRGCRTT     :     IFCTKGCRTT 160		:
g914.pep					220 RNIFICSGVV          RNIFICSGVV 220		
g914.pep	240 LPRIX       LPRIX		. •				

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2775>:

a914.seq 1 ATGAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC 51 ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC 101 ACCGTGTCGC CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT 151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA 201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC 251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA 301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTTGGACGG ATAAAGAAAC 351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTC TGCCGATTCG 401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTC TGCCGATTCG 451 TAGGCTTCGA CGATTTTTG CACCAAAGGA TGCCGGACAA CGTCTTCGCC 501 GGTAAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAGT TTCTCACGCG 551 CATCTTTAA TCCCGATTTG ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG 601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT 651 TTTCATTTGT TCGGGCGTGG TGTTTTGCGC TTCGTCGAGG ATGATGTATG 701 CGCCGTTGAG CGTCCTGCCG CGCATATAG

## This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGSNTVKIDL 51 FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA 101 151 IRCRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFNPDL MFLGRSIWLV 201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```
m914/a914 98.4% identity in 244 aa overlap
```

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAA	MPAFADRIGD	LEARLAQLEH	RVAVLESGGNI	VKIDLFGSNS	TMYVC
• •	[[]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]		11111111111	[] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ] [ ]	11111111111	11111
a914	MKKCILGILTACAA	MPAFADRIGD	LEARLAQLEH	RVAVLESGSNI	'VKIDLFGSNS	TMYVC
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDF	RNEGVARQKVR	QACNRETSAMI	FCEDEAIRCRE	(FDXCIGWTDK	CETDTD
	1111111111111				111111111	111
a914	SVTPFQKTFEASDF	RNEGVARQKVR	QACNRETSAMI	FCEDEAIRCRE	(FDXCIGWTDK	KETD
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGFRICFSLPDE	PCIGFQTALE	CQSCSADSXAS	STIFCTKGCRI	TSSPVKVWKY	SPSTL
			11111111111	11111111111	111111111	1111
a914	TELGFRICFSLPDE	PCIGFQTALE	CQSCSADSXAS	STIFCTKGCRI	TSSPVKVWKY	SPSTP
	120 130	140	150	160	170	
	190	200	210	220	230	240
m914.pep	CSFSRASFNPDLME	LGRSIWLVSP	VMTAFAPKPMI	RVRNIFICSGV	VFCASSRMMY	APLSV
	11111111111111		111111111	1111111111	1111111111	11111
a914	CSFSRASFNPDLME	FLGRSIWLVSP	<b>VMTAFAP</b> KPME	RVRNIFICSGV	VFCASSRMMY	'APLSV
	180 190	200	210	220	230	
m914.pep	LPRIX					
	11111					
a914	LPRIX					
W 7 1 1	240					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2777>:

```
q915.seq
      1 ATGAAGAAAA CCCTGTTGGC AATTGTTGCC GLTTTCGCCT TAAGTGCCTG
      51 CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
    101 qttcqgtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
    151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
    201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
    251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
    301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
    351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
     401 TCGGCAACAA GGAGCAGGCT GAAAAATTTG CAAAGGATAA AGGCGGCAAG
     451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```
MKKTLLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 1
51 KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
```

VVGFDDMPDA YIFK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2779>: m915.seq

1	ATGAAAAAAA	CCCTGTTGGC	AATTGTTGCC	GTTTCCGCCT	TAAGTGC.tG
51	CCGGCAGGCG	GAAGAGGGAC	CGCCGCCTTT	ACCcCGGCAG	ATTAGCGACC
101	GTTCGGTCGG	ACACTATTGC	AGTATGAACC	TGACCGAACA	CAACGGCCCC
151	AAAGCCCAGA	TTTTCTTGAA	CGGCAAACCC	GATCAGCCCG	TtTGGTTCTC
201	CACCATCAAG	CAGATGTTCG	GCTATACCAA	GCTGCCCGAA	GAGCCTAAAG
251	GCATCCGCGT	GATTTACGTT	ACCGATATGG	GCAATGTTAC	CGATTGGACG
301	AATCCCAATG	CCGACACGGA	GTGGATGGAT	GCGAAAAAAG	CCTTTTACGT
351	CATCGACAGC	GGCTTTATCG	GCGGTATGGG	TGCGGAAGAC	GCGCTGCCGT
401	TCGGCAACAA	AGAGCAGGCT	GAGAAATTTG	CAAAGGATAA	AGGCGGTAAG

a915

451				TATATTTTCA		
This correspond	s to the amin	o acid seque	ence <seq i<="" td=""><td>D 2780; ORI</td><td>F 915&gt;:</td><td></td></seq>	D 2780; ORI	F 915>:	
m915.pep		HENT OVERON	EEGDDDI DDO	Tabbananya	COM TRUNCS	
1 51					SMNLTEHNGP TDMGNVTDWT	
101	-				EKFAKDKGGK	
151	VVGFDDMPDT	YIFK*		·		
Computer analy	sis of this am	iino acid seq	uence gave	the following	g results:	
Homology with						
ORF 915 shows	97.0% ident	ity over a 16	64 aa overlap	with a pred	icted ORF (C	)RF 915.ng)
from N. gonorrh	поеае:					
m915/g915						
		10	20 3	0 40	50	60
m915.pep	MKKTLLA				SMNLTEHNGPKA	
	1111111.		1111:11111			
g915	MKKTLLA		-	•	SMNLTEHNGPK/	_
		10	20 3	0 40	50	60
		70	80 9	0 100	110	120
m915.pep	DQPVWFS	rikomfgytkl	PEEPKGIRVIY	VTDMGNVTDWT	NPNADTEWMDA	KKAFYVIDS
	,,,,,,,	[:	1111111111		11111111	
g915	DQPVWFS	-	PEEPKGIRVIY 80 9		NPNADTEWIDAF 110	(KAFYVIDS 120
		70		0 100	110	120
	1	130 1	40 15	0 160		•
m915.pep	GFIGGMG/	AEDALPFGNKE	QAEKFAKDKGG	KVVGFDDMPDT	YIFKX	
~015	CELCOMO			: KVVGFDDMPDA		
g915			40 15		IIFAA	
The following p	artial DNA s	equence was	s identified i	n <i>N. meningi</i>	itidis <seq i<="" td=""><td>D 2781&gt;:</td></seq>	D 2781>:
a915.seq		_			_	
1				GTTTCCGCCT		
51 101				ACCCCGGCAG TGACCGAACA		
151					TTTGGTTCTC	
201				GCTGCCCGAA		
251 301				GCAATGTTAC GCGAAAAAAG		
351				TGCGGAAGAC		
401				CAAAGGATAA		
451	GTTGTCGGTT	TCGACGATAT	GCCTGATACC	TATATTTTCA	AATAA	
This correspond	s to the amin	o acid seque	ence <seo i<="" td=""><td>D 2782: ORI</td><td>F 915 a&gt;·</td><td></td></seo>	D 2782: ORI	F 915 a>·	
a915.pep	b to the tarm	.0 4014 5044	524	2,02, 010	. 715.0	
1	MKKTLLAIVA	VSALSACRQA	EEGPPPLPRQ	ISDRSVGHYC	SMNLTEHNGP	
51				EPKGIRVIYV		
101 151	VVGFDDMPDT		GFIGGMGAED	ALPFGNKEQA	EKFAKDKGGK	
131	VVGLBBIILBI	1111				
m915/a915 99	.4% identity	in 164 aa ov	/erlap			
	•		20 3		50	60
m915.pep					SMNLTEHNGPK/	
a 915					 SMNLTEHNGPK/	
4220	×		20 3		50	60
		70	00 0	0 100	110	100
m915.pep	DOPVWES	· -	80 9 PEEPKGIRVIY		110 NPNADTEWMDAE	120 KKAFYVIDS
					1111111111	

DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS

```
70
                         80
                                 90
                                        100
                                                110
                                                        120
                130
                        140
                                150
          GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX
m915.pep
          GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDDMPDTYIFKX
a915
                        140
                130
                                150
```

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2783>: 9917.seq
```

```
ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttqcaqc
  1
     gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
  51
     accaaAacqt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
     ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
     GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
 201
     GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
 251
     GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
 301
     TCTCAACCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
 351
     AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
     GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
     GGATTTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
     TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACTAT
     TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
     CGCCCTGCTC AAGAAAAACC GCCCCAATAT CAAACGCTTT ACTTCGTCCG
 651
 701
     GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
     GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
 751
 801 GGAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
 901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
 951 CQTEACCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A
```

# This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

```
1 MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51 TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLDSA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
```

251 GGDLNIAKRR AEEAGGKEKI RVMMPKEGVG IWVDSFVIPK DAKNVANAHK

301 YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN

351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2785>: m917.seq

```
ATGACCAAAC ATCTGCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGCAGC
 1
    GTGCGCCGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
   GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
   GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
301
    CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
    AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
    GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
    GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
    TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACTAT
    TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651
    CGCCCTACTC AAGAAAAACC GCCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
```

751 GGCGGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA 801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG 851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG 1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>: m917.pep MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE 51 TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT 151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLK QCGISYLDSA AEIYPMVLNY 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF 251 GGDLNIAKRR AEEAGGKEKI RVMMPKEGVG IWVDSFVIPK DAKNVANAHK 301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. gonorrhoeae

351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae:* 

m917/g917

m917.pep	10 MTKHLPLAVLTA  :        MVKHLPLAVLTA	1111111111111	1111111111	ÎHHHHH		
_	10	20	30	40	50	60
m917.pep	70 IKVTYDVYDSDE	111111111111		ШТИНЦ	110 YQKIDKSLIPN       :    YQKIDKSMIPN	
9917	70	80	90	100	110	120
m917.pep g917	130 EMMRLMDGVDPG          EMMRLMDGVDPD	111111111111	ШИШШ			11 111
m917.pep g917	190 QCGISYLDSAAE           QCGISYLDSAAE 190	111111111111		111111111	11111111111	
m917.pep g917	250 RGDTCVTIGFGG          RGDTCVTIGFGG 250					
m917.pep	310 YINDFLDPEVSA           YINDFLDPEVSA 310		:		: 111111111	111:11

```
ALKFMVRQWQDVKAGKX
m917.pep
            ALKFMVRQWQDVKAGKX
g917
                   370
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2787>:
              ATGACCAAAC ATCTGCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGCAGC
              GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
          51
              ACCGAAACGT ATTGAAAATT TACAACTGGT CGGAATACGT CGATCCGGAA
         101
         151
              ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
              GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCTG
              GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
         251
              GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
         301
              CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
         351
              AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
         401
         451
              GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAGTG
         501
              GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
              TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACTAT
         551
              TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
         601
              CGCCCTACTC AAGAAAAACC GCCCCAATAT CAAACGCTTT ACTTCGTCCG
         651
              GCTTTATCGA TGATTTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
         701
              GGCGGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
         751
              GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
              ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
         851
              TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
         901
              CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
              AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
              AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
        1051
              CCAGTGGCAG GATGTGAAGG CGGGGAAATA A
        1101
This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:
     a917.pep
              MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
           1
              TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
          51
          101
              AGAYOKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
              ERVKKALGTD KLPDNOWDLV FDPEYTSKLK QCGISYLDSA AEIYPMVLNY
         151
              LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
              GGDLNIAKRR AEEAGGKEKI RVMMPKEGVG IWVDSFVIPK DAKNVANAHK
          251
              YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
          301
              SFIMVPIQPA ALKFMVRQWQ DVKAGK*
          351
                 99.7% identity in 376 aa overlap
     m917/a917
                                   20
                                            30
                                                     40
                 MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG
     m917.pep
                 MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG
     a917
                         10
                                   20
                                            30
                                                               50
                                                                         60
                                                     40
                         70
                                   80
                                            90
                                                    100
                                                              110
                                                                        120
                 IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNAFVGROIKAGAYOKIDKSLIPNYKHLNP
     m917.pep
                 a917
                 IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNAFVGRQIKAGAYQKIDKSLIPNYKHLNP
                         70
                                  80
                                            90
                                                    100
                                                              110
                                                                        120
                        130
                                  140
                                           150
                                                     160
                                                              170
                                                                        180
                 EMMRLMDGVDPGHEYAVPFYWGTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLK
     m917.pep
                 EMMRLMDGVDPGHEYAVPFYWGTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLK
     a917
                        130
                                  140
                                           150
                                                    160
                                                              170
                                                                        1.80
```

m917.pep

200

210

QCGISYLDSAAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA

a917	QCGISYLDSAAEI	YPMVLNYLGKI	NPNSSNTEDIF	REATALLKKNF	PNIKRFTSS	GFIDDLA
	190	200	210	220	230	240
	250	260	270	280	290	300
m917.pep	RGDTCVTIGFGGDI	LNIAKRRAEE	AGGKEKIRVMN	1PKEGVGIWVD	SFVIPKDAK	NVANAHK
		нини				
a917	RGDTCVTIGFGGDI	LNIAKRRAEE	AGGKEKIRVMN	1PKEGVGIWVI	SFVIPKDAK	NVANAHK
	2.50	260	270	280	290	300
	310	320	330	340	350	360
m917.pep	YINDFLDPEVSAKI	NGNEVTYAPS	SKPARELMEDE	EFKNDNTIFPT	'EEDLKNSFII	MVPIQPA
	111111111111					111111
a917	YINDFLDPEVSAKI	NGNFVTYAPS	SKPARELMEDE	FKNDNTIFPT	EEDLKNSFI	ATQITAN
432.	310	320	330	340	350	360
	370					
m917.pep	ALKFMVRQWQDVK/	AGKX				
	1111111111111	1111				
a917	ALKFMVRQWQDVK	AGKX				
	370					

The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 2789>: g919.seq

```
ATGAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGCatCG CCGCCgccAT
  1
     CctcqCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
 51
     CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
     GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
     GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
     TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
     TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGGGGTT
     TTTTGAACGC TATTTCACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTTAC GGTATTCCCG ACGATTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGAC ggGGAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaggCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCAt cggaTacgcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGCtcgggc agACCTCGAT GCAGGgcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCCAGC TATATCTTTT
     TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
     ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
     CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
     CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA
```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>: g919.pep

۳					
1	MKKHLLRSAL	YGIAAAILAA	CQSRSIQTFP	QPDTSVINGP	DRPAGIPDPA
51	GTTVAGGGAV	YTVVPHLSMP	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAOAFQTPVH	SFQAKRFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGDGR
151	RTERARFPIY	GIPDDFISVP	LPAGLRGGKN	LVRIRQTGKN	SGTIDNAGGT
201	HTADLSRFPI	TARTTAIKGR	FEGSRFLPYH	TRNQINGGAL	DGKAPILGYA
251		IQGSGRLKTP			
301		KAYMRQNPQR			
351		IDRHYITLGA			
		GDEAGELAGK			
401	AVKVDIEWGI	GDAMBAMIN	SWIIGI AUST	DI MOLDEL DIK	• "

The following partial DNA sequence was identified in N.meningitidis <SEQ ID 2791>:

m919.seq ATGAAAAAT ACCTATTCCG CGCCGCCTG TACGGCATCG CCGCCGCAT 1 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA 101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC 151 GGAACGACGG TCGGCGGCGG CGGGGCCGTC TATACCGTTG TACCGCACCT 201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG 301 TGCGCCCAAG CCTTTCAAAC CCCCGTCCAT TCCTTTCAGG CAAAACAGTT 351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG 451 CGGACGGCAC AAGCCCGCTT CCCGATTTAC GGTATTCCCG ACGATTTTAT 501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA 551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA 601 CATACCGCCG ACCTCTCCcG ATTCCCCATC ACCGCGCGCA CAACAGCAAT 651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC 701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTTACGCC GAAGACCCTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG 851 AACATCCYTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC 901 AAACTCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA 951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCCAGC TATATCTTTT 1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC 1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC 1101 CTTGGGTGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG 1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC 1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT 1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG GTATGAAGCC CGAATACCGC CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2792; ORF 919>: m919.pep

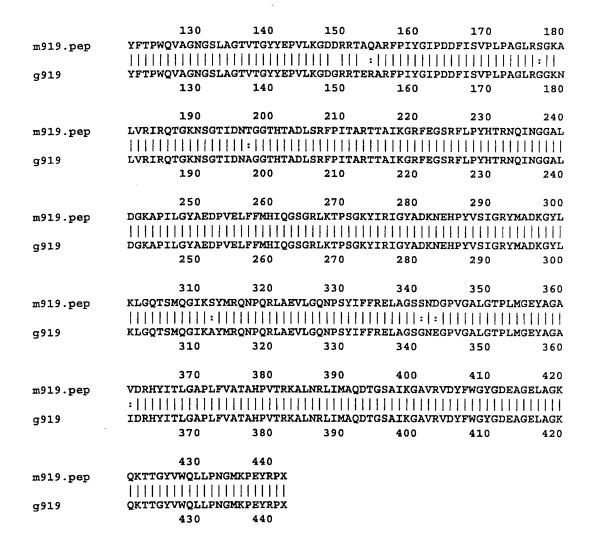
MKKYLFRAAL YGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMRQNPQR LAEVLGQNPS YIFFRELAGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*: m919/g919

	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIA	-				
			1111111111	11111111:	1111111111	:
g919	MKKHLLRSALYGIA	AAILAACQSR	SIQTFPQPDT	SVINGPDRPA	GIPDPAGTTV	/AGGGAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAA	<b>QDFAKSLQSF</b>	RLGCANLKNR	QGWQDVCAQA	FQTPVHSFQ	KQFFER
		[	1111111111	1111111111	1111111111	1:111
g919	YTVVPHLSMPHWAA	QDFAKSLQSF	RLGCANLKNR	.QGWQDVCAQA	.FQTPVHSFQ <i>i</i>	KRFFER
	70	80	90	100	110	120

WO 99/57280

1318



### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2793>:

```
a919.seg
          ATGAAAAAT ACCTATTCCG CGCCGCCCTG TGCGGCATCG CCGCCGCCAT
       1
          CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
      51
    101
          CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
          GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
     151
          GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
     201
          TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
     251
          TGCGCCCAAG CCTTTCAAAC CCCCGTCCAT TCCGTTCAGG CAAAACAGTT
     301
          TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
     351
          CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
     401
     451
          CGGACGCAC AAGCCCGCTT CCCGATTTAC GGTATTCCCG ACGATTTTAT
          CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
     501
          TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
     551
     601
          CATACCGCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
     651
          CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
     701
          AAATCAACGG CGGCGCTT GACGGCAAAG CCCCGATACT CGGTTACGCC
          GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
     751
          GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
     801
          AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
     851
          AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
     901
     951
          CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCCAGC TATATCTTTT
    1001
          TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
          ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
    1051
    1101
          CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
```

	1317
1151 1201 1251 1301	CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGCCGAGCTT CTGCCCAACG GTATGAAGCC CGAATACCGC CCGTAA
•	s to the amino acid sequence <seq 2794;="" 919.a="" id="" orf="">:</seq>
a919.pep  1  51  101	MKKYLFRAAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 201 251 301	RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT HTADLSQFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL KLGQTSMQGI KAYMQQNPQR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 401	TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*
m919/a919	98.6% identity in 441 aa overlap 10 20 30 40 50 60
m919.pep	MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
a919	MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV 10 20 30 40 50 60
m919.pep	70 80 90 100 110 120 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
a919	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER 70 80 90 100 110 120
m919.pep	130 140 150 160 170 180 YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
a919	
m919.pep	190 200 210 220 230 240 LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
a919	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL 190 200 210 220 230 240
m919.pep	250 260 270 280 290 300 DGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
a919	DGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL 250 260 270 280 290 300
m919.pep	310 320 330 340 350 360 KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
a919	
m919.pep	370 380 390 400 410 420 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
a919	

430 QKTTGYVWQLLPNGMKPEYRPX m919.pep a919 QKTTGYVWQLLPNGMKPEYRPX 430 440

Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2795>:
     g920.seq
               (partial)
              ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
                 CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
           51
                 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
          101
                 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
          151
                 ACAAACCCGT ATGTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
          201
                 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACTT GGAAATCGTC
          251
                 CCGCTGGACA ATCccgccga caTTCACgtg ggctaacgCt tcaaaGTccg
          301
                 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
          351
                 TTGacqqctt cGAcaccagc gaccqcagca aaacqcacaa Aaccgaagcc
          401
                 caaqcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
          451
                 CTTGCgccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAtttcc
          501
                 CCGATcaaAG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
          551
                 caaatcgccc attctCacca tTAa
This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:
     q920.pep
               (partial)
                ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY QPTFRSKNKA
                 GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
           51
                 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
          101
                 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTLTF
          151
                 QIAHSHH*
          201
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2797>:
     m920.seq
               ATGAAGAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
            1
               CGCCCACGCC CACCGMGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
           51
          101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
               ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
               CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
          201
               ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
          251
          301 TATCAGCCTA CTTTCTGGTC AAAAWACAAA GCAGGCTGGA AACAGGCGGG
          351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
           401 GCAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
           451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
           501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
           551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
           601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
           651 CACAGACGAC AAAGGCGAAG TGGACATCAT CMCCTTGCGC CAAGGCTTCT
               GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
               CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTCGCA
               CCATTAA
This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:
      m920.pep
            1 MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
            51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
           101 YOPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
               TKPVGONLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
```

```
201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFPDQSVC
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from N. gonorrhoeae:

q920/m920

				10	20	30
g920.pep			PMQI	LVTEKGKENM:	IQRGTYNYQYI	RSNRPVK
÷ •			[ ] ] ]			
m920	GGEYLKADLGYGEF:	PELEPIAKD	RLHIFSKPMQI	LVTEKGKENM:	IQRGTYNYQYE	
	40	50	60	70	80	90
	4.0	50	60	70	80	90
	40					
g920.pep	DGSYLVTAEYQPTF	RSKNKAGWK	QAGI KEMPDAS	SYCEQTRMFG.	KMIANAGHESA	ADIMITI
m920	DGSYLVIAEYQPTF	WSKXKAGWK	QAGIKEMPDAS	SYCEQTRMFG:	KNIVNVGHESA	ADTAIIT
	100	110	120	130	140	150
	•					
	100	110	120	130	140	150
~020 nen	KPVGQNLEIVPLDN	PADIHVGXR	FKVRVLFRGE	PLPNATVTAT	FDGFDTSDRSI	KTHKTEA
g920.pep	111111111111111	11-1111	HHHHHH	111111111		111:11
	KPVGQNLEIVPLDN	ממ <i>יטונונו</i> נוו ו	יייין אין אין אין אין אין אין אין אין אי	ידי מידי לידי מואס. זס די מידי לידי מואס. זס	FUGEULSUBSI	KTHXXEA
m920					200	210
	160	170	180	190	200	210
	160	170	180	190	200	
	QAFSDTTDGEGEVD					псппл
g920.pep		TIPLKOGEN				
		11 111111		:   :		
m920	QAFSDSTDDKGEVD	IIXLRQGFW	KANVEHKTDF:	PDQSVCQKQA		ныних
	220	230	240	250	260	

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2799>:

```
a920.seq
          TGAAAGAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
      1
          CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
     51 CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
     151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
     201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
     251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
     301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
     351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
     401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
     451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
     501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
     551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
     601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
     651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
     701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
     751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTCGCA
         CCATTAA
```

### This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

```
a920.pep

1 *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVC
251 QKQANYSTLT FQIGHSHH*
```

²⁵¹ QKQANYSTLT FQIGHSHH*

m920.pep	10 MKKTLTLLSVSALE	20 FATSAHAHRVV	30 VVETAHTHGGI	40 EYLKADLGYGE	50 EFPELEPIAK	60 DRLHIFS
mszu.pep	1111111:1111	1:1111111		1111111111		111111
a920	XKKTLTLLAVSALI	AASAHAHRV	VVETAHTHGGE	EYLKADLGYGE	FPELEPIAK	DRLHIFS
a 72 0	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENN	/IQRGTYNYQ	YRSNRPVKDG	SYLVIAEYQPI		
a920	KPMQLVTEKGKENN	/IQRGTYNYQ				
	70	80	90	100	110	120
				4.60	4.50	100
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFO	SKNIVNVGHE	SADTAIITKP	VGQNLEIVPLI	ONPANIHVGE	RFKVRVL
a920	MPDASYCEQTRMFO	SKNIVNVGHES				
	130	140	150	160	170	180
					•••	0.40
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTA	rfdgfdtsdr:	SKTHXXEAQA!	FSDS <b>T</b> DDKGE\	/DIIXLRQGF	
		[]]			1111 11111	111111
a920	FRGEPLPNATVTA	rfdgfdtsdr:	SKTHKTEAQA	FSDSTDDKGEV	/DIIPLRQGF	WKANVEH
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQSVCQKQX	ANYSTLTFQI	GHSHHX			
<del>-</del> -	1:1111111111	1111111111				
a920	KADFPDQSVCQKQX	ANYSTLTFQI	GHSHHX			
	250	260				

# The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2801>: g920-1.seq

```
1 ATGAAGAAAA CATTGACACT GCTCGCcgtt TcCGCACTAT TTGCCACATc
    CQCaCACCCC CACCGCGTCT GGGTCGAAAC CGCCCACACG cACGGCGGCG
51
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
    CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCGTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTCG
401 GTAAAAACAT TGTCAACGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTTT
701 GGAAAGCGAG TGTCGAATAC AAAGCCGATT TCCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA
```

## This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>: g920-1.pep

- 1 MKKTLTLLAV SALFATSAHP HRVWVETAHT HGGEYLKADL GYGEFPELEP
- 51 TAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVTAE
- 101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
- 151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
- 201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWKASVEY KADFPDQSLC
- 251 QKQANYTTLT FQIGHSHH*

## The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2803>: m920-1.seq

- 1 ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
- 51 CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
- 101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
- 151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
- 201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
- 251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```
TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
     CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCG
351
     GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
     ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
451
     CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
501
     AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
551
     AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
601
     CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
651
     GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTCGCA
```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>: m920-1.pap

```
MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
  1
    IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
 51
    YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
101
    TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
151
     SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFPDQSVC
201
```

96.3% identity in 268 aa overlap m920-1/q920-1

QKQANYSTLT FQIGHSHH*

751

251

CCATTAA

```
20
                                30
                                        40
                10
          MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
m920-1.pep
          MKKTLTLLAVSALFATSAHPHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
g920-1
                                30
                                        40
                        20
                10
                                90
                                       100
                                               110
                70
                        80
          KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
m920-1.pep
          KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVTAEYQPTFRSKNKAGWKQAGIKE
q920-1
                                90
                                       100
                70
                        80
                       140
                               150
                                       160
                                               170
                                                       180
               130
          MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
m920-1.pep
          MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
g920-1
               130
                       140
                               150
                                       160
                                               170
                                       220
                       200
                               210
          FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
m920-1.pep
          FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDTTDGKGEVDIIPLRQGFWKASVEY
g920-1
                               210
                       200
                190
                250
                        260
          KTDFPDQSVCQKQANYSTLTFQIGHSHHX
m920-1.pep
          1:111131:111111:1111111111111
          KADFPDQSLCQKQANYTTLTFQIGHSHHX
q920-1
                250
                        260
```

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2805>: a920.seq

TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
CGCCCACGCC	CACCGCGTCT	GGGTCGAAAC	CGCCCACACG	CACGGCGGCG
AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTTCCCGA	ACTCGAACCC
ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
CGAAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCAGT
ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
TATCAGCCTA	CTTTCTGGTC	AAAAAACAAA	GCAGGCTGGA	AACAGGCGGG
CATCAAACAA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTCG
GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
ACCAAACCGG	TCGGACAAAA	CTTGGAAATC	GTCCCGCTGG	ACAATCCCGC
CAACATTCAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTTCTG	TTCCGTGGCG
AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CCTTTGACGG	CTTCGACACC
AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTTGCGC	CAAGGCTTCT
GGAAAGCCAA	TGTCGAACAC	AAAGCCGACT	TCCCCGATCA	AAGCGTGTGC
CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTCGCA
CCATTAA				
	CGCCCACGCC AATACCTTAA ATCGCCAAAG CGAAAAAGGC ACCGAAGCAA TATCAGCCTA CATCAAAACAT ACCAAAACAT ACCAACATTCAC AACCGCTGCC AACGCTGCC AGCGACCGCA CACAGACGAC	CACAGACGAC AAAGGCGAAG GGAAAGCCAA TGTCGAACAC CAAAAACAGG CGAACTACTC	CGCCACGGC CACCGGGTCT GGGTCGAAAC AATACCTTAA AGCCGACTTG GGCTACGGCG ATCGCCAAAG ACCGCCTGCA CATCTTCAGC CGAAAAAGGC AAGGAAAACA TGATTCAACG ACCGAAGCAA CCGTCCCGTT AAGGACGGCA TATCAGCCTA CTTTCTGGTC AAAAAACAAA CATCAAACAA ATGCCTGACG CAAGCTATTG GCAAAAACAT CGTCAACGTC GGACACAAA CCAAACCGG TCGGACAAAA CTTGGAAATC CAACATTCAC GTAGGCGAAC GCTTCAAAGT AACGCTGCC CAATGCCACC GTTACCGCA AGCGACCGCA GCAAAACGCA CAAAACCGAA CACAGACGAC AAAGGCGAAG TGGACATCAT GGAAAGCCAA TGTCGAACAC AAAGCCGACT CAAAAACAGG CGAACTACTC GACTTTAACC	CGCCCACGCC CACCGCGTCT GGGTCGAAAC CGCCCACACG AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC ACCGAAGCAA CCGTCCCGTT AAAAAACAAA GCAGGCTGGA CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC GCAAAAACAC CGTCAACGTC GGACACAAA CGCGGGACAC ACCAAACGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG CAACATTCAC GTAGGCGAAC GCTTCAAAGT CGCGTTCTG AACCGCTGCC CAATGCCACC GTTACCGCA CCTTTGACGG AACGCTGCC CAATGCCACC GTTACCGCA CCTTTGACGG CACAGACGAC AAAGCCGAA GCACAGGCTT CACAGACGAC AAAGCCGAAC CCACAGCCTCA CACAAAACAGC CAAAACCGAA CCCCTTGCCC CACAGACCAA TGTCGAACAC CAAAACCGAA CCCCTTGCCC CACAAAACAGG CGAACTACT CCCCTTGCCC CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCC

```
This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:
a920.pep
         *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
      1
        IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
     51
        YQPTFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
    101
        TKPVGONLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
    151
        SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVC
    201
        QKQANYSTLT FQIGHSHH*
    251
             98.9% identity in 267 aa overlap
m920-1/a920
                           20
                                   30
                                            40
                  10
           MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
m920-1.pep
            XKKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920
                                   30
                                            40
                                                    110
                  70
                           80
                                   90
                                           100
                                                             120
           KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
m920-1.pep
           KPMQLVTEKGKENMIQRGTYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ
a920
                                   90
                                           100
                                                    110
                                                             120
                  70
                           80
                          140
                                   150
                                           160
                                                    170
                 130
           MPDASYCEOTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
m920-1.pep
           MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
a 920
                                   150
                                           160
                                                    170
                                                             180
                          140
                 130
                          200
                                   210
                                           220
                 190
           FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
m920-1.pep
           FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
a920
                                   210
                                           220
                                                    230
                                                             240
                 190
                 250
                          260
                                  269
           KTDFPDQSVCQKQANYSTLTFQIGHSHHX
m920-1.pep
           KADFPDQSVCQKQANYSTLTFQIGHSHHX
a920
                 250
                          260
The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 2807>:
q921.seq
          ATGAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
       1
          Ccaqtctatt tatGtgccca cattgacggA aatccccgTg aatcccatca
      51
          ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCTTCG
          CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
          TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
          ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
          TATGAAATCT ACCTGCGTTC GGCGGTAGAC AGCCAGCGCG GCGAAATCAA
          TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
          AGCGTtggAA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
          TTTTTGATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:
g921.pep
          MKKYLIPLSI AAVLSGCOSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
          HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
          YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
     151 FLMEVMKMQP LK*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2809>:
m921.seq
          ATGAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
          CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
      51
          ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
          CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
     151
     201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
```

```
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
         TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
         TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
         AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
         TTTTTGATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:
m921.pep
         MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
     51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
    101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
         FLMEVMKMQP LK*
    151
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N.gonorrhoeae
ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng)
from N. gonorrhoeae:
m921/g921
                                                                  60
                                                         50
                             20
                                      30
                                               40
                   10
            MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD
m921.pep
            MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD
q921
                             20
                                      30
                                               40
                   10
                                              100
                                                        110
                                                                 120
                   70
                             RΛ
                                      90
            EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ
m921.pep
            EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGEINTEQ
g921
                   70
                                      90
                                              100
                                                        110
                   130
                            140
                                     150
            SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX
m921.pep
            SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX
g921
                                     150
                   130
                            140
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2811>:
     a921.seq
              ATGAAAAAT ACCTTATCCC TCTTTCCATT GTGGCAGTTC TTTCCGGCTG
              CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
           51
          101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
              CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
          151
              TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
          201
              ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
              TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
              TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
          351
              AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
          401
              TTTTTGATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:
     a921.pep
              MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
           51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
          101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
              FLMEVMKMQP LK*
            99.4% identity in 162 aa overlap
m921/a921
                                            30
                                                     40
                 MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD
     m921.pep
                  MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD
     a921
                                  20
                                            30
                                                     40
```

WO 99/57280

1326

```
90
                                      100
                                              110
                       80
         EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ
m921.pep
          EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ
a921
                70
                       80
                               90
                                      100
                                              110
                              150
               130
                       140
          SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX
m921.pep
          SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX
a921
               130
                       140
                              150
                                      160
```

The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 2813>:

```
q922.seq
         ATGGAAAAGA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
      1
         TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
      51
         CCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCCGC GTTTGACGCG
         GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
         CCGTTTTGTG GACGATGAAG TCGGGAAAGG GGATTTTTCC CAGGCGGAAT
     201
         GGCAGGATTT TTTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATt
     251
         ATGCACCGAC CCTCCACATC GCGtCCGTGG TATGtgttcc gCacggGAAa
         ttcGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
     351
         qcqcqgttat cgatgatgtg gcgCAAAAat acggcgtGCC TGCCGAGCTT
         ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
     501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
     551 GCGCCGGGTT TTTCCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
     601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCAGCTATG CGGGTGCAAT
         GGGTATGCCG CAATTTATGC CTTCGAGCTA CCGGAAATGG GCGGTGGATT
     701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
         gcatcggTTG CCAATTAtat gaagCAGCAC GGTTGGCGCA CgggcggtAA
     801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CAggcAATCA
     851 TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATTT GAaggCGTAC
     901 ggcatcatcc ccggggaaaC GCTCGCAGAT GATGAAAAGg cgGTTTTGTT
     951 CAAACTGGAA ACCGCACCCG GCGTGTTTGA ATATTATTTG GGCTTGAACA
    1001 ATTTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAACGGCG
    1051 gtcaggGACA TTGCCAATTC GCTCGGCGGC CCGGGATTGT Aa
This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:
g922.pep
          MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KKESRPAFDA
         AAVPVSDSGF AANANVRRFV DDEVGKGDFS QAEWQDFFDK AAYKADIVKI
      51
     101 MHRPSTSRPW YVFRTGNSGR AKFHGARRFY AENRAVIDDV AQKYGVPAEL
     151 IVAIIGIETN YGKNTGSFRV ADALATLGFD YPRRAGFFQK ELVELLKLAK
          EEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
     201
          ASVANYMKOH GWRTGGKMLV SATLAPGADV QAIIGEKTAL TRTVADLKAY
          GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMYVTA
          VRDIANSLGG PGL*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2815>:
```

m922.seq

. acy					
1	ATGAAAAAGA	GAAAAATACT	GCCGCTGGCA	ATTTGTTTGG	CGGCTTTGTC
51	TGCCTGTACG	GCGATGGAGG	CACGCCCACC	CCGGGCAAAT	GAAGCCCAAG
101		GGTTGAAATG			
151		TTGACGCGGC			
201		AATGTCCGCC			
251		GGCGGAATGG			
301		TCAAGATTAT			
351		ACGGGAAATT			
401		GGAAAACCGC			
451		CCGAACTTAT			
501		ACGGGCAGTT			
551	GCTTTGATTA	CCCCCGCCGC	GCCGGGTTTT	TCCAAAAAGA	ATTGGTCGAG

601	CTTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTCG CCTTTAAAGG
651	CAGCTATGCG GGCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701	GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC AACGTCGGCG ATGTCGCGC ATCGGTTGCC AATTATATGA AGCAGCACGG
751	TTGGCGCACG GGCGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
801	TTGGCGCACG GGCGGGAAAA IGCIGGIGIC IGCAACAIIG GCGCCGGGIG CGGATGTTCA GGCAATCATT GGCGAAAAAA CCGCCCTGAC GCGGACGGTG
851	GCGGATGTTCA GGCGAACATC GCGGAAGAGA CCGCGCGAAGAGAC TTGCAGATGA
901	TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACCGGGC GTGTTTGAAT
951	ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1001	CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1051 1101	GGGATTGTAA
This some	sponds to the amino acid sequence <seq 2816;="" 922="" id="" orf="">:</seq>
	spoiles to the annio acid sequence "SEQ ID 2010, Cid >22 .
m922.pep	MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKESRPAFDA
1	AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFFDKAAYK
51	ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
101	GVPAELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
151	LLKLAKEEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
201	NVGDVAASVA NYMKQHGWRT GGKMLVSATL APGADVQAII GEKTALTRTV
251	ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
301 351	RMYVTAVRDI ANSLGGPGL*
	analysis of this amino acid sequence gave the following results:
Computer	analysis of this airmo acid sequence gave the following results.
Homology	y with a predicted ORF from N.gonorrhoeae
<b>ORF 922</b>	shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng)
	onorrhoeae:
m922/g922	·
111922/9922	•
	10 20 30 40 50 60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAVP
mazz.pep	
g922	MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKESRPAFDAAAVP
9722	10 20 30 40 50
	70 80 90 100 110 120
m922.pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
q922	VSDSGFAANANVRRFVDDEVGKGDFSQAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR
3	60 70 80 90 100 110
	130 140 150 160 170 180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL
g922	TGNSGRAKFHGARRFYAENRAVIDDVAQKYGVPAELIVAIIGIETNYGKNTGSFRVADAL
	120 130 140 150 160 170
	190 200 210 220 230 240
m922.pep	ATLGFDYPRRAGFFQKELVELLKLAKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
g922	ATLGFDYPRRAGFFQKELVELLKLAKEEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
	180 190 200 210 220 230
	000 000 000
	250 260 270 280 290 300
m922.pep	
g922	DGDGHRDIWGNVGDVAASVANYMKQHGWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV
	240 250 260 270 280 290
	220 220 240 250 260
	310 320 330 340 350 360
m922.pep	
g922	ADLKAYGIIPGETLADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI

310 320 330 340 350 300 370 ANSLGGPGLX m922.pep ANSLGGPGLX q922 360 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2817>: a922.seq ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC 1 TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG 51 CCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCCGC GTTTGACGCG 101 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC 151 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG 201 ATTTTTCCCG GGCGGAATGG CAGGATTTTT TTGACAAAGC GGCTTACAAG 251 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA 301 TGTGTTCCGC ACGGGAAATT CGGGCAAGGC GAAATTTCGC GGCGCGCCC 351 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC 401 GGCGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA 451 CGGCAAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG 501 GCTTTGATTA CCCCCGCCGC GCCGGGTTTT TCCAAAAAGA ATTGGTCGAG 551 CTTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTCG CCTTTAAAGG 601 CAGCTATGCG GGCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC 651 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC 701 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG TTGGCGCACG GGCGGGAAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG 801 CGGATGTTCA GGCAATCATT GGCGAAAAAA CCGCCCTGAC GCGGACGGTG 851 GCGGATTTGA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCCGATGA 901 TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACCCGGC GTGTTTGAAT 951 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT 1001 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC **GGGATTGTAA** 1101 This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>: a922.pep MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KKESRPAFDA 1 AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFFDKAAYK 51 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY 101 GVPAELIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE 151 LLKLAKEEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG 201 251 NVGDVAASIA NYMKQHGWRT GGKILVSATL APGADVQAII GEKTALTRTV 301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS RMYVTAVRDI ANSLGGPGL* 98.9% identity in 369 aa overlap m922/a922 50 20 40 10 30 MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAVP m922.pep MKNRKILPLAICLAALSACTAMEARPPRANEAQAPRADEMKKESRPAFDAAAVFDAAAVP a922 50 60 10 20 30 70 80 90 100 110 VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR m922.pep VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR a922 100 110 120 80 90 70 150 160 170 130 140 TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL m922.pep TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPAELIVAVIGIETNYGKNTGSFRVADAL a922 150 160 170 180 130 140

190

200

210

220

230

m922.pep	ATLGFDYPRRAGFF	QKELVELLKI	AKEEGGDVFA	AFKGSYAGAMO	GMPQFMPSSYI	RKWAVDY
a922	ATLGFDYPRRAGFF	QKELVELLKI 200	LAKEEGGDVFF 210	AFKGSYAGAMO 220	EMPQFMPSSYI 230	RKWAVDY 240
m922.pep a922	250 DGDGHRDIWGNVGD            DGDGHRDIWGNVGD 250	1411:4111				111111
m922.pep	310 ADLKAYGIIPGEEL            ADLKAYGIIPGEEL 310	111111111			111111111	
m922.pep a922	370 ANSLGGPGLX           ANSLGGPGLX 370					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2819>:

```
q923.seq
        ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
      51 CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
     101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
     151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
     201 CGGTTGGACG GGCGCATACT TGGGTAGTAG GATGTTCAGG CATAAAACGG
     251 CGAAAAAGCG TTTTGTTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
```

301 CTGGCGACCT GCATCCTGAT TGATTATTTC GTTCCGCCCG AACTTTTTGT

351 AAAACTCGGG CAACATCTCT GA

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

g923.pep

- MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRAVR 1 51 GKRRIPEHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFVV LFRLTVSGNV
- 101 LATCILIDYF VPPELFVKLG QHL*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2821>:

m923.seg

ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT 51 101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG 151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG 201 CGGCTGGGTG GGCGCGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG 251 CGAAAAAGCG TTTTGTTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC 301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG 351 CGTTGCCTCG CCTTGCCGTA CTATTTGTAC TGTCTGCGGC TTCGTCGCCT 401 TGTCCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATTT 451 TTCGTAAAAC TCGGGCAGAA TACCTGA

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

- m923.pep MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCAIR 51 GORRIPEHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFVV LFRLTVSGNV
  - 101 LATLILIYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPPEF
  - 151 FVKLGQNT*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from N. gonorrhoeae: g923/m923 50 40 20 30 MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLYAFALYGIDKRRAVRGKRRIPEHRL g923.pep MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLYAFALYGIDKRCAIRGQRRIPEHRL m923 40 10 30 90 100 70 LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRLTVSGNVLATCILID------q923.pep 1111:11:11:11:11 LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLTVSGNVLATLILIYSGLNLNQYGVAS m923 80 90 110 70 110 120 -YFVPPELFVKLGQHLX q923.pep PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX m923 130 140 150 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2823>: a923.seq ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT 51 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG 101 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTTGTTCGG CGGTTGGGCG GGCGCATACT TGGGCAGCAG GATATTCAGG CATAAAACGG CGAAAAAGCG TTTTGTTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC 251 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTTAA ACCAGTACGG 301 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC 351 401 ACCAAGTGAA TCGGTTCCGT ACTATTTGTA CTGTCTGCGG CTTCGTCGCC TTGTCCTGAT TTTTGTTAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT TTTCGTAAAA CTCGGGCAGA ATACCTGA This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>: a923.pep MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRAVR GKRRIPEHRL LLPALFGGWA GAYLGSRIFR HKTAKKRFVV LFRLTVSGNV LATLILIYSG LNLNQYGVAS PXAQRERFSK VLKHQVNRFR TICTVCGFVA LS*FLLIHYX YFVPPEFFVK LGQNT* 84.6% identity in 175 aa overlap m923/a923 40 30 MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLYAFALYGIDKRCAIRGQRRIPEHRL m923.pep MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLYAFALYGIDKRRAVRGKRRIPEHRL a 923 60 30 40 50 20 10 120 110 90 100 70 LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLTVSGNVLATLILIYSGLNLNQYGVAS m923.pep 11111:111:11 LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRLTVSGNVLATLILIYSGLNLNQYGVAS a923 90 100 70 80 130 140 150 -----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX m923.pep PXAQRERFSKVLKHQVNRFRTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX a923

130

140

150

160

WO 99/57280

1331

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2825>:
q925.seq
          ATGAAACAAA TGCTTTTGGC cgtcggcgtg ggcGCGGTGT TGGCGGGCTG
       1
      51 CGGCAaggat gcCGGCGGtt acgagggtTA TTGGCGCGAA AAGTCGGACA
     101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCCTTAAT
     151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
     201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
     251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
     301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
     351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
     401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
     451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
     501 GACATTGTTG TTTTAG
This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:
       1 MKQMLLAVGV_GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
      51 KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
     101 TDAAMKDKII AHQKKCGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
     151 EAEFDELEKE IKCNGKPTLL F*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2827>:
m925.seq (partial)
          ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
      51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
     101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:
          (partial)
m925.pep
       1 MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNYFL..
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng)
from N. gonorrhoeae:
m925/g925
                                          3.0
                                20
              MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNYFL
m925.pep
              MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYFLNKINVFTGKE
 q925
                                20
                                                     40
                      10
              ESLLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT
 g925
                                                               110
                       70
                                 8.0
 The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2829>:
 q925-1.seq
       1 ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
      51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGCAA AAGTCGGACA
     101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCCTTAAT
     151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
     201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
     251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
     301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGCGG
      351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
      401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
          GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
      451
          GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>: g925-1.pep

```
1 MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
      51 KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
     101 TDAAMKDKII AHQKKCGQTA QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
         EAEFDELEKE IKCNGKPTLL F*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2831>:
m925-1.seq
       1 ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
      51 CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
     101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
     201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
     251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
     351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
     401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
         TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
     501 AAGCCCGGCA TTGTTGCTTT AG
This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:
m925-1.pep.
          MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNYFL
       1
          NKIHVVTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
      51
          KTDAAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
     151 FEAEFDELEK EIKCNGRSPA LLL*
             92.5% identity in 173 aa overlap
m925/q925
                               20
                                         30
                                                   40
             MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNYFLNKIHVVTGKE
m925-1.pep
             MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYFLNKINVFTGKE
g925-1
                                                   40
                     10
                               20
                                         30
                                         90
                                                  100
                                                            110
             ESLLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRQYVKTDAAMKDK11AHQKKCGQT
m925-1.pep
             ESLLLSEKDGALSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT
g925-1
                                80
                                          90
                                                   100
                                                             110
                      70
                              140
                                        150
             AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX
m925-1.pep
             1411 | 111441411111411: | 11141444411111444441141111: 4:14:1
             AQAYLDARNALPSNQTYQQRQAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
g925-1
                                         150
                                                   160
                               140
                     130
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2833>:
a925-1.seq
       1 AATAAAATCA ACGTGTTTAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
      51 AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
     101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
      151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
     201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
      251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
          TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
      301
      351 ACCGACATTG TTGTTTTAG
This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:
a925-1.pep
       1 NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
       51 KTDAAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
      101 FEAEFDELEK EIKCNGKPTL LF*
                 92.7% identity in 123 aa overlap
a925-1/m925-1
                                                    10
                                                             20
                                            NKINVFTGKEESMLLSEKDGALSINTGIGE
 a925-1.pep
                                            111:1-111111:111111111111111111
              AGGYEGYWREKSDKKEGMIAVKKEKGNYFLNKIHVVTGKEESLLLSEKDGALSINTGIGE
m925-1
                                                   60
                      30
                                40
                                          50
                                                              80
                                50
                                          60
                                                    70
                                                                        90
                      40
```

g926.pep

```
IPIKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
a925-1.pep
            1PIKLSDDGKELYVERRQYVKTDAAMKDK11AHQKKCGQTAQAYRDARNALPSNQTYQQH
m925 - 1
                                              120
                                                       130
                                                                140
                           100
                                    110
                            110
                                      120
                  100
            QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
a925-1.pep
             LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX
m925-1
                                     170
                  150
                           160
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2835>:
g926.seq (partial)
        ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
     51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
    101 GCAGTTTTGC AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
    151 TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
    201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGACAGGG
         ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
    301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACTGC CAATCCAATA
    351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GGCGGGCGCG CCTtaccGCA
         TCCGTTCAGA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
         tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...
This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:
g926.pep (partial)
      1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
      51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEG
         TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGWTIGQN
     101
         CROWGASPNV ATE...
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2837>:
m926.seq
         ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
         GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
      51
         GCAGTTTTGC AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
     101
         TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
         TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
     201
         ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCGGAAAGT
     251
         GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACTGC CAATCCAATA
     301
     351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GGCGGGCGCG CCTTACCGCA
         TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
         GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
     451
         GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
     501
         CCCCGGAACG CTGTGCGGCG CGCACGAGAT AA
This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:
m926.pep
         MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
       1
         SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
     101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGWTVGRT
         ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*
           91.6% identity in 155 aa overlap
 g926/m926
                                       30
                                                40
                                                         50
                             20
            MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
 g926.pep
            MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
 m926
                           . 20
                                       30
                                                40
                                                         50
                    10
                                       90
                                               100
                                                        110
                    70
                              80
             PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGTEDLSRQLVGFKLPIQYLHI
 g926.pep
             PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
 m926
                                               100
                                                        110
                    70
                              80
                                       90
                   130
                             140
                                      150
                                               160
             WAEGRRVAGAPYRIRSDGILEQYGWTIGQNCRQWGASPNVATE
```

```
WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
m926
                                        160
                      140
                                150
                130
    a926.seg
             ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
             GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
          51
             GCAGTTTCAC GGCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
         101
             TCGTATGCAA ATTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
         201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
         251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCGGAAAGT
             GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACTGC CAATCCAATA
             TCTGCATATC TGGGCAGATG GCAGGCCTGT GGCGGGCGCG CCTTACCGCA
             TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
             GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
             GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
             CCCAAGAACA ATGCGCGGCA CGCATACAGT AA
         551
    a926.pep
             MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
           1
             SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
          51
             AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
             ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETQEQCAA RIQ*
           96.9% identity in 191 aa overlap
m926/a926
                                                            50
                                                                     60
                                          30
                                 20
                MKHTVSASVILLLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
     m926.pep
                 MKHTVSASVILLLTACAQLPQNNENLWQPSEHTRSFTAEGRLAVKAEGKGSYANFDWTYQ
     a926
                                                   40
                                                            50
                                          30
                                 20
                        10
                                                                    120
                                          90
                                                  100
                                                           110
                                 80
                        70
                 PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
     m926.pep
                 PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEELSRQLVGFKLPIQYLHI
     a 926
                        70
                                 80
                                          90
                                                  100
                                                           110
                                                                    120
                                                                    180
                                                           170
                                140
                                         150
                                                  160
                      130
                 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
     m926.pep
                 WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
     a926
                                         150
                                                  160
                                                           170
                                                                     180
                                140
                       130
                       190
                 ETETPERCAARTRX
     m926.pep
                 1111 1:1111
                 ETETQEQCAARIQX
     a926
                       190
```

# The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>: 9927.seq

.seq					
1	atqaaaacct	acGCAcAggC	ACTCTATacc	GCAGCCCTGC	TCACCGCCTG
		GCcgatTcaa			
101		cgacGgaaAA			
151	gtGACACGGT	ATTTttacaa	agaatacgac	cacTtgtttg	tcggaaCATA
201		CACCCGGCA			
251		ACAGGCATTA			
301		ACCAATCTTC			
351	GGTAGAAAAA	GGCTGGCAAC	AAGCCCTCCC	CGATCACGCC	GCACCCTACA

PCT/US99/09346 WO 99/57280

1335

```
CCAGCACTAT GGTTTTCCTT GTCCGAAAAA ACAACCCcaa ACAGAtccgC
         GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
          CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
         AAGCCAACAA CGGCaaCGAG CAGGAAGCCC AAAAACTCGT CGCATCCATC
     601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGC.C CGCCGCCACC
         ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
         agCcaactac gtCAGCAAAA AACTGA
This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:
g927.pep
         MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
         VTRYFYKEYD HLFVGTYQSE HPGTSVSIQQ SHGGFSKQAL SVANGLOADV
         VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKOIR
     101
         DWNDLAKDGV NIVIAKTSGN GRYAFLGAYG YGLKANNGNE QEAQKLVASI
         LKNTPVFENG GRXPPPPPSH NATSATYSSL LKTKPTTSAK N*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2841>:
m927.seq
         ATGAAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
       1
         CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
      51
     101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
         GTGGCACGGG ATTTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
     201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
         GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
         GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
         GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
         CCAGCACTAT GGTTTTCCTT GTCCGAAAAA ACAACCCCAA ACAGATCCGC
         GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
     501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
     551 GTCTGAAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
     601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GCKCGCCACC
     651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTTGAAAA
     701 CGAAGCCAAC TACGTCAGCr AAAAACtGA
This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:
m927.pep
         MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
      1
         VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
     51
         VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKOIR
         DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
         SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N.gonorrhoeae
ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng)
from N. gonorrhoeae:
q927/m927
                              20
                                       30
                                                 40
                                                          50
                                                                    60
            {\tt MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD}
q927.pep
            MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
m927
                    10
                              20
                                       30
                                                 40
                                                          50
                                                                    60
                    70
                              80
                                       90
                                                100
                                                         110
            \verb|HLFVGTYQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK|
q927.pep
             PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
m927
                    70
                              80
                                       90
                                                100
                                                         110
                   130
                             140
                                      150
                                                160
                                                           170
            GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSGNGRYAFLGA
9927.pep
            GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
m927
                   130
                            140
```

150

160

170

g927.pep	30 190 200 210 220 230  GYGLKANNGNEQEAQKLVASILKNTPVFENGGRXPPPPPSHNATSATYSSLLKTKPTTS       ::
24 g927.pep <i>F</i>	AKNX
	 AKNX
240	
The following p	partial DNA sequence was identified in N. meningitidis <seq 2843="" id="">:</seq>
a927.seq	- · ·
1	ATGAAAACCT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCAGCGCCTG
51 101	CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
151	
201	
251	· ·
301	
351	
401	CCAGCACTAT GGTTTTCCTT GTCCGAAAAA ACAACCCCAA ACAGATCCGC
451	GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
501	CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
551	
601	
651	
701	CGAAGCCAAC TACGTCAGCA AAAAACTGA
This correspond	ds to the amino acid sequence <seq 2844;="" 927.a="" id="" orf="">:</seq>
1	MKTYAPALYT AALLSACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
51	VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
101	<del>-</del>
151	
201	SILKNTPVFE NGGRAPPPPS HNATSATYSS LLKTKPTTSA KN*
m927/a927 99	9.2% identity in 242 aa overlap
	10 20 30 40 50 60
m927.pep	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
222	
a927	MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN 10 20 30 40 50 60
	10 20 30 40 50 60
	70 80 90 100 110 120
m927.pep	70 80 90 100 110 120 PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
maz r. pep	
a927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
4,52,	70 80 90 100 110 120
	120
	130 140 150 160 170 180
m927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
· · · · · · · · · · · · · · · · · · ·	
a927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
	130 140 150 160 170 180
	190 200 210 220 230 240
m927.pep	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
a927	YGYGLKTTNGNEQEAQKLVASILKNTPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
	190 200 210 220 230 240

```
m927.pep
              KNX
              111
a927
              KNX
```

```
The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 2845>:
g929.seq
```

```
ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
   1
  51 CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAAcgctggG CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAACT GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GGCGGCATTA TACATCcgaT TATGCagtcg attgCcggCA GttacggctC
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
 551 tcaattaTCA TTCcaaTCCC atttcgtcgg ctAtggctat taCTGcaact
 601 gCCCCcaaCC CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 tttccgtCTT TCttgggggg cgTGGGcgtg ggcaaTGGCT Gttcccggcg
 701 ttatcgcctt TTtcgTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGTCTGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGGCAAT
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTTaAATA AActcggact gattaaatGG TTCTCCGGAG TGTTGGCGGA
1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
     TGCTTGCtta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGATATTG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>: g929.pep

```
MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
```

- 151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMAITAT 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
- 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
- 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
- 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
- 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2847>: m929.seq

```
ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
  1
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
    TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAACT GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
```

```
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
 501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
 551 TCAACTATCA TTCCAATCCC ATTTCGTCGG CTATGTTTAT TACTGCAACT
 601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
 651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
 701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTWYT GTATCCGCCT
 751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
 801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGGCAAT
 901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTTGGCGGA
1101 AAGTGTCGGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
     TGGGGTATTG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>: m929.pep

1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from N.gonorrhoeae

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from N. gonorrhoeae:

	10	20	30	40	50	. 60
g929.pep	MKLGFKPIPLAIAA	VLCALVLALP	VPDGVKPQAV	YTLLAMFVGVI	AAIIGKVMPI	LGALSII
		111111111			11111:11	
m929	MKLGFKPIPLAIAA	VLCALVLALP	VPDGVKPQAV	VTLLAMFVGVI	AAIIGKAMPI	GALSII
	10	20	30	40	50	60
	70	80	90	100	110	120
g929.pep	AVGLVAVTGVTADK	PGAAMSDALS.	AFANPLIWL	AIAVMISRGI	LKTGLGMRI	GYLFIAV
					1111111111	
m929	AVGLVAVTGVTADK	PGAAMSDALS.	AFANPLIWLI	AIAVMISRGI	LKTGLGMRIC	YLFIAV
	70	80	90	100	110	120
	130	140	150	160	170	180
g929.pep	FGRKTLGIGYSLAL	SELLLAPVTP	SNTARGGGI 1	HPIMOSIAGS	YGSNPAKGTE	EGKMGKY
J		1111111111	111111111		111111111	
m929	FGRKTLGIGYSLAL	SELLLAPVTP	SNTARGGGII	HPIMOSTAGS	YGSNPAKGTE	CKMCKV
	130	140	150	160	170	180
					1,0	100
	190	200	210	220	230	240
g929.pep	LALVNYHSNPISSA	MAITATAPNP:	LIVNLIAENI			
J - 1 1		1 11111111	11111111			
m929	LALVNYHSNPISSA	MFITATAPNP	LIVNI.TAENI	.GSSFRLSWGA	THILLIT	 
					HISHES IN CO.	THERM

	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKET	'PNAVQFAKD	RLSEMGKMSA	DEIIMAVIFO	GILLLLWADV	PALITGN
			11 [11] [1	111111111		
m929	PLILYXLYPPEIKET	'PNAVQFAKD	RLREMGKMSA	DEIIMAVIFG	ILLLLWADVE	PALITGN
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGL	SLLLLSGVL	TWDDVLKEKS	AWDTIIWFGA	LIMMAAFINE	
JEE		111111111				
m929	HAFSINATATAFIGL	SLLLLSGVI	TWDDVLKEKS	AWDTITWFGA	LIMMAAFLNE	(T.CT.T.VI)
111.52.5	310	320	330	340	350	
	210	320	330	340	350	360
	270	200	200			
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGLGVS	GTAAGVILV:	LAYMYAHYMF	ASTTAHITAM	IFGAFLAAAVS	SLNAPAM
		11111111		!	1111:1111	
m929	FSGVLAESVGGLGVS	GTAAGVILV:	LAYMYAHYMF	ASTTAHITAM	FGAFFAAAVS	LNAPAM
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMT	LTHYATGTS	PVIFGSGYTTI			
2		111111111				111111
m929	PTALMMAAASNIMMT	ΙΙΙΙΙΙΙΙΙ Ι.ΤΗΥΔΤΩΤΟΙ	▎▎▎▎▎▎▎ ₽▓▞▐▞▞▞▞▞▜▜			
111929	430	440	450	_		
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2849>:

```
a929.seq
         ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
     51
         CGCCTTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
         GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
         GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
    201 AACCGGCGTA ACCGCCGACA AACCGGGTGC GGCGATGAGC GATGCGTTGA
    251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
         TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
    301
    351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
    401 TTTCCGAACT GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
    451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
    501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
    551 TCAACTATCA TTCCAATCCC ATTTCGTCGG CTATGTTTAT TACTGCAACT
         GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
         TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
    651
    701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
    751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
    801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
    851 GTATCTTGTT GCTGTTGTGG GCAGATGTTC CCGCCCTTAT TACCGGCAAT
    901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
    951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
         GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
   1001
         TTTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTTGGCGGA
   1051
         AAGTGTCGGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
   1101
         TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
   1151
   1201
         ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
   1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
   1301
         TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTCG
         GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
   1351
   1401
         AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
         TGGGGTATTG GTAA
   1451
```

This corresponds to	the amino ac	cid sequence	<seq 2850;<="" id="" th=""><th>ORF 929.a&gt;:</th></seq>	ORF 929.a>:

	is to the annue acid sequence SEQ 1D 2850, OKF 929.a>.
a929.pep	
1	MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
51	AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101	SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151	GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHSNP ISSAMFITAT
201	ADMDITING TABLICOCEDI CUCMANAN MACUNATHAN ISSAMFITAT
	APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251	EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301	HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351	FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401	ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451	GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*
	ETTT-TOOTW MANDETW
020/-020 00	60/ identity in 497 as assolute
m929/a929 99	.6% identity in 487 aa overlap
	10 20 30 40 50 60
m929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPQAWTLLAMFVGVIAAIIGKAMPLGALSII
mana Pap	11111111111111111111111111111111111111
a929	
a929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPQAWTLLAMFIGVIAAIIGKAMPLGALSII
	10 20 30 40 50 60
	70 80 90 100 110 · 120
m929.pep	AVGLVAVTGVTADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV
a 929	
a929	AVGLVAVTGVTADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV
	70 80 90 100 110 120
	· · · · · · · · · · · · · · · · · · ·
	130 140 150 160 170 180
m929.pep	FGRKTLGIGYSLALSELLLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
- 020	
a929	FGRKTLGIGYSLALSELLLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
	130 140 150 160 170 180
	190 200 210 220 230 240
m929.pep	LALVNYHSNPISSAMFITATAPNPLIVNLIAENLGSSFRLSWGAWAWAMAVPGVIAFFVM
	11111111111111111111111111111111111111
-020	
_. a929	LALVNYHSNPISSAMFITATAPNPLIVNLIAENLGSSFRLSWGAWAWAMAVPGVIAFFVM
	190 200 210 220 230 240
	250 260 270 280 290 300
m929.pep	PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPALITGN
a929	DI TI VELL VEDER LYEMPAN OF PROPERTY OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE
a 3 2 3	PLILYFLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADVPALITGN
	250 260 270 280 290 ₃₀₀
	310 320 330 340 350 360
m929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW
-	
a929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW
4323	310 330 330 5.5
	310 320 330 340 350 360
	370 380 390 400 410 420
m929.pep	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASTTAHITAMFGAFFAAAVSLNAPAM
a929	FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASTTAHITAMFGAFFAAAVSLNAPAM
4323	270 200 200
	370 380 390 400 410 420
	430 440 450 460 470 480
m929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW
• •	
a929	PTALMMAAASNIMMTITHVATCTCOUTTCCCCUTTCCCCCTTTCCCCCTTTCCCCCTTTCCCCCTTTCCCCCTTTCCCC
4747	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW
	430 440 450 460 470 480
m929.pep	WKVLGYWX
, -	

WO 99/57280 PCT/US99/09346

1341

WKVLGYWX a929

g930.seq not found yet q930.pep not found yet

### The following partial DNA sequence was identified in N.meningitidis <SEQ ID 2851>:

```
ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
   CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
```

- 251 AACCGTGTTT TGCCATTAAC GAALGGGTGT TGGAAGGCGA ACACCATGCT
- 301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC 351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
- 401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
- 451 CCACAGGATT TGAATAGTGG aAGCTTCAAT TAA

#### This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>; m930.pep

- 1 MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
- 51 EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWVLEGEHHA
- 101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
- 151 PODLNSGSFN *

#### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2853>: g930-1.seq (partial)

```
1 GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
  51 AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
 101 CACAGGATTT GAATAGTGGC AAGCTTCAAT TAACCCTGAT GCCGGGCTAT
 151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
     ACGTATTGCA GCATTCCAAA ACAAATTTCC CACCCGCTCG AACGATCTGT
 251 TGAATCTGCG TGATTTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
 351 AAGTGATGTC GTGGTGCAAT GGCGGTAACG TCTGCTGCCC TACTGTGTGA
     GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
 451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTTCTA
 501
     TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
     ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
 551
     GCCCCTTTCG GTAAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
 601
     CCATCAGGCG GTTTCCGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
 701
     GTTACAACAC TGATTTCGGC TTCAACCGCC TGTTGTATCG TGATGCCAAA
     CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAAGTTA
 801 CATTGATGAT GCCGAACTGA CTGTACAACG GCGTAAAACC ACAGGTTGGT
 851 TGGCAGAACT TTCCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
     AAGTTGAAAT ATAAACACGG CACCGGCATG AAAGATGCTC TGCGCGCGCC
     TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
 951
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
     CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCGCAACGA TTTGAGCTGG
     CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTTATCGGG CCAAACTCTA GCCGGCACAG
     CAATTGGGAT ACGCGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTTATTC GTTTTGA
```

#### This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>: g930-1.pep (partial)

- 1 GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLOLTLMPGY
- LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
- 101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
- 151 NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
- 201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK 251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
- 301 KLKYKHGTGM KDALRAPEEA FGEGTSRMKI WTASADVNTP FQIGKQLFAY
- 351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
- 401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD

```
451 IFTGRALKKP EYFQTKKWVT GFQVGYSF*
```

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2855>:
 m930-1.seq
       1 ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
          CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
          ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
      101
      151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
      201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
      251 AACCGTGTTT TGCCATTAAC GAAGTGGTGT TGGAAGGCGA ACACCATGCT
          CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
      301
      351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
      401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
          CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCCTGA TACCGAGCTA
      451
          TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
      551 GACGTATTGC AGCATTCCAG AACAAATTTC CCACCCGCTC GAACGATCTG
          TTGAATCTGC GTGATTTGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
      651 GACTGCGGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAAACC
     701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
     751
          AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
          AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
     801
     851 ATGTAAATTA TGGACGTTCG ATTGGCGGTA CGCCCGATGA GGAAAGTTTT
     901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
          AGCCCCTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
    1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
    1051 AGTTACAATA CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA
    1101 ACGCAAAACC TATCTCGGTG TAAAACTGTG GATGAGGGAA ACAAAAAGTT
          ACATTGATGA TGCCGAACTG ACTGTACAAC GGCGTAAAAC TGCGGGTTGG
    1151
          TTGGCAGAAC TTTCCCACAA AGAATATATC GGTCGCAGTA CGGCAGATTT
    1201
    1251
          TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
          CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA
    1301
          TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA
    1351
         TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
    1401
         ACAAACTGGC TATCGGCGGA CACCACACC TACGTGGCTT CGACGGTGAA
    1451
         ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
    1501
         GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
    1551
    1601 TTTCAGGACA ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGTCGGCACA
    1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GGCGGCAACC TGCATTACGA
         TATATTTACC GGCCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
    1751 AATGGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA
This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:
m930-1.pep
       1 MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
         EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
      51
         RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
     101
     151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL
     201 LNLRDLEQGL ENLKRLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLLPYRV
         SVGMDNSGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
         DGHRKEGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQAVSG LSEVYDYNGK
     301
     351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKSYIDDAEL TVQRRKTAGW
         LAELSHKEYI GRSTADFKLK YKRGTGMKDA LRAPEEAFGE GTSRMKIWTA
         SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
         MSLSAERGWY WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
     501
     551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*
m930-1/q930-1
               95.4% identity in 478 aa overlap
             90
                      100
                               110
                                         120
                                                  130
            \verb|AINEVVLEGEHHARFQFALKRALRETGFQAGKCLHAGNINQIMSLAQNALIGRGYTTRI|
m930-1.pep
                                         g930-1.pep
                                         GKCLHAGDINQIMSLAQNALIGRGYTTTRI
                                                10
                                                          20
                      160
                               170
                                         180
                                                  190
            {\tt LAAPQDLNSGKLQLTLIPSYLRSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDLLNLRDLE}
m930-1.pep
            g930-1.pep
            LAAPQDLNSGKLQLTLMPGYLRSIRIDRSNDDQTHAGRIAAFQNKFPTRSNDLLNLRDLE
                    40
                             50
                                                          80
            210
                     220
                               230
                                         240
                                                  250
            QGLENLKRLPTAEADLQIVPVEGEPNQSDVVVQWRQRLLPYRVSVGMDNSGSEATGKYQG
m930-1.pep
```

```
QGLENLKCLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
g930-1.pep
                100
                        110
                                120
                                        130
                                                140
           270
                   280
                           290
                                   300
                                          310
                                                  320
          NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
m930-1.pep
           NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
g930-1.pep
                160
                        170
                                180
                                        190
          330
                  340
                           350
                                  360
                                          370
          NHNGYRYHQAVSGLSEVYDYNGKSYNTDFGFNRLLYRDAKRKTYLGVKLWMRETKSYIDD
m930-1.pep
          g930-1.pep
          NHNGYRYHQAVSGLSEVYDYNGKSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDD
                220
                        230
                                240
                                        250
                                                260
          390
                  400
                          410
                                  420
                                          430
                                                  440
          AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTGMKDALRAPEEAFGEGTSRMKI
m930-1.pep
          AELTVQRRKTTGWLAELSHKGYIGRSTADFKLKYKHGTGMKDALRAPEEAFGEGTSRMKI
g930-1.pep
                280
                        290
                                300
                                        310
                                                        330
          450
                  460
                          470
                                  480
                                          490
          WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
m930-1.pep
          WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
g930-1.pep
                340
                        350
                                360
                                       370
                                               380
          510
                  520
                          530
                                  540
                                          550
          GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAIGIRGQIKLGGNLHYD
m930-1.pep
          g930-1.pep
          GWYWRNDLSWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLAGTAIGIRGQIKLGGNLHYD
                400
                        410
                                420
                                       430
                                               440
                  580
                          590
          IFTGRALKKPEFFQSRKWASGFQVGYTF
m930-1.pep
          a930-1.pep
          IFTGRALKKPEYFQTKKWVTGFQVGYSFX
               460
                       470
```

a930-1.seq not yet found a930-1.pep not yet found

The following partial DNA sequence was identified in N.gonorrhoeae <SEQ ID 2857>:

```
ATGAAACCCA AATTCAAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
 1
     CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
 51
     ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAAC CGTTGCCAAT
1.01
151
     TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201
     CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
    TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
251
    AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
301
    CGCCGCCGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
351
    ACAAAAACGG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
401
    ATGGACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
451
    TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTTGTCG
501
    GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCCAAAA
551
    AACGCCGTTT AA
```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>: g931.pep

- 1 MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
- 51 FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
- 101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
- 151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2859>:
         ATGAAACCCA AATTCAAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
       1
         CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
      51
         ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
     101
         TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
         CGTTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
         CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
         AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
     351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
         ACAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
     451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
     501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTTGTCG
     551 GGCAGTAA
This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:
m931.pep..
      1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
     51 FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
     101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGOYG YTVFGRVESG
     151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N.gonorrhoeae
ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng)
from N. gonorrhoeae:
g931/m931
                             20
                    10
                                       30
                                                 40
                                                          50
            {\tt MKPKFKTVLTALLLAVSLPSMAATRVLMETDMGNIRLVLDESKASKTVANFVRYARKGFY}
g931.pep
            m931
            MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLDESKAPKTVANFVRYARKGFY
                    10
                             20
                                       30
                                                40
                                                          50
                             80
                                       90
                                               100
                                                         110
                                                                   120
            \verb|DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA|
g931.pep
            DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS
m931
                    70
                           · 80
                                       90
                                               100
                                                         110
                   130
                            140
                                      150
                                               160
                                                         170
q931.pep
            QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYONVPVOPVKIRR
                     QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVPVQPVKIRR
m931
                   130
                            140
                                      150
                                               160
                                                         170
            VVVGQX
q931.pep
            111111
m931
            VVVGOX
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2861>:
     a931.seq
              ATGAAACCCA AATTCAAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
              CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
          51
              ATATCCGTTT GGTTTTGGAC GAATCCAAAG CACCCAAAAC CGTTGCCAAT
         101
         151
              TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
              CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
         201
         251
              CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
         301 AAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
```

351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT 401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC

```
451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
              TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTTGTCG
          551
              GGCAGTAA
This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:
              MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
           51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
          101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
          151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
m931/a931
          94.6% identity in 185 aa overlap
                                  20
                                           30
                                                     40
                                                              50
                 MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLDESKAPKTVANFVRYARKGFY
     m931.pep
                 MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLDESKAPKTVANFVRYARKGFY
     a 931
                                  20
                                                     40
                                                              50
                         70
                                  80
                                           90
                                                    100
                                                             110
                 DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS
     m931.pep
                 DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS
     a931
                         70
                                           90
                                                   100
                                                             110
                       130
                                 140
                                          150
                                                   160
                                                             170
                 QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVPVQPVKIRR
     m931.pep
                 QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVPVQPVKIRR
     a931
                       130
                                 140
                                          150
                                                   160
                                                             170
     m931.pep
                 VVVGQX
                 11111
     a 931
                 VVVGQX
g932.seq not found yet
g932.pep not found yet
The following partial DNA sequence was identified in N.meningitidis <SEQ ID 2863>:
m932.seq
         ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
      1
         GTTTGGGGGA TTTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
         TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACTTGAC
         CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
    201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
         GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAACAAA
         AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA
This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:
m932.pep
        MKYIVSISLA MGLAACSFGG FKPNPWDAAS FWELKNYANP YPGSASAALD
        OYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDPYPENK
        KYEWPREEGK TK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N.gonorrhoeae
ORF 932 shows ___% identity over a ___ as overlap with a predicted ORF (ORF 932.ng)
from N. gonorrhoeae:
```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>: 9934.seq

¹ ATGAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCACCGC

110

120

130

140

```
51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
      101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
      151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
      201 CGGCAACAAC GGTCAGCCCG TTACCGGCAA .AGAcggGCA GCAGTATATT
           TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
           GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
          GCAACCAAGA CAGCCCCGTC GCCCGTCGCG CGCGTGCTGC CTACCATCAG
           TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
          CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
          GCCCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
          cggtaaaCCC GGCGCGTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATTT
          TTGTATTTGT TAGGGGCATT GTTATGTTGC CGTTTGATTT TCAGACGGCA
          TTTTGTTTCC AAGCGTTTGA TGTCGGGATG GCAATTCTGA
 This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:
 g934.pep
          MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
       51 LTPEAVKDTI PAQAQANGNN GQPVTGKRRA AVYLRPIDRK LAAAKPDWRG
          GRRVYRQRAG KQIHTGGQPR QPRRPSRACC LPSVRTPQCA HQQGFEHAQP
      101
          PCKTTGGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
          LYLLGALLCC RLIFRRHFVS KRLMSGWQF*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2867>:
m934.seq (partial)
          ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
       1
            ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
      51
            ACACCATTCC TGCCGAAGCA CAGGCAAACG GCAACAACGG GCAACCCGTT
      101
            ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
     151
            GGCTGCTGCA AAGCCTGGTC GGCGCGGCGG CAGGCGCGTT TATCGGCAAC
            GCGCTGGCAA ACAAATTCAC ACGGGCAGGC AACCAAGACA GTCCCGTCGC
            CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
     301
            yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
     351
            CAKGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
     401
            CCCCGCTATG CGCGGTTTCG GCAGGAGGCG GTAAACCCGG CGCGCCAATG
     451
            CCGTCTGAAG AGCTTTCAGA CGGCATTTnT GCATTTGTTA GGGACATTGT
     501
            TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
     551
     601
            TCGGGATGGC AATTCTGA
This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:
m934.pep
          (partial)
          ..RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
       1
            TGXRRAAVYL RPIDRKLAAA KPGRRGGRRV YRQRAGKQIH TGRQPRQSRR
      51
            PARACSLPSV RTPQCAHQQG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
     101
            PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
     151
     201
            SGWQF*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N.gonorrhoeae
ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng)
from N. gonorrhoeae:
m934/g934
                                            10
                                                      20
m934.pep
                                     RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                     {\tt MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI}
q934
                     10
                                        30
                                                  40
                                                                      60
               40
                                  60
                                            70
                                                      80
            {\tt PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAAKPGRRGGRRVYRQRAGKQIHTGRQPR}
m934.pep
            {\tt PAQAQANGNNGQPVTGKRRAAVYLRPIDRKLAAAKPDWRGGRRVYRQRAGKQIHTGGQPR}
q934
                    70
                              80
                                        90
                                                 100
                                                           110
                                                                     120
```

	SRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF    :
1	160 170 180 190 200  QEAVNPARQCRLKSFQTAFXHLLGTLLCCRLIFRRHFVSKRLMSGWQFX   :
The following p	partial DNA sequence was identified in N. meningitidis <seq 2869="" id="">:</seq>
a934.seq	
1 51 101 151 201 251 301 351 401 451 501 551 601 651	ATGAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCGCCGC CTGCCAAGAC GACGCCAGG CGCGCTCGA ACAGCAGCAG AAACAGATTG AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA CTGACTCCCG AAGCAGTCA AGACACCATT CCTGCCGAAG CACAGGCAAA CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGGCGGCGC GGCAGCCAACAC CAGTCCCGTC GCCCGGCGC CACACGACAC GCCAACCAAGA CAGTCCCGTC GCCCGGCGC CGCGTGCCGC CTACCATCAG TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT CCGTGCAAAA CAACAGGCGG CGCCGCCGC CAATTACCGC CGCCTGCCGC CAATTACCGC CGCCCGCCA TGCGCGTTT CCGCCACAACGC GCCCGCCCGC CAATTACCGC CGCCCGCCA TGCGCGTTTC CGGCAGAAGG CGGTAAATCC GGCGTGCCAA TGCCGTCTGA AGGGCTTTCA GACGGCATTT TTTTTTTTTTTT TAGGGACATT GTTATGTTGC CGTTTGATTT TTAGACGGCA  Is to the amino acid sequence <seq 2870;="" 934.a="" id="" orf="">:</seq>
a934.pep	•
1 51 101 151 201	MKKIIASALI ATFALAACQD DAQARLEQQQ KQIEALQQQL AQQADDTVYQ LTPEAVKDTI PAEAQANGNN GQPVTX*RRA AVYLRPIDRK LAAAKPGRRG GRRVYRQRAG KQIHTGRQPR QSRRPARACR LPSVRTSQCA HQQGFEHAQP PCKTTGGAGA ALPPDNAPAR QLPPPRHARF RQKAVNPACQ CRLKGFQTAF LYLLGTLLCC RLIFRRHFVS KSLMSGWQF*
m934/a934 94	1.1% identity in 205 aa overlap
m934.pep a934	10 20 30  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
m934.pep a934	40 50 60 70 80 90  PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAAKPGRRGGRRVYRQRAGKQIHTGRQPR
m934.pep	100 110 120 130 140 150 QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
m934.pep a934	160 170 180 190 200  RQEAVNPARQCRLKSFQTAFXHLLGTLLCCRLIFRRHFVSKRLMSGWQFX   :

```
not found yet
 The following partial DNA sequence was identified in N.meningitidis <SEQ ID 2871>:
 m935.seg
          ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
        1
       51 TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
      101 TGTTGCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
      151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTTGGC
      201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCGCTC AACGGCAATC
     251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
     301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
     351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAACTG CACGGGGAAA
     401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
     451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
     501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
     551 CGGAGGGCT GACGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
     601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
     651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGCCGGCA GGGTTGAATT
         ATGAAATCGA GGCGGAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
          TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
     801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTTGGGTTGG CAGTATAAAA
     851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCG
     901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCGCCT
     951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
    1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
    1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
    1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
    1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
    1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGTTG
    1251 GGCGCAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTTCCGCGT
    1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTTCTC GACAGAGGCG
    1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
    1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
    1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCG
    1501 GCGGATTGGC GGTTTTGA
This corresponds to the amino acid sequence <SEQ ID 2872; ORF 935>:
m935.pep
         MLYFRYGFLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
      51 KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
     101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
     151 DFRLKSAERH FAEAAKLDLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
     201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
     251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
     301 GSDGFDAKTK RVNNRRLPPY MLAHGVGVQL SHTYRPNPGW QFSVALEHYR
         QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
         GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
         QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
     501 ADWRF*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2873>:
     a935.seg
               ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
            1
           51 TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
          101 TGTTGCAGGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
          151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTTGGC
               GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
          251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
          301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
          351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAACTG CACGGGGAAA
          401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
          451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCCGAGG CGGAAAAATT
              GGATTTGCCG GCGCCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
```

CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

601	AATAGAAATG CCAA	ATAATGC CGCGCCGCA	G TATTGCCGGC	AAAACGGAGG
651		AGTGTCA GCCGGGCGG		
701		GAAAAA CTGACGGCG		
751	TTGTTCCGTT CCAF	ATATCGG CGGCACGAG	C TATTATTTCA	GTAAAAAATC
801	AGCTTATGAC GACG	GGTTCG GCAGAGCGT	A TTTGGGTTGG	CAGTATAAAA
851		GCGGGG ATTTTGCCG		
901		TTGATGC GAAAACAAA		
951		TGGCGC ACGGAGTCG		
1001		GGGATGG CAATTTTCG		
1051		ACAGGA TAGGGCGGA		
1101	CGGGTTTTAT GTTT	CGTCGG CAAAACGTT	r GGGCGAATCG	GCAACTGTGT
1151		STTTGTG CGGTTTGTG		
1201		ATGCCGC CTACCGGCG		
1251		CGGCAGT TGGGCGGTT		
1301 1351		CAACTAT AAGGGCGTT AATGGAA TGTCTCGCT		
1401		ATCGTGC CCGCGTTGA		
1451		STATGCG AAACGCCGC		
1501	GCGGATTGGC GGTT		A ACAGCGAGGI	GIIIGIGICG
a935.pep		d sequence <seq< td=""><td></td><td></td></seq<>		
1		AGVSAA YGADAPAIL		
51		FLLAHPK MLEHSLRDV		
101		KLAGRP AEAVARYRE		
151 201		EKLDLP APVLENVGR		
251		NGGRQI CSVSRAERA KKSAYD DGFGRAYLG		
301		RRLPPY MLAHGVGVQ		
351		GRODGEY VSSAKRLGE		
401		AGWAQE WRQLGGLNS		
451		IDKLSYK GIVPALNYR		
	OUNTERNATE ADDIT	DREDIK GIVERENTK	GRIEDHVEIA	KKKNAEAEA2
501	ADWRF*			
501 m935/a935 98	ADWRF*  3.8% identity in 50	)5 aa overlap		
	3.8% identity in 50	20	30 40	50 60
	3.8% identity in 50	20		50 60 VSDKWAESDWKVENDAPRVV
m935/a935 98	6.8% identity in 50 10 MLYFRYGFLVVW	20 CAAGVSAAYGADAPAT	LDDKALLQVQRS\	/SDKWAESDWKVENDAPRVV
m935/a935 98	6.8% identity in 50 10 MLYFRYGFLVVW	20 CAAGVSAAYGADAPAT	LDDKALLQVQRS\	/SDKWAESDWKVENDAPRVV
m935/a935 98	6.8% identity in 50 10 MLYFRYGFLVVW	20 ICAAGVSAAYGADAPAI               CAAGVSAAYGADAPAI	LDDKALLQVQRS\	/SDKWAESDWKVENDAPRVV
m935/a935 98	3.8% identity in 50 10 MLYFRYGFLVVW 11111111111111111111111111111111111	20 ICAAGVSAAYGADAPAI                 CAAGVSAAYGADAPAI   20	LDDKALLQVQRS\ 	/SDKWAESDWKVENDAPRVV               SDKWAESDWKVDNDAPRVV
m935/a935 98 m935.pep a935	5.8% identity in 50 10 MLYFRYGFLVVW 11111111111111111111111111111111111	20 CAAGVSAAYGADAPAI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	LDDKALLQVQRSV 	7SDKWAESDWKVENDAPRVV 
m935/a935 98	3.8% identity in 50 10 MLYFRYGFLVVW 11!!!!!!!! MLYFRYGFLVVW 10 70 DGDFLLAHPKMI	20 ICAAGVSAAYGADAPAI	LDDKALLQVQRSV	VSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep	3.8% identity in 50 10 MLYFRYGFLVVW            MLYFRYGFLVVW 10 70 DGDFLLAHPKML	20 ICAAGVSAAYGADAPAI	LDDKALLQVQRSV	7SDKWAESDWKVENDAPRVV 
m935/a935 98 m935.pep a935	1.8% identity in 50 10 MLYFRYGFLVVW 11!!!!!!!! MLYFRYGFLVVW 10 70 DGDFLLAHPKML 1!!!!!!!!	20  CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	VSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep	3.8% identity in 50 10 MLYFRYGFLVVW            MLYFRYGFLVVW 10 70 DGDFLLAHPKML	20  CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	7SDKWAESDWKVENDAPRVV 
m935/a935 98 m935.pep a935 m935.pep	1.8% identity in 50 10 MLYFRYGFLVVW 11!!!!!!!! MLYFRYGFLVVW 10 70 DGDFLLAHPKML 11!!!!!!!	20 CAAGVSAAYGADAPAI               CAAGVSAAYGADAPAI 20  80 LEHSLRDALNGNQADLI       :       LEHSLRDVLNGNQADLI 80	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935	2.8% identity in 50  10  MLYFRYGFLVVW             MLYFRYGFLVVW 10  70  DGDFLLAHPKMI           DGDFLLAHPKMI 70  130	20 CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep	2.8% identity in 50 10 MLYFRYGFLVVW                         MLYFRYGFLVVW 10  70 DGDFLLAHPKML                       DGDFLLAHPKML 70  130 AEAVARYRELHG	20 CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep	2.8% identity in 50 10 MLYFRYGFLVVW                         MLYFRYGFLVVW 10  70 DGDFLLAHPKML                       DGDFLLAHPKML 70  130 AEAVARYRELHG	20 CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935	2.8% identity in 50 10 MLYFRYGFLVVW                         MLYFRYGFLVVW 10  70 DGDFLLAHPKML                       DGDFLLAHPKML 70  130 AEAVARYRELHG	20 CAAGVSAAYGADAPAI                CAAGVSAAYGADAPAI 20  80 EHSLRDALNGNQADLI EHSLRDVLNGNQADLI 80  140 140 ENAADERILLDLAAAE	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep	2.8% identity in 50 10 MLYFRYGFLVVW                         MLYFRYGFLVVW 10  70 DGDFLLAHPKML                       DGDFLLAHPKML 70  130 AEAVARYRELHG	20 CAAGVSAAYGADAPAI                CAAGVSAAYGADAPAI 20  80 EHSLRDALNGNQADLI EHSLRDVLNGNQADLI 80  140 140 ENAADERILLDLAAAE	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep	1.8% identity in 50 10 MLYFRYGFLVVW 11          MLYFRYGFLVVW 10 70 DGDFLLAHPKML 1         DGDFLLAHPKML 70 130 AEAVARYRELHG 1          AEAVARYRELHG	20 CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935	3.8% identity in 50  10  MLYFRYGFLVVW                          MLYFRYGFLVVW 10  70  DGDFLLAHPKML                        DGDFLLAHPKML 70  130  AEAVARYRELHG                        AEAVARYRELHG 130  190	20 CCAAGVSAAYGADAPAI CCAAGVSAAYGADAPAI CCAAGVSAAYGADAPAI 20  80 LEHSLRDALNGNQADLI LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep	3.8% identity in 50  10  MLYFRYGFLVVW                          MLYFRYGFLVVW 10  70  DGDFLLAHPKML                        DGDFLLAHPKML 70  130  AEAVARYRELHG                          AEAVARYRELHG 130  190  RKKTEGLTGWRE	20 CAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935 m935.pep	1.8% identity in 50 10 MLYFRYGFLVVW                         MLYFRYGFLVVW 10  70 DGDFLLAHPKML                     DGDFLLAHPKML 70  130 AEAVARYRELHG                     AEAVARYRELHG 130  190 RKKTEGLTGWRE	20 CAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935	1.8% identity in 50 10 MLYFRYGFLVVW                         MLYFRYGFLVVW 10  70 DGDFLLAHPKML                     DGDFLLAHPKML 70  130 AEAVARYRELHG                     AEAVARYRELHG 130  190 RKKTEGLTGWRE       :                 RKKAEGLTGWRE	20 CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935 m935.pep	1.8% identity in 50 10 MLYFRYGFLVVW                         MLYFRYGFLVVW 10  70 DGDFLLAHPKML                     DGDFLLAHPKML 70  130 AEAVARYRELHG                     AEAVARYRELHG 130  190 RKKTEGLTGWRE	20 CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935 m935.pep	1.8% identity in 50  10  MLYFRYGFLVVW              MLYFRYGFLVVW  10  70  DGDFLLAHPKML              DGDFLLAHPKML  70  130  AEAVARYRELHG               AEAVARYRELHG               RKKTEGLTGWRF     :          RKKAEGLTGWRF  190	20 CAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935 m935.pep a935	1.8% identity in 50  10  MLYFRYGFLVVW              MLYFRYGFLVVW  10  70  DGDFLLAHPKML              DGDFLLAHPKML  70  130  AEAVARYRELHG               AEAVARYRELHG  130  190  RKKTEGLTGWRF     :          RKKAEGLTGWRF  190  250	20 CAAGVSAAYGADAPAI CAAGVSAAYGADAPAI 20 80 LEHSLRDALNGNQADLI LEHSLRDVLNGNQADLI 80 140 140 15ENAADERILLDLAAAE 1111111111111111111111111111111111	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935 m935.pep	1.8% identity in 50  10  MLYFRYGFLVVW              MLYFRYGFLVVW  10  70  DGDFLLAHPKML              DGDFLLAHPKML  70  130  AEAVARYRELHG               AEAVARYRELHG  130  190  RKKTEGLTGWRF     :          RKKAEGLTGWRF  190  250  LTPLADNHYLLE	20 CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935 m935.pep a935	1.8% identity in 50  10  MLYFRYGFLVVW               MLYFRYGFLVVW  10  70  DGDFLLAHPKML                DGDFLLAHPKML  70  130  AEAVARYRELHG                 AEAVARYRELHG                 RKKTEGLTGWRE     :            RKKAEGLTGWRE  190  250  LTPLADNHYLLE	20 CAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV
m935/a935 98 m935.pep a935 m935.pep a935 m935.pep a935 m935.pep a935	1.8% identity in 50  10  MLYFRYGFLVVW               MLYFRYGFLVVW  10  70  DGDFLLAHPKML                DGDFLLAHPKML  70  130  AEAVARYRELHG                 AEAVARYRELHG                 RKKTEGLTGWRE     :            RKKAEGLTGWRE  190  250  LTPLADNHYLLE	20 CCAAGVSAAYGADAPAI	LDDKALLQVQRSV	ZSDKWAESDWKVENDAPRVV

m935.pep a935	310 GSDGFDAKTKRVNNI          GSDGFDAKTKRVNNI	 RRLPPYMLAH	11111111	[] [] [] [] [] [] [] [] [] [] [] [] [] [		
	310	320	330	340	350	360
m935.pep	370 YNNGRQDGFYVSSAI	380 (RIGESATVE	390	400	410	420
m333.pcp						
a935	YNNGRQDGFYVSSAF	KRLGESATVF	GGWQFVRFVI	PKRETVGGAVN	INAAYRRNGV	
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASY			. <b></b>	DKLSYKGIVI	PALNYRF
a935	WRQLGGLNSRVSASY	'ARRNYKGVA	AFSTEAQRNE			PALNYRF
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPYAKRRNS	EVFVSADWR	FX			
a935			 FX			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

```
1 ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTGCCCTC GGCGGCTGCT TCAGCGCAGT CGTCGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGCCGAACCA CCGGCGGGG GCCGCCGTCG
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACGTCCAAA GTCCGCGCCC CGCCGAAG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACTACGTC
```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>: g936.pep

- 1 MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
- 51 NVMALRIETT ARSYLRONNO TKGYTPQISV VGYNRHLLLL GOVATEGEKO
- 101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
- 151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
- 201 OR*

The following partial DNA sequence was identified in N.meningitidis <SEQ ID 2877>: m936.seq (partial)

- 1 ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
- 51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
- 101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
- 151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
- 201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
- 251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
- 301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
- 351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>: m936.pep (partial)

- 1 MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAOTDD
- 51 NVMALRIETT ARSYLRONNO TKGYTPQISV VGYNRHLLLL GQVATEGEKO
- 101 FVGQIARSEQ AAEGVYNYIT VASLPRTA...

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N.gonorrhoeae

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from N. gonorrhoeae: m936/g936

m936.pep	10 MKPKPHTVRTLIA <i>F</i> 	::   :	[	1111::1111	1111111111	111111
g936	MKPKPHTVRTLIA	VLSLALGGCF	SAVVGGAAV	GAKSVIDRRTT	ן ון ון ון ווון GAOTO	ייייים דכו.ז.
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLRONNOTKGY	TPQISVVGYN	RHLLLLGQVA	ATEGEKQFVGQ	IARSEQAAEG	VYNYIT
g936			11111111		111111111	111111
	70	80	90	100	110	120
	130					
m936.pep	VASLPRTAXXX					
g936	VASLPRTAGDIAGD	TWNTSKVRAT	LLGISPATQA	RVKI I TYGNV	TYVMGILTPE	EOAOTT
	130	140	150	160	170	180

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2879>:

a936.seq ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG 1 51 CCTTGCCCTC GGCGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCG GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC 101 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA 151 201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG 251 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG 351 401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT 451 501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACTACGTC 551 601 CAACGCTGA

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

a936.pep

- MKPKPHTVRT LTAAVLSLAL GGCVSAVVGG AAVGAKSAVD RRTTGAQTDD NVMALRIETT ARSYLRONNO TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
- FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP 101
- ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV 151

201 QR *

m936/a936 95.3% identity in 128 aa overlap

	10	20	30	4.0		
m036 non				40	50	60
m936.pep	MKPKPHTVRTLIAA	IFSLALSGCV	SAVIGSAAVG	AKSAVDRRTT	GAQTDDNVMA	LRIETT
		::	111:1:111	311111111	11111111111	111111
a936	MKPKPHTVRTLTAA	VLSLALGGCV	SAVVGGAAVG	AKSAVDRRTT	וווווווווווווו	ן           מתחים TDT
	10	20	30			
		20	20	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLRQNNQTKGY	TPOTSWAYN	DUITTICOUN	MECEROPIA-	110	120
		111111111	MADDITION W	TEGERÓFAGÓ	TARSEQAAEG	VYNYIT
- 026		111111111	1	11111111	1111111111	ELLIPS
a936	ARSYLRQNNQTKGY	TPQISVVGYN)	RHLLLLGOVA	TEGEROEUCO	TADCECAARC	*
	70	80	00			AANAT.L
	. 0	80	90	100	110	120

m936.pep VASLPRTA

```
VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
       a 936
                            130
                                     140
                                            150
                                                           1.60
                                                                                 180
 The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2881>:
 g936-1.seq
       1 ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
       51 CCTTGCCCTC GGCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
      101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
      151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
      201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
      251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
          TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
     351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
     401 ACACTTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
     451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
     501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
     551 GCACCACCGT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACTACGTC
     601 CAACGCTGA
This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:
       1 MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
         NVMALRIETT ARSYLRONNO TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
      51
     101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
     151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2883>:
       1 ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
      51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
         GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
     151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
     201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
     251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
     301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
     351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
     401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
     451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
     501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
     551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACTACGTC
     601 CAACGCTGA
This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:
m936-1.pep
      1 MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
     51 NVMALRIETT ARSYLRONNO TKGYTPQISV VGYNRHLLLL GQVATEGEKO
    101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
    151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
    201 OR*
m936-1/a936-1
                95.5% identity in 202 aa overlap
                             20
                                      30
                                                40
            MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT
m936-1.pep
            MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVIDRRTTGAQTDDNVMALRIETT
g936~1
                   10
                             20
                                               40
                   70
                             80
                                      90
                                              100
                                                        110
           ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
m936-1.pep
            ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
g936-1
                   70
                            80
                                      90
                                                        110
```

m936-1.pep

VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT

160

PCT/US99/09346 WO 99/57280

1353

VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT g936-1 150 160 170

200 190 QKVSTTVGVQKVITLYQNYVQRX m936-1.pep 1111111111111111111111111 QKVSTTVGVQKVITLYQNYVQRX g936-1 190 200

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2885>:

1 ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG CCTTGCCCTC GGCGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCG 51 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA 151 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA 201 251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA 301 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG 351 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC 401 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA 501 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACTACGTC 551 CAACGCTGA

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>: a936-1.pep

- 1 MKPKPHTVRT LTAAVLSLAL GGCVSAVVGG AAVGAKSAVD RRTTGAQTDD
- NVMALRIETT ARSYLRONNO TKGYTPQISV VGYNRHLLLL GOVATEGEKO 51
- FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP 101
- 151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
- 201 OR*

97.0% identity in 202 aa overlap a936-1/m936-1

20 30 10 40 50 60 MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVDRRTTGAQTDDNVMALRIETT m936-1.pep a936-1 MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAVGAKSAVDRRTTGAQTDDNVMALRIETT 10 20 30 40 70 90 80 100 ARSYLRONNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT m936-1.pep ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT a936-1 70 80 90 100 140 150 160 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEOAOIT m936-1.pep a936-1 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT 130 140 150 160 170 190 200 m936-1.pep QKVSTTVGVQKVITLYQNYVQRX 1111111111111111111111111111 a936-1 QKVSTTVGVQKVITLYQNYVQRX 190 200

The following partial DNA sequence was identified in N.gonorrhoeae <SEO ID 2887>: q937.seq

- atgaaaata ttctcttagt atttgttagc tttgtgccat tatgtgtccg
- 51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
- 101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
- 151 GCACTTGCCT CACCGGTTTA CATTCAGACC GGCTCCGCTT CCTTTATCCC
- CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG 201
- GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccgA CATTTACGGC 251
- 301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAACTCGacg GCAACGGCAA

```
351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
          TCCttaAAGa cgGCAAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCACG
          GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAAAAT CGTGGCTCAT
          CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCCTT TCCCTCACCG
          CCGCCTACCG CATCAACGGC AGCAAAACCC TTTCAGACGA CGTCAAATAC
          AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
          CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCG
          ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
          CATTTCGGCG CAGGTTTCGG TTTCACCAAA ACCGCGGCTT TAAACGCATC
     801 CGCACGTTTC AACGTTTCAG GGCAAAGCAG TTCCGAACTG AAATTGGGCG
          TACAGCATAC ATTTTAA
This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:
g937.pep
          MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETSL TYLNSENSRA
          ALASPVYIQT GSASFIPVPT EIQENGSNTD MLAGTLGLRY GLTGNTDIYG
     101 SGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
     151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTLSDDVKY
     201 KAGNYWMLNP NISFAANDRI SLTGGIQWLG KQPDRIDGKK ESARNTSTYA
          HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVQHTF*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2889>:
m937.seg
         ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
      51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
     101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
     151 GCCGAACTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
     201 CCCCATTCCG ACCGAAATCC AAGAAAaCGG CAGCAATACC GATATGCTCG
          TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTTAC
          GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACAG
     351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
     401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
     451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
     501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
     551 CCGCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
     601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
     651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
     701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
     751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
     801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
     851 GCGTACAGCA TACATTTTAA
This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:
m937.pep..
       1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
      51 AELAAPVYIQ TGATSFIPIP TEIQENGSNT DMLVGTLGLR YGLTGNTDIY
     101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
     151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTLSDGIR
     201 YKSGNYLLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
     251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N.gonorrhoeae
ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng)
from N. gonorrhoeae:
g937/m937
                     10
                                         30
            	t MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETSLTYLNSENSRAALASPVYIQ
q937.pep
            MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
m937
                    10
                              20
                                        30
                                                  40
                                                            50
           60
                                         90
                                                  100
            TGSASFIPVPTEIQENGSNTDMLAGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTR
g937.pep
```

	11	::1111:11	11111111111	ыйнын			
m937	TG	ATSFIPIPTE	IOENGSNTDMI	VGTLGLEVGL			:
		70	80	90	100	110	
					100	110	120
	120	130	140	150	160	170	170
g937.pep					KCDNKVCCCK	I/U SWLIGATTYKAI	179
3	1.1	1111:1 111		11.11111111		IIIIIIIIIII	-DPIV
m937	NK	RMSDVSLGTS	HTFIKDDKNDA	 			1111
	****	130	140	150			
		130	140	150	160	170	180
	180	190	200	210	220	000	
g937.pep					220	230 GIQWLGKQPDR	239
g557.pcp	11	1111111111	IIIII	III .IUIII	FAANDRISLIC	GIQWLGKQPDR	IDGK
m937	1.1 T.C	1111111111 1.TA A VOTNICO	··  : VTI COCTOVYC	CNVITINDATO			
111237	ப	190	20171			GIQWLGRQPDR	
		190	200	210	220	230	240
	240	250	260				
. 03.5	240	250	260	270	280	289	
g937.pep	KE	SARNTSTYAH	FGAGFGFTKTA	ALNASARFNVS	GOSSSELKLGV	QHTFX	
	: 1	1:	<u> </u>	111111111	11111111111111		
m937	RE:		FGAGFGFTKTT	ALNASARFNVS	GQSSSELKFGV	QHTFX	
		250	260	270	280		
The follow	ing pa	rtial DNA s	sequence wa	s identified i	n N. menino	itidis <seq< td=""><td>ID 28015.</td></seq<>	ID 28015.
a937.	sea		•			man blo	11) 20)12.
	1 .	ATGAAGCGCA	TCTTTTTGCC	ССССТТСССС	CCCATCCTC	CTTTATCCGC	
	51	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATCACA	GACAAGGGCA	
	101	AATGGAAACT	GGAAACTTCC	CTTACCTACC	TGAACAGCCA	AAACAACCGC	
	151	GCCGAACTTG	CCGCACCGGT	TTACATCCAA	ACCGCCCCAA	CCTCGTTTAT	
	201	CCCCATTCCG	ACCGAAATCC	AAGAAAACGG	CACCADATACC	GATATGCTCG	
	251	TTGGCACGCT	CGGTTTGCGC	TACGGACTGA	CCGCGATACC	CGACATTTAC	
	301	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACTCC	ACGGCAACGG	
	351	CAAAACCCGA	AACAAACGGA	TGTCCGACGT	ATCCCTCCC	ATCAGCCACA	
	401	CCTTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCACCTCGGC	TCTTGAAAGC	
	451 7	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTCGGGAA	AATCCTGGCT	
	501 (	CATCGGCGCC	ACCACCTACA	AAGCCATCGA	CCCCGTCGTC	CTCTCATTGA	
	551 (	CCGCTGCCTA	CCGTATCAAC	GGCAGCAAAA	CCCCTTTCAAC	CAACACCAAA	
	601	racaaagcag	GCAATTACTG	GATGCTGAAT	СССТТТСДАС	CCTTCGCCGC	
	651 (	CAACGACAGA	ATCAGCCTCA	CGGGCGGCAT	CCAATGGCTC	GGCAAGCAGC	
•	701 (	CCGACCGTCT	GGACGGCAAA	AAAGAATCCG	CAAGAAACAC	ATCCACCTAT	
•	751 (	SCCCATTTCG	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACCC	
1	801 <i>F</i>	ATCCGCACGT	TTCAACGTTT	CAGGGCAAAG	CAGTTCCGAA	CTGAAATTTC	
8	851 0	GCGTACAGCA	TACGTTTTAA		0.1011000111	CIGAAAIIIG	
This corresp	onds	to the amin	o acid seque	nce <seo ii<="" td=""><td>D 2892 ORI</td><td>3 037 05.</td><td></td></seo>	D 2892 ORI	3 037 05.	
a937.				01Q II	5 2072, OIG	751.a	
		KRIFLPALP	AILPLSAYAD	I.PI.TTFDIMT	DRCKMAL BEG	TOUTHOUSE	
	51 P	ELAAPVYIO	TGATSFIPIP	TETOENGSNT	DMIVCTICIB	LIYLNSENNR	
1	101 0	SSGSYLWHEE	RKLDGNGKTR	NKRMSDVSLG	TSHAELKUUK	MUNITORIEC	
1	151 Т	VYEKSRNKA	SSGKSWLIGA	TTYKATDPVV	I.SI.TAVATA	NEWTI SETTE	
	201 Y	KAGNYWMLN	PNISFAANDR	ISLTGGIOWL	CKODDBI DCK	G2V1T22M1K	
2	251 A	HFGAGFGFT	KTTALNASAR	FNVSGOSSSE	I.KECVOHTE*	RESARNISTY	
					HILL GA ÖLLİT		
m937/a937	95.2	% identity	in 289 aa ov	erlan			
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	, J <b></b>	-		*			
m937.p	ner.			0 30	40	50	60
m33/.F	ne h	TINKIFLPA	LEHILLELSTYE	NUTERITEDIMI	DKGKWKLETSI	LTYLNSENNRAE	LAAPVYIQ
a 937		MUDITION		[	11111111111		111111
a 33 /		HUKILPPA	LPAILPLSAYA 10 2	O		TYLNSENNRAE	LAAPVYIQ
			10 2	30	40	50	60
			70 8	90			
m937.p	nen				100	1,10	120
	-CP	10012515	1	THEFT	TGLTGNTDIYG	SGSYLWHEERK	LDGNSKTR
a937		TGATSFIP	TPTETOENGON	*			1111:111
			70 8	O GULGER		SGSYLWHEERK	
				0 90	100	110	120

	•	
	130 140 150 160 170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGAT	TYKAIDPIV
a 937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGAT	TYKAIDPVV
	130 140 150 160 170	180
m037 non	190 200 210 220 230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLLNPNISFAANDRISLTGGIQWLG	
a 937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLG	KQPDRLDGK
	220 230	240
m937.pep	250 260 270 280 290 RESSRNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX	
a937	KESARNTSTYAHFGAGFGFTKTTALNASARFNVSGQSSSELKFGVQHTFX 250 260 270 280 290	
	230 230	
g939.seq not	found yet found yet	
	partial DNA sequence was identified in <i>N.meningitidis</i> <seq ii<="" td=""><td>7.20025</td></seq>	7.20025
m939.seq (part:	ial)	J 2893>:
1 ATGA	AACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC	
51 CGCC 101 TTTG	TCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG	
101 111G.	TGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT GTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACTATCGG	
	CGCGAC GTAAACGCAC CC	
This correspond	s to the amino acid sequence <seq 2894;="" 939="" id="" orf="">:</seq>	
m939.pep (parti	ial)	
	TLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY	
51 PRLA	AQHTAY IYHQTIGIRD VNAP	
The following pa	artial DNA sequence was identified in N. meningitidis <seq ii<="" td=""><td>D 2895&gt;·</td></seq>	D 2895>·
a939.seq		J 20752.
1	ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC	
51 101	CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG	
151	TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACCATCGG	
201	CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG	
251	TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT	
301	GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA	
351	ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG	
401 451	CGTGTATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGGCGGA	
501	AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT TGTTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA	
551	TGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGGTCGCC	
601	AACTTTATCC AAGGTTTGCG TTAA	
This corresponds	s to the amino acid sequence <seo 2004,="" 220<="" id="" ode="" td=""><td></td></seo>	
a 939. pep	s to the amino acid sequence <seq 2896;="" 939.a="" id="" orf="">:</seq>	
a 939. pep 1	MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY	
	PRLAAQHTAY IYHQTIGIRD GKRTHGSAAV MKPVVMNLSD QDILNVSAFY	
101	AKQQPKSGEA NPKENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG	
151	SEIQAYPRLG GQHQAYIVEQ MNAYKSGQRK NTIMEDIANR MSEEDLKAVA	
201	NFIQGLR*	
m939/a939 100	0.0% identity in 70 aa overlap	
	10 20 30 40 50	60
m939.pep	MKRLTLLAFVLAAGAVSASPKADVEKGKOVAATVCAACHAADGNSGTAMVPDT	י עשטטעע.
a939		
	MKRLTLLAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRI	"AAQHTAY

```
10
                                         20
                                                   30
                                                              40
                                                                        50
                                                                                   60
                              70
       m939.pep
                     IYHQTIGIRDVNAP
                     111111111
                     IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDQDILNVSAFYAKQQPKSGEANPKENPELGA
       a939
                                        80
                                                   90
                                                                       110
 The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2897>:
 g950.seq
           ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
          GGCCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
       51
          TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
      101
          TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
          TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
          AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
      301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA
 This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:
 g950.pep
          MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
          SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
       51
         EGKCGEGKCG SK*
 The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2899>:
 m950.seq
          ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
       1
          GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
      51
     101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
     151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
     201 CARATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
          AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
     301 ТСТАВАТАВ
This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:
m950.рер
          MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAHG SCGASKSAEG
         SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
      51
     101
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from
N. gonorrhoeae
m950/q950
            86.6% identity in 112 aa overlap
                             20
                                       30
            MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAHGSCGASKSAEGSCGA-
m950.pep
            MNKNIAAALAGALSLSLAAGAVAAHKPASNATGVQKSAQGSCGASKSAEGSCGASKSAEG
                             20
                                       30
                             70
                                       80
                                                        100
            ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
m950.pep
                g950
            SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
                             80
                                       90
                                               100
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2901>:
a950.seq
        ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
         GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
    101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
    151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
        CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
         AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
    251
    301 ТСТАААТАА
```

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>: a950.pep

- 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAHG SCGASKSAEG
- 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG

101 SK

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from N. meningitidis

```
a950/m950
         100.0% identity in 102 aa overlap
                10
                        20
                                30
          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAHGSCGASKSAEGSCGAAGSKAG
a950.pep
          MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAHGSCGASKSAEGSCGAAGSKAG
m950
                        20
                                30
                70
                                90
          EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
a950.pep
          EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
m950
                70
                               90
                       80
                                      100
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2903>:

```
ATGATTATGT TACCCGCCCG TTTCACTATT TTATCTGTCC TCGCAGCAGC
   1
   51 CCTGCTTGCC GGACAGGCGT ATGCTGCCGG CGCGGCGGAT GTGGAGCTGC
       CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
 101
 151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
 201 CAGGGTGTTT ACGCTGTTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
 251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTTGGAACG CACAAAATCC
      CCCGAAGTCG CCGAACGCGC CTTGGAAATG GCCGTGTCGC TGAACGCGTT
 301
      TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
 351
      CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TGCGGAACGT ATTGAGGGAA
      GGGGGAAATC AGCATCTGGA CGGGTTGGAA GAGGTGCTGG CGCAATCGGA
 451
      CGATGTGCAA AAACGCAGGA TATTTTTGCT GCTGGTGCAA GCCGCCGTGC
 501
 551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTCG CCGTGCGGCG
      TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCGG
 601
      CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
 701 CGAAGCTCGA TACGGAAATA TTGCCCCCCA CTTTAATGAC GTTGCGTCTG
 751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
 801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAATT ATGAATCTGG
 851
      TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGAA CGTGCTGTTG
 901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
 951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGGCAT
1001 ACGGCAGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGGTTGAA
1101 AAAAGTGTCC GCGCCGGAAT ACCTGTTCGA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACTTTC GGCGGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
      ACAGTTCGGC AAACGGGGAA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1401
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAATC AACCCGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCATT TGGGCGAAGT
     GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTTGACGTA TGGACGCAGG
1701
     CGGCACACCT TAGGGGAGAC AAGAAAATAT GGCGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>: g951.pep

¹ MIMLPARFTI LSVLAAALLA GQAYAAGAAD VELPKEVGKV LRKHRRYSEE

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1359
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```
51 EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHLDGLE EVLAQSDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTQN LSAVWQEMEI MNLVSLRKPD DAYARLNVLL
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKVS APEYLFKGV LAAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSKLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2905>:

```
m951.seq
         ATGATTATGT TACCTAACCG TTTCAAAATG TTAACTGTGT TGACGGCAAC
      51 CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
     101 AACAGCCGAA GGAAGTCGGA AAGGTTTTCA GAAAGCAGCA GCGTTACAGC
     151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGGCGAGCG
     201 GGTTAATCAG ATATTTACGT TGCTGGGAGG GGAAACCGCC TTGCAAAAGG
     251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
     301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
     351 CGCGTTTGAA CAGGCGGAAA TGATTTATCA GAAATGGCGG CAGATTGAGC
     401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
     451 AGGGAAAGAG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
     501 GGCGGACGAA GGACAGAACC GCAGGGTGTT TTTATTGTTG GCACAAGCCG
     551 CCGTGCAACA GGACGGGTTG GCGCAAAAAG CATCGAAAGC GGTTCGCCGC
     601 GCGGCGTTGA AATATGAACA TCTGCCCGAA GCGGCGGTTG CCGATGTGGT
     651 GTTCAGCGTA CAGGGACGCG AAAAGGAAAA GGCAATCGGA GCTTTGCAGC
     701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCCACTTT AATGACGTTG
     751 CGTCTGACTG CACGCAAATA TCCCGAAATA CTCGACGGCT TTTTCGAGCA
     801 GACAGACACC CAAAACCTTT CGGCCGTCTG GCAGGAAATG GAAATTATGA
     851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTG
     901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
     951 GGCGGCAAAC CGAAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
    1001 AGGCATACGG CAGGGGACG GAGGAACAGC GGAGCAGGGC GGCGCTAACG
    1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAAG TCAGGCAGTG
    1101 GCTGAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
   1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
    1201 ATCGGCAGGG TGCGGAAACT TCCCGAACAG CAGGGGCGGT ATTTTACGGC
   1251 AGACAATTTG TCCAAAATAC AGATGCTCGC CCTGTCGAAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCCTGCC
   1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAGTTGT
    1401 TTACGATCGG CTTGGCAAGC GGAAAAAAT GATTTCAGAT CTTGAAAGGG
    1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
   1501 AGCCTGCTGA CCGATTCCAA ACGTTTGGAC GAAGGTTTCG CCCTGCTTCA
    1551 GACGGCATAC CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
    1601 GCTGGGCGTA TTACCTGAAA GGCGACGCGG AAAGCGCGCT GCCGTATCTG
    1651 CGGTATTCGT TTGAAAACGA CCCCGAGCCC GAAGTTGCCG CCCATTTGGG
    1701 CGAAGTGTTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
    1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAAACGCTC
         AAACGTCACG GCATCGCATT GCCCCAACCT TCCCGAAAAC CTCGGAAATA
```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>: m951.pep

```
1 MIMLPNRFKM LTVLTATLIA GQVSAAGGGA GDMKQPKEVG KVFRKQQRYS
51 EEEIKNERAR LAAVGERVNQ IFTLLGGETA LQKGQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRRVFLLL AQAAVQQDGL AQKASKAVRR
201 AALKYEHIPE AAVADVVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLTARKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAAILAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLAAAAAVE LDGGRAALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALSK LPDKREALRG LDKIIEKPPA
451 GSNTELQAEA LVQRSVVYDR LGKRKMISD LERAFRLAPD NAQIMNNLGY
551 RYSFENDPEP EVAAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPOP SRKPRK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from N. gonorrhoeae

O	
m951/g951	88.6% identity in 616 aa overlap
m951.pep	10 20 30 40 50 60  MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKEVGKVFRKQQRYSEEEIKNERAR
m951.pep g951	70 80 90 100 110 120 LAAVGERVNQIFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE         ::
m951.pep g951	130 140 150 160 170 180 QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRRVFLLL
m951.pep g951	190 200 210 220 230 240 AQAAVQODGLAQKASKAVRRAALKYEHLPEAAVADVVFSVQGREKEKAIGALQRLAKLDT :
m951.pep g951	250 260 270 280 290 300 EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
m951.pep g951	310 320 330 340 350 360 LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTEEQRSRAALTAAMMYADRRD    :   :
m951.pep	370 380 390 400 410 420 YAKVRQWLKKVSAPEYLFDKGVLAAAAAVELDGGRAALRQIGRVRKLPEQQGRYFTADNL
m951.pep g951	430 440 450 460 470 480 SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTELQAEALVQRSVVYDRLGKRKKMISD
m951.pep g951	490 500 510 520 530 540 LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK     :: :
m951.pep	550 560 570 580 590 600 GDAESALPYLRYSFENDPEPEVAAHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
m951.pep g951	610 KRHGIALPOPSRKPRK   :    :       KRYGIALPEPSRKPRKX 600 610

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2907>:
            ATGTTACCCG CCCGTTTCAC CATTTTATCT GTGCTCGCGG CAGCCCTGCT
           TGCCGGGCAG GCGTATGCCG CCGGCGCGCG GGATGCGAAG CCGCCGAAGG
        51
           AAGTCGGAAA GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
       101
       151 AAAAACGAAC GCGCACGGCT TGCGGCAGTG GGCGAGCGGG TTAATCAGAT
201 ATTTACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
           CGGCTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
       301
           GTCGCCGAAC GCGCCTTGGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
           GGCGGAAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
       351
       401 AGGCGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAAGAGGA
       451 AATCAGCATC TAGACGGACT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
      501
           ACAGAACCGC AGGGTGTTTT TATTGTTGGC ACAAGCCGCC GTGCAACAGG
      551 ACGGGTTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCGTTGAGA
      601 TATGAACATC TGCCCGAAGC GGCGGTTGCC GATGTGGTGT TCAGCGTACA
      GGGACGCGAA AAGGAAAAGG CAATCGGAGC TTTGCAGCGT TTGGCGAAGC
TCGATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
      751 CGCAAATATC CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
      801 AAACCTTTCG GCCGTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
           TGCACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGGAACGC
      851
      901 AATCCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAAACCG
      951 AAAAGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
           GGGGGACGGG GGAACAGCGG GGCAGGGCGG CAATGACGGC GGCGATGATA
     1001
     1051 TATGCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
     1101 GTCCGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGGCGG
     1151 CTGTCGAGTT GGACGGCGGC AGGGCGGCTT TGCGGCAGAT CGGCAGGGTG
     1201 CGGAAACTTC CCGAACAGCA GGGGCGGTAT TTTACGGCAG ACAATTTGTC
     1251 CAAAATACAG ATGTTCGCCC TGTCGAAGCT GCCCGACAAA CGGGAGGCTT
     1301 TGAGGGGGTT GGACAAGATT ATCGAAAAAC CGCCTGCCGG CAGTAATACA
          GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
     1351
          TGGCAAGCGG AAAAAATGA TTTCAGATCT TGAAAGGGCG TTCAGGCTTG
     1401
          CACCCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CCTGCTTTCC
     1501 GATTCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
     1551 AATCAACCCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
     1601 ACCTGAAAGG CGACGCGGAA AGCGCGCTGC CGTATCTGCG GTATTCGTTT
     1651 GAAAACGACC CCGAGCCCGA AGTTGCCGCC CATTTGGGCG AAGTGTTGTG
          GGCATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
     1751 ACCTTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
     1801 ATCGCATTGC CCCAACCTTC CCGAAAACCT CGGAAATAA
This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:
a951.pep
          MLPARFTILS VLAAALLAGQ AYAAGAADAK PPKEVGKVFR KQQRYSEEEI
          KNERARLAAV GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
      51
     101 VAERALEMAV SLNAFEQAEM IYQKWRQIEP IPGKAQKRAG WLRNVLRERG
     151 NQHLDGLEEV LAQADEGQNR RVFLLLAQAA VQQDGLAQKA SKAVRRAALR
     201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTEILP PTLMTLRLTA
          RKYPEILDGF FEQTDTQNLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
     251
     301 NPNADLYIQA AILAANRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
     351 YADRRDYTKV RQWLKKVSAP EYLFDKGVLA AAAAVELDGG RAALRQIGRV
     401 RKLPEQQGRY FTADNLSKIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
     451 ELQAEALVQR SVVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
     501 DSKRLDEGFA LLQTAYQINP DDTAVNDSIG WAYYLKGDAE SALPYLRYSF
          ENDPEPEVAA HLGEVLWALG ERDQAVDVWT QAAHLTGDKK IWRETLKRHG
     551
          IALPQPSRKP RK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. meningitidis
ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from
N. meningitidis
a951/m951
             96.4% identity in 614 aa overlap
                       10
                                 20
                                             30
                                                       40
              MLPARFTILSVLAAALLAGQAYAAG--AADAKPPKEVGKVFRKQQRYSEEEIKNERAR
a951.pep
               MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKEVGKVFRKQQRYSEEEIKNERAR
m951
                    10
                               20
                                                   40
                                                             50
                                   80
                                             90
                                                      100
a951.pep
            LAAVGERVNQIFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
```

PCT/US99/09346

1362

m951	
a951.pep	120 130 140 150 160 170  QAEMIYQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRRVFLLL
a951.pep	180 190 200 210 220 230 AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVFSVQGREKEKAIGALQRLAKLDT !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
a951.pep	240 250 260 270 280 290 EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
a951.pep	300 310 320 330 340 350  LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQRGRAAMTAAMIYADRRD
a951.pep	360 370 380 390 400 410 YTKVRQWLKKVSAPEYLFDKGVLAAAAAVELDGGRAALRQIGRVRKLPEQQGRYFTADNL  :
a951.pep	420 430 440 450 460 470  SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTELQAEALVQRSVVYDRLGKRKKMISD      :
a951.pep	480 490 500 510 520 530  LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
a951.pep	540 550 560 570 580 590  GDAESALPYLRYSFENDPEPEVAAHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
a951.pep	600 610 KRHGIALPQPSRKPRK   !

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2909>: g952.seq (partial)

	(bor crar)				
1	TTGTCTTATC	GTTTGAATGC	TGCACCGATG	TTTAACGATA	ATCCTGTTGT
51	TTACGGAAAA	ATCAAATTGC	AGAGTTGGAA	AGCGCGGCGG	GATTTCAATA
101	TTGTAAAGCA	GGATTTGGAT	TTTTCCTGCG	GGGCGGCTTC	GGTGGCGACG
151	CTTTTGAACA	ATTTTTACGG	GCAAAAGCTG	ACGGAAGAAG	AAGTGTTGGA
201	AAAACTGGGT	AAGGAACAGA	TGCGCGCGTC	GTTTGAGGAT	ATGCGGCGCA
251		TTTGGGTTTT			
301	CAGCTCGCGC	AGTTGAAAAT	CCCCGTCATC	GTGTATCTGA	AATACCGCAA
351		TTTTCGGTAT			
4C1	TTGCCGACCC	GTCGCCGGGT	CATGTTTCGA	TGAGCAGGGC	GCAGTTTTTG
451	GAGGCTTGGC	AAACCCGTGA	GGGAAATTTG	GCAGGCAAAA	TTTTGGCGGT
501	CGTGCCGAAA	AAAGCGGAGG	CGATTTCAAA	TAAATTGTTT	TTCACACATC
551	ATCCCAAGCG	GCAGACGGAG	TTTGCAGTCG	GACAGGTAAA	ATGGTGGCGT

```
GCTTATTGA
```

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>: g952.pep (partial)

```
.. LSYRLNAAPM FNDNPVVYGK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
       LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPDLGF EAKGYALSFE
 51
       QLAQLKIPVI VYLKYRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
101
       EAWQTREGNL AGKILAVVPK KAEAISNKLF FTHHPKRQTE FAVGQVKWWR
151
201
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2911>: m952.seq

```
ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
 51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGGCGGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCTGATT TGGGTTTTGA GGCGAAGGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGGCA TGTTTCAATG AGCAGGGCGC AGTTTTTGGA
    TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>: m952.pep

- 1 MMKFKYVFLL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
- 51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
- 101 MPDLGFEAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
- 151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH 201 PKRQTEFTVG QIRQARAE*

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from N. gonorrhoeae

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from N. gonorrhoeae

```
92.5% identity in 201 aa overlap
q952/m952;
                                     20
g952.pep
                       LSYRLNAAPMFNDNPVVYGKIKLQSWKARRDFNIVKQDLDFSCG
                       MMKFKYVFLLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG
m952
                10
                         20
                                 30
                                        40
                                                50
             50
                     60
                             70
                                     80
                                             90
                                                    100
          AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
g952.pep
          m952
          AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
                70
                        80
                                 90
                                               110
                                                       120
                    120
                            130
                                    140
                                            150
          {\tt LKIPVIVYLKYRKDDHFSVLRGVDGNTVLLADPSPGHVSMSRAQFLEAWQTREGNLAGKI}
q952.pep
          m952
          {\tt LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFLDAWQTREGNLAGKI}
                       140
                               150
                                       160
            170
                    180
                            190
                                    200
          LAVVPKKAEAISNKLFFTHHPKRQTEFAVGQVKWWRAYX
g952.pep
          m952
          LAVIPKKAETISNKLFFTQHPKRQTEFTVGQIRQARAE
               190
                       200
                               210
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2913>: a952.seq

ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT

```
51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTTCAATATT
    GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
    TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
    ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
301
351
    GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
    ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
401
451 GCCGACCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTTNGGA
    TGCTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCG
501
    TGCCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

- MMKFKYVFLL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
- VKQDLDFSCG AASVATLLNN FYGQTLTEEE YLKKLDKEQM RASFEDMRRI 51
- 101 MPDLGFEAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
- 151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH 201 PKRQTEFAVG QIRQARAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from N. meningitidis

```
a952/m952
          97.7% identity in 218 aa overlap
                        20
                                30
                                        40
          MMKFKYVFLLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG
a952.pep
          m952
          MMKFKYVFLLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG
                        20
                                30
                                       40
                70
                        80
                                90
                                       100
                                              110
          AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
a952.pep
          m952
          AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
                70
                        80
                                       100
                                              110
               130
                       140
                               150
                                       160
                                              170
          {\tt LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFXDAWQTREGNLAGKI}
a952.pep
          m952
          LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFLDAWQTREGNLAGKI
               130
                       140
                               150
                                       160
                                              170
               190
                       200
                               210
          LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAEX
a952.pep
          m952
         LAVIPKKAETISNKLFFTQHPKRQTEFTVGQIRQARAE
               190
                       200
                               210
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2915>: g953.seq

```
ATGAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
  1
    CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
 51
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCCGTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
    CATTCCCGTC GCCAACCTGC AAAGCGGTTC GCAACCCTTC ACCGGCCACC
    TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
251
301 GTTTCCACCA AATTCAACTT CAACGGCAAA AAACTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGCGGCA AAACCGCCCC CGTCAAACTC AAAGCCGAAA
    AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 СААААСААТА А
```

WO 99/57280 1365

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>: g953.pep

- MKKIIFAALA AAAVGTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT GSVEFDQAKR DGKIDITIPV ANLQSGSQPF TGHLKSADIF DAAQYPDIRF 51 VSTKFNFNGK KLVSVDGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVCGG 101
- DFSTTIDRTK WGVDYLVNAG MTKNVRIDIQ IEAAKQ*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2917>: m953.seq

```
ATGAAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
 1
51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCG
101 CCATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
151 ACCGGTTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCC ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAAACTGG TTTCCGTTGA
351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCGTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGG AGAAAACCGA AGTTTGTGGC
451 GGCGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

- MKKIIFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
- TGSVEFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAAQYPDIR 51
- FVSTKFNFNG KKLVSVDGNL TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG
- 151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from N. gonorrhoeae

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from N. gonorrhoeae

```
93.0% identity in 187 aa overlap
m953/q953
                        20
                                30
                10
                                        40
          MKKIIFAALAAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDOAK
m953.pep
          MKKIIFAALAAAAVGTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK
a953
                10
                         20
                                 30
                                        40
                                                50
                        80
                                90
                                       100
                                               110
m953.pep
          RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSVDGNL
          RDGKIDITIPVANLQSGSQPFTGHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSVDGNL
g953
                                 90
                                        100
                       140
                               150
                                       160
                                               170
                                                       180
          TMHGKTAPVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
m953.pep
          TMRGKTAPVKLKAEKFNCYQSPMAETEVCGGDFSTTIDRTKWGVDYLVNAGMTKNVRIDI
g953
        120
                130
                        140
                                150
m953.pep
          QIEAAKQX
          1111111
a953
          OIEAAKOX
        180
```

The following partial DNA sequence was identified in N. . meningitidis <SEQ ID 2919>: a953.seq

- ATGAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC 1
- 51 CTCCGCCGCC ACCTACAAAG TGGACGAATA TCACGCCAAC GCCCGTTTCT
- 101 CTATCGACCA TTTCAACACC AGCACCAACG TCGGCGGTTT TTACGGTCTG
- 151 ACCGGTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
- 201 CACCATCCCC GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
- 251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
- 301 TTTGTTTCCA CCAAATTCAA CTTCAACGGC AAAAAACTGG TTTCCGTTGA

WO 99/57280 PCT/US99/09346

1366

- CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCGTCAAA CTCAAAGCCG AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
- GGCGACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT 451
- 501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
- 551 CAGCCAAACA ATAA

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>: a953.pep

- MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
- TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
- 101 FVSTKFNFNG KKLVSVDGNL TMHGKTAPVK LKAEKFNCYQ SPMLKTEVCG
- GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKO*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from N. meningitidis

```
a953/m953
          97.3% identity in 187 aa overlap
                         20
                                 30
          MKKIIIAALAAAAIGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK
a953.pep
          MKKIIFAALAAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
m953
                         20
                                 30
                                         40
                 70
                         80
                                 90
                                        100
                                                110
                                                        120
          {\tt RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSVDGNL}
a953.pep
          m953
          RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNGKKLVSVDGNL
                70
                        80
                                90
                                        100
                                                110
                130
                        140
                                150
                                        160
                                                170
          TMHGKTAPVKLKAEKFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
a953.pep
          TMHGKTAPVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
m953
                        140
                                150
                                       160
                                               170
          QIEAAKQX
a953.pep
          1111111
m953
          QIEAAKQX
```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2921>: m954.seq

- ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
- 51 GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
- 101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
- CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT 151 201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
- TTACTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
- 301
- TACCGCGTCT GCAAACAGGC TGCGCAAGAT GCAGAAATCC TGATGAAGAG TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
- 401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAAC AATAACGGAA
- GCTGAAGCCA ATTTGCCGAA AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>: m954.pep

- MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
- RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP 51
- YRVCKQAAQD AEILMKSMVT SGGGGTTDLD KESYQNYRKS MQECRKTITE 101
- 151 AEANLPKK*

```
a954.seq not found yet a954.pep not found yet
```

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2923>: g957.seq (partial)
```

```
ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
 51 TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCGGT ATTTGATGCG GCGGGGCGCG GGAAAATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
    ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG GGGGatgaaG gcgaacagtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
    qaaaaaaacc ccaaagtgtc gaatattatt tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaacc tatcatgcgc aacaaacgtt gtatttggat ggg...
```

# This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>: g957.pep (partial)

```
1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51 AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGCYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS VDNGKKPQSV EYYLKNGNLF
```

301 IAQSSTVTLK TDGVTADMQT YHAQQTLYLD G...

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2925>: m957.seq

```
ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
     TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
  51
      TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
 101
 151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
 201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACT GTGGATGACG
     GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
 301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
 351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
     TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
     TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
 501 CGGGGAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
 551 ACGGTTCGGT ATTTGATGCG GCGGGGCGCG GGAAAATCGG GGAAGATGTT
     TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
 651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
 701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
 751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
     CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
 851 GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
 901 ATTGCACAAT CTTCGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
     TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
 951
     TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

# This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>: m957.pep

1 MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51 AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGCYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN

- 251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
- 301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
- 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from N. gonorrhoeae

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from N. gonorrhoeae

```
q957/m957
                               95.2% identity in 331 aa overlap
                                                                         20
                                                                                                                       40
                               MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNAFVAKLARLFRNA
 g957.pep
                               MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
 m957
                                                                         20
                                                                                                30,
                                                                                                                       40
                                                 70
                                                                         80
                                                                                                90
                                                                                                                    100
                                                                                                                                           110
                               DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV
 g957.pep
                               m957
                               DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV
                                                 70
                                                                         80
                                                                                                90
                                                                                                                    100
                                                                                                                                           110
                                                                                                                                                                  120
                                              130
                                                                      140
                                                                                             150
                                                                                                                    160
                                                                                                                                           170
                                                                                                                                                                  180
                              WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV
 g957.pep
                               WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
m957
                                              130
                                                                      140
                                                                                             150
                                                                                                                    160
                                                                                                                                           170
                                                                                                                                                                  180
                                              190
                                                                     200
                                                                                             210
                                                                                                                    220
                                                                                                                                           230
                                                                                                                                                                  240
                              WQPDGSVFDAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS
g957.pep
                               * [ * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ] * [ * ]
                              WQPDGSVFDAAGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS
m957
                                              190
                                                                     200
                                                                                             210
                                                                                                                    220
                                                                                                                                                                  240
                                                                     260
                                              250
                                                                                             270
                                                                                                                    280
                                                                                                                                           290
                                                                                                                                                                  300
                              DSRDYVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSVDNGKKPQSVEYYLKNGNLF
q957.pep
                              DSRNSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF
m957
                                              250
                                                                     260
                                                                                            270
                                                                                                                   280
                                                                                                                                          290
                                              310
                                                                     320
                              IAQSSTVTLKTDGVTADMQTYHAQQTLYLDG
g957.pep
                              m957
                              IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR
                                              310
                                                                     320
                                                                                            330
                                                                                                                                          350
                                                                                                                                                                  360
                              YAEAAARRSGGRRDLSHX
m957
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2927>: a957.seq

```
ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
     TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
 51
     TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAAACTT
101
     GCCCGCCTGT TCCGAAATGC CGACAGGGCG GTTGTCATCG TGAAGGAATC
151
     GATGAGGACG GAGGAAAGTC TTGCCGGAGC TGTGGATGAC GGTCCGTTGC
201
     AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
     GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGGAAGAGGT
301
     TTGGCTGGAT TACTATATCG GCGAGGGCGG TTTGGTTGCG GTTTCGCTTT
351
     CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
401
     GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
451
     TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
501
     TATTTGATGC GTCGGGGCGC GGGAAAATCG GGGAAGATGT TTATGAGCAT
551
     TGCCTCGGGT GTTATCAGAT GGCCCAGGTA TATTTGGCGA AATATCGGGA
601
651
     TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
     GGATTGCGTC GGACTCGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
701
751
    TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
     GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
801
851
     GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
     TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
```

```
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCGGG
```

1101 CGGCAGGCGC GACCTTTCTC ACTGA

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>: a957.pep

- MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL 51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
- 101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VSLSQRSPEA FVNAEYLYRN
- DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
  CLGCYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
- 251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
- 301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
- 351 LEKEVSRYAE AAARRSGGRR DLSH*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from N. meningitidis

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from N. meningitidis

a957/m957	96.3% identity in 377 aa overlap
a957.pep m957	10 20 30 40 50  MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATENPNAFVAKLARLFRNA
a957.pep	00 70 80 90 100 110  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV
a957.pep	120 130 140 150 160 170' WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
a957.pep	180 190 200 210 220 230  WQPDGSVFDASGRGKIGEDVYEHCLGCYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS
a957.pep	240 250 260 270 280 290  DSRDSVFYQNMRELMPRGMKANSLVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF    :
a957.pep m957	300 310 320 330 340 350  IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDLEKEVSR
a957.pep m957	360 370 YAEAAARRSGGRRDLSHX                 YAEAAARRSGGRRDLSHX 370

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2929>:

- 1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
- 51 TTTCGGCACG CATTGCGCCG CCGATACCGT TGCGGCGGAA GAGGCGGACG

```
101 GGCGTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAGCT
 151
      TCCGATTTGA CCCTCGGTTC GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
 201 CAGCCCCGAG AGAACCGAAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
 251 TCCCCGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
      AAGGTTAAGG TGCGCGCGGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
 351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
 401 CCGTAGGCGA CCGGTTCGCC CTCCAACAGG ACGGTACGCT GATTCGGGGC
      GAAACCCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACGT
 451
      CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAGC GTCAGCCGCA
 501
      CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAATTC
      AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
 601
      CGAAGCCGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
 651
      TGTTCGGCGG CGTTCCCCTT TTCTATACGC CTTGGGCGGA CTTCCCGCTT
 701
 751 GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
      GGACGGCGTT TCCCTTTCCG TCCCCTATTA TTTCAACCTT GCCCCCAACT
      TCGATGCCAC TTTCGCCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
 851
      GACGGACAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
      GACCTGGTTG CCGCACGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
 951
1001
      CAAAATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GGCGGGTGTC
      GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1051
1101 CGAAGAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
      ATGGCGGCAG GGCGGCGGA GGCAGCCTGA ATGCCGGCCT TTCGGTTCAG
1151
      AAATACCAGA CGCTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1201
1251 CATCATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
      GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAAATGGG ATTTCAGCAA
1401 CAGCTGGGGC TACGTCCGCC CCAAACTCGG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCGGCGGC AAAGCATCCC GCAGCGTCGG GCGCGTTTTG
1501 CCCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
      GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAACT
1601 ATATTCCTGC CAAATCTCAA AACGACCTGC CCAATTTCGA TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
     CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCCGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TGCGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTCGCCTCC GGCGGCATAG
     GCGGGCGTTT CACCCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCCGT CGGCGCAGGC TACCGCCCCG CCCCCGGAAA
2001 AGTGTTGAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGCGGACGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
     GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCGTCC GCTACAACTA
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GGCGCGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCCGTC TTTTTTTCAC TTCAGTTGAA
     AGACCTCAGC AGCGTCGGCA GAAACCCCGC AGGCAGGATG GATGTCGCCG
2301
2351 TTCCCGGCTA CATCCCCGCC CACTCTCTTT CCGCCGGACG CAACAAACGG
```

# This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>: g958.pep

```
LARLFSLKPL VLALGFCFGT HCAADTVAAE EADGRVAEGG AQGASESAQA
    SDLTLGSTCL FCSNESGSPE RTEAAVQGSG EASVPEDYTR IVADRMEGOS
 51
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQQDGTLIRG
151 ETLTYNLDQQ TGEAHNVRME TEQGGRRLQS VSRTAEMLGE GRYKLTETQF
201 NTCSAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
    DGQIRYLRPD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
    DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
351
    KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSHDGRO
401
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
    PVVNIDGGTT FERNTRLFGG GVVQTIEPRL FYNYIPAKSQ NDLPNFDSSE
501
    SSFGYGQLFR ENLYYGNDRI NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSVGKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLQADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAORYV
    TGENTYKNAV FFSLQLKDLS SVGRNPAGRM DVAVPGYIPA HSLSAGRNKR
```

# The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2931>: m958.seq

- 1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
  51 CTTCGGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
- 101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATACAG

```
1371
```

```
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
 201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
      CCATCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
 301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAACCG
 351 GACGACCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
      TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCGG
      GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
 451
      CGTCCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
 551
      GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
      TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
      TGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
      TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
      CTTGACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
 801 TTCGGACGGC GTTTCCCTTT CCGTTCCCTA TTATTTCAAC CTTGCCCCCA
 851 ATCTCGATGC CACGTTCGCG CCCAGCGTGA TCGGCGAACG CGGCGCGGTC
      TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
 951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGG CAGGGCGGCG GGCGGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTCGAGTG GCGTAAAAAC ACCGGCAGGG
1301 CGCAAATCGG CGTGTCCGCA CAATTTACCC GATTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCCGCCTGGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAACT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATTG TCAACATCGA CAGCGGCGCA ACTTTTGAGC GGAATACGCG
1551 GATGTTCGGC GGAGAAGTCC TGCAAACCCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCGTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAGCC
1751 GTATTTTGGA CGGCGCGACG GGGGAAGAGC GTTTCCGCGC CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGCAGCCG CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
      CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAAACGCT GTCTTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTCG GCAGAAACCC CGCAGACAGG ATGGATGTCG
     CCGTTCCCGG CTATATCACC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
2351
```

#### This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```
m958.pep
           LARLFSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
      51 PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
     101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQQDGTLIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGGRRLQ SVSRTAEMLG EGHYKLTETQ
     201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP
     251 LDGNRKSGLL VPSLSAGSDG VSLSVPYYFN LAPNLDATFA PSVIGERGAV
     301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
     351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSLNAGLSV
     401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSHDSR
     451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFG SQEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLEPR LFYNYIPAKS QNDLPNFDSS
     551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
     601 QKFYFKDDAV MLDGSVGKKP RNRSDWVAFA SGSIGSRFIL DSSIHYNQND
           KRAENYAVGA SYRPAQGKVL NARYKYGRNE KIYLKSDGSY FYDKLSQLDL
          SAQWPLTRNL SAVVRYNYGF EAKKPIEVLA GAEYKSSCGC WGAGVYAQRY
     701
           VTGENTYKNA VFFSLOLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
     751
     801
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

CGACCCTGA

2401

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from N. gonorrhoeae

m958/g958	89.3% identity in 802 aa overlap
m958.pep	10 20 30 40 50 60 LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC
m958.pep	70 80 90 100 110 120 LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL
m958.pep	130 140 150 160 170 180 NTDWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMEIEQGGRRLQ
m958.pep g958	190 200 210 220 230 240 SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP
m958.pep	250 260 270 280 290 300 IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPSVIGERGAV :
m958.pep	310 320 330 340 350 360  FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG     :
m958.pep	370 380 390 400 410 420 YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM       ::
m958.pep	430 440 450 460 470 480 PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH     :: :  :
m958.pep	490 500 510 520 530 540 ATYYSLNRFGSQEARRVSRTLPIVNIDSGATFERNTRMFGGEVLQTLEPRLFYNYIPAKS
m958.pep	550 560 570 580 590 600 QNDLPNFDSSESSFGYGQLFRENLYYGNDRINTANSLSAAVQSRILDGATGEERFRAGIG
m958.pep	610 620 630 640 650 660  QKFYFKDDAVMLDGSVGKKPRNRSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA
m958.pep g958	670 680 690 700 710 720 SYRPAQGKVLNARYKYGRNEKIYLKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF :

```
730
                       740
                              750
                                      760
         EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
m958.pep
         EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
a958
        720
                       740
                               750
                                      760
               790
                      800
         MDVAVPGYITAHSLSAGRNKRP
m958.pep
         MDVAVPGYIPAHSLSAGRNKRPX
g958
                790
                       800
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2933>:

```
a958.seq
         TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
         TTTCGGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
     51
    101
         ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
    151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
    201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
         CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
    301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
    351 GACGACCCTC AATGCCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
    401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCGG
         GGCGAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
    501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
    551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
         TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
    651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
    701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
    751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCCGCCGG
         TTCGGACGGC GTTTCCCTTT CCGTTCCCTA TTATTTCAAC CTTGCCCCCA
    851 ATCTCGATGC CACGTTCGCG CCCGGCGTGA TCGGCGAACG CGGCGCGGTC
    901 TTTGACGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
    951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
         AGGCGAAATG GCAGCACCGG CACGACATTT CCGACACGCT TCAGGCGGGT
   1001
   1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
   1101 CAACAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
         ATTATGGCGG CAGGGCGGCG GGCGGCAGCC TGAATGCCGG CCTTTCGGTT
   1151
         CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAACCGTA
   1201
         TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAAC ACCGGCAGGG
   1301 CGCAAATCGG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
         CAAGACGGCA GCCGCCTCGT CGTCTATCCC GACATCAAAT GGGATTTCAG
   1401 CAACAGCTGG GGTTACGTCC GTCCCAAACT CGGACTGCAC GCCACCTATT
   1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
   1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
   1551 GATGTTCGGC GGCGGAGTCC TGCAAACCCT CGAGCCGCGC CTGTTCTACA
   1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCGTCG
   1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTTT CGTGAAAACC TCTATTACGG
         CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAGCC
   1751 GTATTTTGGA CGGCGCGACG GGGGAAGAGC GTTTCCGCGC CGGCATCGGG
   1801 CAGAAATTCT ACTTCAAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCGG
   1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTCGCC TCCAGCGGCA
   1901
         TCGGCAGCCG CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAAACGAC
   1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
   2001 CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
   2051
         TGAAGTCCGA CGGTTCCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
   2101
         TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
   2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
   2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
   2251
         GTTACCGGCG AAAACACCTA CAAAAACGCT GTCTTTTTCT CACTTCAGTT
   2301 GAAAGACCTC AGCAGTGTCG GCAGAAACCC CGCAGACAGG ATGGATGTCG
   2351 CCGTTCCCGG CTATATCCCC GCCCACTCTC TTTCCGCCGG ACGCAACAAA
   2401 CGGCCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>: a958.pep

```
LARLFSLKPL VLALGFCFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIO
 51 PTSLSLGSTC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGTLIR
151 GETLTYNLEQ QTGEAHNVRM ETEHGGRRLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGGVP IFYTPWADFP
```

WO 99/57280

251 LDGNRKSGLL VPSLSAGSDG VSLSVPYYFN LAPNLDATFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFG SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLQTLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDAV MLDGSVGKKP RSRSDWVAFA SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGKVL NARYKYGRNE KIYLKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLA GAEYKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. meningitidis* 

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from N. meningitidis

a958/m958	98.1% identity in 802 aa overlap
a958.pep m958	10 20 30 40 50 60  LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC
a958.pep m958	70 80 90 100 110 120 LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGQSQVQVRAEGNVVVERNRTTL
a958.pep m958	130 140 150 160 170 180 NADWADYDQSGDTVTAGDRFALQQDGTLIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ I:
a958.pep	190 200 210 220 230 240  SVSRTAEMLGEGHYKLTETOFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFVFGGVP
a958.pep	250 260 270 280 290 300 IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPYYFNLAPNLDATFAPGVIGERGAV
a958.pep	310 320 330 340 350 360  FDGQVRYLRPDYAGQSDLTWLPHDKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG
a958.pep	370 380 390 400 410 420 YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
a958.pep	430 440 450 460 470 480 PRLSADWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH     ::
a958.pep	490 500 510 520 530 540 ATYYSLNRFGSQEARRVSRTLPIVNIDSGMTFERNTRMFGGGVLQTLEPRLFYNYIPAKS

	490	500	510	520	530	540
	550	560	570	580	590	600
a958.pep	ONDLPNFDSSESSF					
0.50						
m958	QNDLPNFDSSESSF 550	560				
	330	360	570	580	590	600
	610	620	630	640	650	660
a958.pep	QKFYFKNDAVMLDG	SVGKKPRSRS	DWVAFASSGI	GSRFILDSSI	HYNQNDKRAI	ENYAVGA
•	111111:111111	11:111111	1111111::1	1111111111	111111111	
m958	QKFYFKDDAVMLDG	SVGKKPRNRS	DWVAFASGS I	GSRFILDSSI	HYNONDKRAI	ENYAVGA
	610	620	630	640	650	660
	670	680	690	700	710	720
a958.pep	SYRPAQGKVLNARY					
m958	SYRPAQGKVLNARY			KLSQLDLSAQW	PLTRNLSAV	JRYNYGF
	670	680	690 ·	700	710	720
	730	740	750	760	770	780
a958.pep	EAKKPIEVLAGAEY					
					111111111	
m958	EAKKPIEVLAGAEY					GRNPADR
	730	740	750	760	770	780
	200					
	790	800				
a958.pep	MDVAVPGYIPAHSL:					
m958	MDVAVPGYITAHSL:					
	790	800				

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2935>: g959.seq

- 1 ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
  - 51 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
  - 101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
  - 151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
  - 201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
- 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
  301 GTGATTTCCT CCCGCCGCGA CGACTGA
- 301 GIGATITECT CCCGCGGGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>: g959.pep

- 1 MNIKHLLITA AATALLGISA PALAHHDGHG DDDHGHAAHQ HGKQDKIISR
- 51 AQAEKAAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
- 101 VISSRRDD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

- 1 ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
- 51 CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
- 101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
- 151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
- 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
- 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>: m959.pep

- 1 MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAAHQ HNKQDKIISR
- 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
- 101 VISSRRDD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from N. gonorrhoeae

```
m959/g959
          95.4% identity in 108 aa overlap
                10
                        20
                                30
                                        40
          MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAAHQHNKQDKIISRAQAEKAALAR
m959.pep
          MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAAHQHGKQDKIISRAQAEKAAWAR
g959
                10
                        20
                                30
                                       40
                                               50
                70
                        80
                                       100
          VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
m959.pep
          VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
q959
                        80
                                90
                                       100
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2939>: a959.seq

- ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG 1 CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC 51
- ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC 101 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
- 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
- 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
- 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEO ID 2940; ORF 959.a>: a959.pep

- MNFKRLLLTA AATALMGISA PALAHHDGHG DDDHGHAAHQ HSKODKIISR
- 51 AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
- 101 VISSRRDD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from N. meningitidis

```
a959/m959
          94.4% identity in 108 aa overlap
                10
                        20
                                30
                                       40
          MNFKRLLLTAAATALMGISAPALAHHDGHGDDDHGHAAHQHSKQDKIISRAQAEKAALAR
a959.pep
          m959
          MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAAHQHNKQDKIISRAQAEKAALAR
                10
                        20
                                30
                                       40
                                               50
                        80
                                90
                                       100
          VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
a959.pep
          m959
          VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
                               90
                                      100
```

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2941>: m960.seq

ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT 1 51 TAAGCCCCCC TTGTTTGAAG CTCCGCGGCT CCTGCCGAGC TTCACCGACC CCGTTGTGCC CAAGCTCTCT GCTCCCGGCG GCTACATTGT CGACATCCCC 101 AAAGGCAATC TGAAAACCGA AATCGAAAAG CTGGCCAAAC AGCCCGAGTA 151 TGCCTATCTG AAACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAACCAGG 201 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA 251 GCCGGTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG 351 401 ATGCCGCCTT TGCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC 451 NATAAAGGCG ATGTCGGCAA AACCCTGAAG GAACTGGGCA GAAGCCGCAC

GGTAAAAAAT CTGGTTGTAG CGGCGGCAAC GGCAGGCGTA TCCAACAAAC

WO 99/57280 PCT/US99/09346

```
1377
```

```
551 TCGGTGCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
     601 CTCAACGTTA ACCTGGCCAA TGCGGGCAGT GCCGCGCTGA TCAACACCGC
          TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
     701 CATTGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
     751 GATCAGCACT ATGTCGCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
          GGCTGCAGCG GCGAATAAGG GCAAATGTCA GGACGGCGCG ATCGGTGCGG
     851 CTGTGGGTGA GATTGTCGGG GAGGCTTTGG TTAAAAATAC CGATTTTAGC
     901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
    951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAAACGCGG TAGAAAATAA TGCGGTTAAA
    1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
    1101 AAAAAACGGG AAAATCAACG TTAGAGATTT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCGA CGAAACATTG
    1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
          GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTTAG
          AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
    1351 ACATACATGA AAAATAATCC TTTTGGAAAA CAGCTGGCTC AAATTTCAGA
    1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
    1451
          GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATTT AGATGGCCAA
    1501 CATAAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAACT TTAAGTTTGT
    1551 TCTAAATATG GATGGTTCGC TTAACCAAAT GAAAACTGGG GCAGCAAAAG
    1601 GTCGTAAATT AAACTTAAAA TAG
This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:
m960.pep
          MQVNIQIPCM LYRRGSVKPP LFEAPRLLPS FTDPVVPKLS APGGYIVDIP
      51 KGNLKTEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDYKOEGLTR
     101 AGAAIIALAV TVVTAGAGVG AALGLNGAAA AAADAAFASL ASQASVSLIN
     151 NKGDVGKTLK ELGRSRTVKN LVVAAATAGV SNKLGASSLA TWSETPWVNN
     201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKCQDGA IGAAVGEIVG EALVKNTDFS
     301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
     351 AVVTAAKVVY KVARKGLKNG KINVRDLKQT LKDEGYNLAD NLTTLFDETL
     401 DWNDAKAVID IVVGTELNRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
     451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVF LVKRNOGLLK TGDRFYLDGO
     501 HKNHLEVFDK NGNFKFVLNM DGSLNQMKTG AAKGRKLNLK *
a960.seq not found yet
a960.pep not found yet
g961.seq not found yet
g961.pep not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2943>:
m961.seq
          ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
      51 CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
     101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
     151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTTGAAGCC GACGACTTTA
     251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
     301 GAAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
     351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
     401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
     451 AATATAACGA CATTTGCTGA AGAGACTAAG ACAAATATCG TAAAAATTGA.
     501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
     551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
     601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAACA
     651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAGCCG
     701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
     751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAAGCTGA
     801 · TATTGCTAAA AACTCAGCAC GCATCGACAG CTTGGACAAA AACGTAGCTA
     851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
     901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
     951 CGGCGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
    1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
    1051 GGTTCTTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA
```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>: m961.pep

MSMKHFPAKV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGOEI

WO 99/57280

```
51 NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
        ENKONVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
        NITTFAEETK TNIVKIDEKL EAVADTVDKH AEAFNDIADS LDETNTKADE
    201 AVKTANEAKQ TAEETKQNVD AKVKAAETAA GKAEAAAGTA NTAADKAEAV
    251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEOAALS
    301 GLFQPYNVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
    351 GSSAAYHVGV NYEW*
a961.seq not found yet
a961.pep not found yet
          not found yet
g972.seq
g972.pep
          not found yet
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2945>:
m972.seq
          TTGACTAACA GGGGGGGGC GAAATTAAAA ACCARTTCCA AGAGTAGTGA
       1
         ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
         GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
     151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
     201 CGGTTGCCCT TTATTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
     251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
     301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCGG ATGATGTTGA
     351 TTATGGAGAG GTGCATTTCG GArGTCAGCG CAATACTGTT TTAGTTGAGT
     401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
     451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
     501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
     551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
     601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
     651 TGTAGGTCGC AAGAAAATT CTCGTTTTGT TCGTGTTTAT GAGAAAGGCA
     701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCGA GATCCAGTTT
     751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
     801 GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
     851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTCGAG
         CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAAACTGG TCAATTTCAT
     951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
    1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
   1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
   1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
   1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
   1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
   1251 AGATTATGAT TATTTTTAA
This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:
m972.pep
         LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGKLLEIP ORRGKODGVF
     51 VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
     101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
     151 KQFLDDSIRT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
     201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIOF
     251 NYGDIEIPLD ILINQGSYFC GAFPICRKFK NMPVPERFDQ RKKKLNLTFE
     301 HKLHYAKNAV GKLVNFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
     351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
     401 KERKYQEYLS KVYHQNVDYD YF*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2947>:
     a972.seq
               TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
```

```
51 ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
    GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
101
    GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
    CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
```

	•
251	AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301	GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCGG ATGATGTTGA
351	TTATGGAGAG GTGCATTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401	TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451	AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501	AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551	ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601	ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651	TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTTTAT GAGAAAGGCA
701	GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCGA GATCCAGTTT
751	AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801	GTATTTCTGT GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851	TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901	CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAAACTGG TCAATTTCAT
951	GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001	ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051	TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101	TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
1151	ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201	AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC~ATCAAAATGT
1251	AGATTATGAT TATTTTTAA
1231	AGAITAIGAI TATTITTAA
m1 *	de to the amine said comment of CDO ID 2040, ODE 070
i nis correspond	Is to the amino acid sequence <seq 2948;="" 972.a="" id="" orf="">:</seq>
a972.pep	
1	LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKGKLLEIP QRRGKQDGVF
51	VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101	GNKFYESMYR LGSDDVDYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151	KQFLDDSIRT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201	TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251	NYGDIEIPLD ILINQGSYFC GAFPICRKFK NMPVPERFDQ RKKTLNLTFE
301	HKLHYAKNAV GKLVNFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351	LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401	KERKYQEYLS KVYHQNVDYD YF*
.01	
m072/2072 00	0.3% identity in 422 aa overlap
1117/2/03/2 99	*
	10 20 30 40 50 60
m972.pep	LTNRGGAKLKTXSKSSERMSEVEYFSHFISDGKGKLLEIPQRRGKQDGVFVDWISFTFHE
a 972	LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGKGKLLEIPQRRGKQDGVFVDWISFTFHE
	10 20 30 40 50 60
	70 80 90 100 110 120
m972.pep	DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE
a972	DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE
	70 80 90 100 110 120
	130 140 150 160 170 180
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSIRTRITRIDLALDFFDGEYTPDQ
• •	
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSIRTRITRIDLALDFFDGEYTPDQ
	130 140 150 160 170 180
	190 200 210 220 230 240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKKNSRFVRVYEKGRQLGDKE
4372	
	190 200 210 220 230 240
	250 260 270 280 290 300
m972.pep	250 260 270 280 290 300 SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFPICRKFKNMPVPERFDQRKKKLNLTFE
m3/2.pep	
a 972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFPICRKFKNMPVPERFDQRKKTLNLTFE
ayız	250 260 270 280 290 300

```
310
                       320
                               330
                                       340
                                               350
          HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI
m972.pep
          HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI
a 972
               310
                       320
                               330
                                       340
                       380
                               390
                                       400
                                               410
          HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVDYD
m972.pep
          a 972
          HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVDYD
                       380
                               390
                                       400
          YFX
m972.pep
          \Pi
a 972
          YFX
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2949>: g973.seq

```
ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
  1
 51 actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
    CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
    TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
401
    CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
    TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
    ACGAGTTTGA CGAAGACGAA AGCGCcgacg acatCCACTC cgTTTccqCC
    GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
    TTTCGGTACG GAatacggca gcgaagaagc cgacaccatc ggcggctTGG
    TCATTCAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTAtc
701
    qqcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
    GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgccgttT
851
    CTGCacAGTT TAG
```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>: q973.pep

```
1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
```

- KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED 51
- 101 KDEVLGILHA KDLLKYMFNP EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
- QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
- ERWRIHAATE IEDINAFFGT EYGSEEADTI GGLVIQELGH LPVRGEKVLI
- 251 GGLQFTVARA DNRRLHTLMA TRVK*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2951>: m973.seq

```
ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCG
 1
    ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
 51
101
    AGGCGCACGA GCAGGAAGTT TTTGATGCGG ATACGCTTTT AAGATTGGAA
CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
201
    CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
    CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
    ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
    GaACGCTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT
```

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CTTCGGCACG GAATACAGCA KCGAAGAAGC CGACACCATT GGCGGCCTGG
        TCATTCAAGA GTTGGGACAT CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
    701
        GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
        GCTGATGGCG ACCCGCGTGA AGTAA
This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:
m973.pep
        MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLLRLE
        KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
        KDEVLGILHA KDLLKYMFNP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
    151 ORNHMAIVID EYGGTSGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
    201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVLI
    251 GGLQFTVARA DNRRLHTLMA TRVK*
Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from N. gonorrhoeae
ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng)
from N. gonorrhoeae:
m973/g973
                            20
                                    30
                                             40
                                                      50
                                                               60
                   10
           MDGAOPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSDLEV
m973.pep
           MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLTRLEKVLDFAELEV
g973
                                    30
                           20
                                             40
                                                      50
                                                               60
                  10
                   70
                            80
                                    90
                                            100
                                                     110
                                                              120
           RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFNP
m973.pep
           RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFNP
g973
                  70
                                            100
                                   150
                                            160
                                                     170
                  130
                           140
           EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
m973.pep
           EQFHLKSVLRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
g973
                           140
                                   150
                                            160
                                                     170
                  130
                  190
                           200
                                   210
                                            220
           ETEDEFDEDDSADNIHAVSSERWRIHAATETEDINTFFGTEYSXEEADTIGGLVIQELGH
m973.pep
           DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFFGTEYGSEEADTIGGLVIQELGH
q973
                                   210
                                            220
                                                     230
                  190
                           200
                           260
                                   270
                  250
           LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
m973.pep
           LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
q973
                                   270
                  250
                           260
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2953>:
    a973.seq
             ATGGACGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
             ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
         101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
         201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
             CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGTGAAGAC
         301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT
         351
             GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CCTGCCGTCT
             TCGTCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
         401
         451
             CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
             TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
         501
```

ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

```
601
              GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
               TTTCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
               TCATTCAGGA ATTGGGACAC CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
               GGCGGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
              GCTGATGGCG ACCCGCGTGA AGTAA
This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:
     a973.pep
              MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLLRLE
            1
              KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
           51
              KDEVLGILHA KDLLKYMFNP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
              QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
          201
              ERWRIHAATE IEDINAFFGT EYSSEEADTI GGLVIQELGH LPVRGEKVLI
          251
              GGLQFTVARA DNRRLHTLMA TRVK*
          97.8% identity in 274 aa overlap
m973/a973
                         10
                                   20
                                            30
                                                      40
                                                               50
                 MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLLRLEKVLDFSDLEV
     m973.pep
                 a973
                 MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLLRLEKVLDFSDLEV
                         10
                                   20
                                            30
                                                      40
                                                               50
                                                                         60
                         70
                                   80
                                            90
                                                     100
                                                              110
                                                                        120
                 RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFNP
     m973.pep
                 RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFNP
     a973
                         70
                                   80
                                            90
                                                     100
                                                              110
                        130
                                  140
                                           150
                                                     160
                                                              170
                                                                        180
                 EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
     m973.pep
                 EOFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
     a973
                        130
                                  140
                                           150
                                                    160
                                                              170
                                                                        180
                        190
                                  200
                                           210
                                                    220
                                                              230
                                                                        240
     m973.pep
                 EIEDEFDEDDSADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH
                 DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFFGTEYSSEEADTIGGLVIQELGH
     a973
                        190
                                  200
                                           210
                                                    220
                                                              230
                        250
                                 260
     m973.pep
                 LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
                 a973
                 LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
                        250
                                 260
                                           270
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2955>:
g981.seq
        ATGAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCAC TCGCGCTGTC
     1
        TGCCTGCGGC GGTCAGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
     51
        GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
    151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
    201
        GATGGCGAAG GCGGGCAATT TTAAAATCGA ATTCAAACAC CAGCCGTGGG
    251
        ACAGCCTTTT CCCCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
    301 GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
   351 GTATTTGAA ATCACCCAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
    401 CTTCTTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTTACCGGC
    451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
    501
        AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAAGAA CTGGAAAACG
        GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
    601
        AAAAACAACC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
   651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
   701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
    751 AAGATCTACG CCAAATATTT TGCCAAAGAG GGCGGACAGG CTGCGAAATA
    801
```

WO 99/57280

```
This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:
g981.pep
         MKKWIAAALA CSALALSACG GQGKDAAAPA ANPGKVYRVA SNAEFAPFES
      1
         LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMS
     51
         GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK KMNKVGVVTG
     101
         HTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANYV
     201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
    251 KIYAKYFAKE GGQAAK*
The following partial DNA sequence was identified in N. meningitidis <SEO ID 2957>:
m981.seq
         ATGAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
      1
         TGCCTGCGGC GGTCAGGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
     51
    101
         ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
         TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
    201
         GATGGCGAAG GCGGGCAATT TTAAAATCGA ATTCAAACAC CAGCCGTGGG
    251 ACAGCCTTTT CCCCGCCTTA AACAACGGCG ATGCGGACGT TGTGATGTCG
         GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
         GTATTTTGAA ATCACCCAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
         CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
         TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAATCCGAA
    451
    501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
    551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG
    601 AAAAACAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
    651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
         AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
    751 AAGATTTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:
m981.pep
         MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
      1
        LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMS
     51
         GVTITDDRKO SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK NMNKVGVVTG
    151 YTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANYV
         KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
         KIYAKYFAKE DGQAAK*
m981/g981
            98.1% identity in 266 aa overlap
                            20
                                     3.0
                                              40
                   10
                                                       50
            MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
981.pep
            MKKWIAAALACSALALSACGGQGKDAAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF
g981
                            20
                                     30
                   10
                                              40
                                                       50
                   70
                            80
                                     90
                                             100
                                                      110
            DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSGVTITDDRKQSMDFSDPYFE
981.pep
            DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSGVTITDDRKQSMDFSDPYFE
a981
                   70
                            80
                                     90
                                             100
                  130
                           140
                                    150
                                             160
                                                      170
981.pep
            ITQVVLVPKGKKVSSSEDLKNMNKVGVVTGYTGDFSVSKLLGNDNPKIARFENVPLIIKE
            ITOVVLVPKGKKVSSSEDLKKMNKVGVVTGHTGDFSVSKLLGNDNPKIARFENVPLIIKE
g981
                  130
                           140
                                    150
                                             160
                           200
                                    210
                  190
                                             220
                                                      230
                                                               240
            LENGGLDSVVSDSAVIANYVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
981.pep
            LENGGLDSVVSDSAVIANYVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
g981
                           200
                  190
                                    210
                                             220
                                                      230
                                                               240
                           260
                  250
981.pep
           EKVRESGEYDKIYAKYFAKEDGQAAKX
            q981
           EKVRESGEYDKIYAKYFAKEGGQAAKX
                  250
                           260
```

```
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2959>:
     a981.seq
              ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
          51
              TGCCTGCGGC GGTCAGGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
              ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
              TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
              GATGGCGAAG GCGGGCAATT TTAAAATCGA ATTCAAACAC CAGCCGTGGG
              ACAGCCTTTT CCCCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
              GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
              GTATTTTGAA ATCACCCAAG TCGTCCTCGT TCCGAAAGGC AAAAAAATAT
              CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
              TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
         501 AATCGCGCGC TTTGAAAACG TTCCCCTGAT TATCAAAGAA CTGGAAAACG
         551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
         601 AAAAACAATC CGACCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
         651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
         701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
             AAAATCTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
         801
This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:
     a981.pep
              MKKWIAAALA CSALALSACG GQGKDAAAPA ANPDKVYRVA SNAEFAPFES
             LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVVMS
          51
             GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKISSSEDLK NMNKVGVVTG
         151 YTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SDSAVIANYV
         201 KNNPTKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
             KIYAKYFAKE DGQAAK*
           98.5% identity in 266 aa overlap
m981/a981
                                          30
                                                   40
                                                            50
                                                                     60
                MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
    m981.pep
                 MKKWIAAALACSALALSACGGQGKDAAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
    a981
                        10
                                 20
                                                   40
                        70
                                 80
                                          90
                                                  100
                DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSGVTITDDRKQSMDFSDPYFE
    m981.pep
                DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVVMSGVTITDDRKQSMDFSDPYFE
    a981
                        70
                                 80
                                          90
                                                  100
                                                           110
                                                                    120
                       130
                                140
                                         150
                                                  160
                                                           170
                                                                    180
                ITQVVLVPKGKKVSSSEDLKNMNKVGVVTGYTGDFSVSKLLGNDNPKIARFENVPLIIKE
    m981.pep
                a981
                ITQVVLVPKGKKISSSEDLKNMNKVGVVTGYTGDFSVSKLLGNDNPKIARFENVPLIIKE
                       130
                                140
                                         150
                                                  160
                                                           170
                                                                    180
                       190
                                200
                                                  220
                                         210
                                                           230
                                                                    240
                LENGGLDSVVSDSAVIANYVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
    m981.pep
                LENGGLDSVVSDSAVIANYVKNNPTKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
    a981
                       190
                                200
                                         210
                                                  220
                                                           230
                       250
                                260
    m981.pep
                EKVRESGEYDKIYAKYFAKEDGQAAKX
                a981
                KKVRESGEYDKIYAKYFAKEDGQAAKX
                      250
                                260
```

## The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2961>:

```
q982.seq
          atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
         caacggcgTg aatattttgc cggccgcCga ttgggtagcC ttgGGcgcCA
     101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
         AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
         AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAAcgaCq
         tagCCGgcga cggtacgact accgCCACCG TATTGGCACA ATCCATCGTT
         GCCGAAggcA TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
         ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
         TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
         TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
         AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
         AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
     551
     601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
         TCCGTTTGTT TTGCTGTTCG ACAAAAAAT CAGCAACATC CGCGACCTGC
         TGCCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCCGCT GTTGATTATC
         GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
         CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
         GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
         ATTtccGAAG Aagtcggcct GTCTTTGGAA AAAgcgactT TGgacgaCTT
         Gggtcaaacc aaACGcatCG AAATCGGtga agaaaacact ACCGTCATcg
         acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTGC CGAAATCCGC
    1001
         CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
   1051
   1101 GCGCGTTGCC AAACTGGCAG GAGGCGTGGC AGTGATCAAA GTCGGCGCGG
   1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
   1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
   1251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
   1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
   1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
    1401 CAAAGTGTTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
   1451 AATACGGCGA CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
   1501 CGTTCCGCGC TGCAACACGC CGCGTCTAtC GCCGGTCTGA TGCTGACGAC
    1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
        TGGGGGGAAT GGGCGGTATG GGCGGCATGA TGTAA
```

#### This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```
q982.pep
         IASONLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
      1
         KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
     51
    101 AEGMKYVTAG MNPTDLKRGI DKAVAALVEE LKNIAKPCDT SKEIAQVGSI
         SANSDEOVGA IIAEAMEKVG KEGVITVEDG KSLENELDVV EGMQFDRGYL
         SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLII
    251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
    301 ISEEVGLSLE KATLDDLGQT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
    351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
    401 HATRAAVEEG VVAGGGVALL RARAALENLH TGNADQDAGV QIVLRAVESP
         LROIVANAGG EPSVVVNKVL EGKGNYGYNA GSGEYGDMIG MGVLDPAKVT
         RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGGM GGMM*
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2963>:

```
m982.seg
         ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
      1
      51 AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
     101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
     151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
     201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TGCGTCCAAA ACCAACGACG
     251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
     301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
     351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAACA
         TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
         TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
         AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
         AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
         TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA
```

651	TCCGTTTGTA	TTGTTGTTCG	ACAAAAAAAT	CAGCAACATC	CGCGACCTGC
701	TGCCTGTTTT	GGAACAAGTG	GCAAAAGCCA	GCCGTCCGCT	GTTGATTATC
751	GCTGAAGACG	TAGAAGGCGA	AGCCTTGGCG	ACTTTGGTCG	TGAACAACAT
801	CCGAGGCATC	CTGAAAACCG	TTGCCGTCAA	AGCCCCTGGC	TTCGGCGACC
851	GCCGCAAAGC	GATGTTGCAA	GACATCGCCA	TCCTGACCGG	CGGCGTGGTG
901	ATTTCCGAAG	AAGTCGGTCT	GTCTTTGGAA	AAAGCGACTT	TGGACGACTT
951	GGGTCAAGCC	AAACGCATCG	AAATCGGTAA	AGAAAACACC	ACCATCATCG
1001	ACGGCTTTGG	CGACGCAGCC	CAAATCGAAG	CGCGTGTTGC	CGAAATCCGC
1051	CAACAAATCG	AAACCGCAAC	CAGCGATTAC	GACAAAGAAA	AACTGCAAGA
1101	GCGCGTGGCT	AAATTGGCAG	GCGGCGTGGC	AGTCATCAAA	GTCGGTGCCG
1151	CGACCGAAGT	CGAAATGAAA	GAGAAAAAAG	ACCGCGTGGA	AGACGCGCTG
1201	CACGCTACCC	GCGCAGCCGT	TGAAGAAGGC	GTGGTTGCAG	GCGGCGGCGT
1251	AGCCCTGTTG	CGTGCCCGTG	CTGCTTTGGA	AAACCTGCAC	ACCGGCAATG
1301	CCGACCAAGA	CGCAGGCGTA	CAAATCGTCT	TGCGCGCCGT	TGAGTCTCCG
1351	CTGCGCCAAA	TCGTTGCCAA	CGCAGGCGGC	GAACCCAGCG	TGGTTGTGAA
1401	CAAAGTATTG	GAAGGCAAAG	GCAACTACGG	TTACAACGCT	GGCAGCGGCG
1451	AATACGGCGA	TATGATCGAA	ATGGGCGTAC	TCGACCCCGC	CAAAGTAACC
1501	CGTTCTGCGC	TGCAACACGC	CGCATCTATC	GCCGGCTTGA	TGCTGACCAC
1551	TGATTGCATG	ATCGCTGAAA	TCCCCGAAGA	CAAACCGGCT	GTGCCTGATA
1601	TGGGCGGCAT	GGGTGGTATG	GGCGGCATGA	TGTAA	

### This corresponds to the amino acid sequence <SEQ ID 2964; ORF 982>:

```
m982.seq
          ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
      51 AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
     101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
     151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
     201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TGCGTCCAAA ACCAACGACG
     251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
     301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
     351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAACA
         TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
         TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
     501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
     551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
     601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA
     651 TCCGTTTGTA TTGTTGTTCG ACAAAAAAT CAGCAACATC CGCGACCTGC
         TGCCTGTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
         GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
         CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCCTGGC TTCGGCGACC
          GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
         ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
     901
         GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
     951
         ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTTGC CGAAATCCGC
    1001
         CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
    1051
    1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
    1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
    1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
    1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
    1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
    1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
    1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
    1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
    1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
          TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCCTGATA
    1551
         TGGGCGCAT GGGTGGTATG GGCGGCATGA TGTAA
    1601
```

# Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

g982	IASQNLRFDNRFLQKMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI 10 20 30 40 50 60
m982.pep g982	70 80 90 100 110 120 ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRGI
m982.pep g982	130 140 150 160 170 180 DKAVAALVDELKNIAKPCDTSKEIAQVGSISANSDEQVGAIIAEAMEKVGKEGVITVEDG
m982.pep g982	130 140 150 160 170 180  190 200 210 220 230 240  KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
m982.pep g982	250 260 270 280 290 300  AKASRPLLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
m982.pep g982	310 320 330 340 350 360  ISEEVGLSLEKATLDDLGQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY  !!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
m982.pep g982	370 380 390 400 410 420 DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
m982.pep g982	430 440 450 460 470 480 RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKGNYGYNA
m982.pep g982	490 500 510 520 530 540  GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM
m982.pep g982	GGMMX       GGMMX
The following p  a982.seq  1  51  101  151  201  251  301  351	ATGGCAGCAA AAGACGTACA ATTCGGCAAT GAAGTCCGCC AAAAAATGGT AAACGGCGTG AACATTTTGG CAAACGCCGT GCGCGTAACC TTGGGTCCCA AAGACCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC AAAGACGCCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA AAATATGGGC GCGCAAATGG TGAAAGAAGT CGCGTCCAAA ACCAACGACG TGGCGGGCGA CGGTACGAT ACCGCCACG TATTGGCGCA ATCCATCGTT GCCGAAGGTA TGAAATACGT TACCGCCGGT ATGAACCCGA CCGACCTGAA ACGCGGTATC GACAAAGCCG TCGCCGCTTT GGTTGAAGAGC CTGAAAAACA

401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA

451	TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501	AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551	AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
` 601	TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCCG GCTTGGACAA
651	TCCGTTTGTA TTGCTGTTCG ACAAAAAAT CAGCAATATC CGCGACCTGC
701	·
751	GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801	CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851	GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901	ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951	GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001	ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTGC CGAAATCCGC
1051	CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101	GCGCGTTGCC AAACTGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGCCG
1151	CGACCGAAGT GGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
	·
1201	CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251	AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301	CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351	CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401	CAAAGTGTTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451	AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501	
1551	AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601	TGGGCGGCAT GGGTGTATG GGCGGCATGA TGTAA
This correspond	is to the amino acid sequence <seq 2966;="" 982.a="" id="" orf="">:</seq>
•	is to the minimo acid sequence (SEQ ID 2500, Old 502.2).
a982.pep	
1	MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51	KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101	AEGMKYVTAG MNPTDLKRGI DKAVAALVEE LKNIAKPCDT SKEIAQVGSI
151	SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLENELDVV EGMQFDRGYL
201	SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLII
251	AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301	ISEEVGLSLE KATLDDLGQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351	QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401	HATRAAVEEG VVAGGGVALL RARAALENLH TGNADQDAGV QIVLRAVESP
451	LRQIVANAGG EPSVVVNKVL EGKGNYGYNA GSGEYGDMIE MGVLDPAKVT
501	RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*
301	North Market North Transferred Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market
m982/a982	99.3% identity in 544 aa overlap
m982/a982	99.3% Identity in 344 da overlap
	10 20 30 40 50 60
m982.pep	MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
a982	MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
	20 20 30 40 30 60
	70 80 90 100 110 120
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRGI
a982	ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRGI
	70 80 90 100 110 120
	1
	130 140 150 160 170 180
m002 non	DKAVAALVDELKNIAKPCDTSKEIAQVGSISANSDEQVGAIIAEAMEKVGKEGVITVEDG
m982.pep	
	##!# <b>!##:</b> !!!#!!#!!#!#!##!##!###########
a982	DKAVAALVEELKNIAKPCDTSKEIAQVGSISANSDEQVGAIIAEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
	190 200 210 220 230 240
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
2002	
a982	

m982.pep	250 AKASRPLLIIAEDVE                 AKASRPLLIIAEDVE 250	11111111111	111111111		11:1
m982.pep	310 ISEEVGLSLEKATLDI IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1111111111	111111111		1111
m982.pep	370 DKEKLQERVAKLAGGV 11111111111111111111111111111111111		111111111	111111111	1111
m982.pep a982	430 RARAALENLHTGNADO	шшіш	1111111111	11111111	1111
m982.pep a982	490 GSGEYGDMIEMGVLDE		1111111111	1111:1111	1111
m982.pep a982	GGMMX           GGMMX			·	

### The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2967>:

<b>—</b> ,		-		•	•
g986.seq					
1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTTCA	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701		CGACGTTGCC			
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTCGC	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCGG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101		AAAGAAGTCA			
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAgcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	CGCAGGCTTA

```
AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
               agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
               TGGTCAtgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA
This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:
     g986.pep
               VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
            1
               SMLLPDFAQL VQSEGPAVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
           51
          101 EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKNGYILTN THVVAGMGSI
          151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
          201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
               FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
               LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
          351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
          401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
          451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*
The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2969>:
     m986.seq
               GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
               GCTGGCAGGC TGCGACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAG
          . 51
              AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
              AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
          201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCG
          251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
          301 GAATTTTCA AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
          351 AGCAGATGAC GGCGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
          401 ACGGCTACAT CCTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
          451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
          501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
          551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
          601 GTCGCCGCCA TCGGCGCCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
          651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
          701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
          751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAAA TATACAGCCG
          801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
          851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
          901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
          951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
         1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
         1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
               TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
         1151
               TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
         1201
               TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
         1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
         1301
               GACACCTCGT CGTCGTACGG GTTTCCGACG CGGCAGAACG CGCAGGCTTG
         1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
         1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
               TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA
This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:
     m986.pep..
               VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
            1
               SMLLPDFAQL VQSEGPAVVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
               EFFKRLVPNM PEIPQEEADD GGLNFGSGFI ISKDGYILTN THVVTGMGSI
          151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
          201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
          251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
```

Computer analysis of this amino acid sequence gave the following results:

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

### Homology with a predicted ORF from N. gonorrhoeae

m986/g986	97.0% identity in 49	9 aa overlap			
m986.pep	10 2 VFKKYQYLALAALCAASLA		40 KEASFVERIEHTKI	50 DDGSVSMLL	60 PDFAQL
				ППППП	14444
g986	VFKKYQYFALAALCAALLA				
	10 2	30	40	50	60
	70 8		100	110	120
m986.pep	VQSEGPAVVNIQAAPAPRT				
~006				, , , , , , , , ,	
g986	70 8		100	110	120
	· ·				
	130 140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILT			~	
226					
g986	GGLNFGSGFIISKNGYILTI 130 140		LINDKREYTAKLIC 160	3SDVQSDVA: 170	180
	130 140	) 150	100	170	100
	190 200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGE	VVAAIGAPFGFDNS	SVTAGIVSAKGRSI	JPNESYTPF:	IQTDVA
g986	TEELPVVKIGNPKNLKPGE				~ ~
	190 200	210	220	230	240
	250 260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVG:	INSQIYSRSGGFMG	SISFAIPIDVAMNV	/AEQLKNTG	KVQRGQ
					11111
g986	INPGNSGGPLFNLKGQVVG				
	250 260	270	280	290	300

	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAÇ	SFGLDKAGG	ALIAKILPGSE	PAERAGLQAGI	OIVLSLDGGE:	IRSSGDL
q986	LGVIIQEVSYGLAÇ	SFGLDKASG <i>F</i>	ALIAKILPGSP	PAERAGLQAGE	DIVLSLDGGE:	IRSSGDL
-	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVS	SLGVWRKGEEI	TIKVKLGNAA	EHIGASSKT	EAPYTEQQS	GTFSVES
	- 111111111111111	1111111111		11 111111		
g986	PVMVGAITPGKEVS	LGVWRKGEEI	TIKAKLGNAA	EHTGASSKT	EAPYTEQQS	GTFSVES
,	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSG	HLVVVRVSDA	AERAGLRRGD	EILAVGQVPV	NDEAGFRKA	MDKAGKN
		11111111111		11111111111	111111111	11111
q986	AGITLQTHTDSSGK	CHLVVVRVSDA	AERAGLRRGD	EILAVGQVPV	NDEAGFRKA	MDKAGKN
3	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFI	ALNLQX				
	1111:11111111	111111				
g986	VPLLVMRRGNTLFI	ALNLOX				
9	490	500				
		<del>-</del>				

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2971>:

```
GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCCTC
  1
  51
     GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
     AAGCATCCTT TGTAGAACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
 151 AGTATGCTGC TGCCCGACTT TGTCCAACTG GTTCAAAGCG AAGGCCCGGC
 201 AGTCGTCAAT ATTCAGGCAG CCCCCGCCCC GCGCACCCAA AACGGCAGCA
 251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
     GAATTTTTCA AACGCCTCGT CCCGAACATG CCCGAAATCC CCCAAGAAGA
     AGCAGATGAC GGNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
     ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGGCAGTATC
     AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
     GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
     TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
 551
     GTCGCCGCCA TCGGCGCGC CTTCGGCTTC GACAACAGCG TGACCGCCGG
     CNTCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
     TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
     TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAAA TATACAGCCG
     CAGCGGCGA TTCATGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
 851 TGAATGTCGC CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
 901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
 951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051
     GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101
     TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAAA GGCGAAGAAA
1151
     TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
      TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
     GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
     GACACCTCGT CGTCGTACGG GTTTCCGACG CGGCAGAACG CGCAGGCTTG
1301
     AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1351
     AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1401
1451
     TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA
```

#### This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

a986.pep					
1	VFKKYQYLAL	AALCAASLAG	CDKAGSFFGA	DKKEASFVER	IKHTKDDGSV
51	SMLLPDFVQL	VQSEGPAVVN	IQAAPAPRTQ	NGSSNAETDS	DPLADSDPFY
101	EFFKRLVPNM	PEIPQEEADD	GGLNFGSGFI	ISKDGYILTN	THVVTGMGSI
151	KVLLNDKREY	TAKLIGSDVQ	SDVALLKIDA	TEELPVVKIG	NPKDLKPGEW
201	VAAIGAPFGF	DNSVTAGXVS	AKGRSLPNES	YTPFIQTDVA	INPGNSGGPL
251	FNLKGQVVGI	NSQIYSRSGG	<u>FMGISFAIPI</u>	DVAMNVAEQL	KNTGKVQRGQ

301 351 401 451	LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*
m986/a986	98.2% identity in 499 aa overlap
m986.pep	10 20 30 40 50 6 VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQ
a 900	10 20 30 40 50 6
m986.pep	70 80 90 100 110 120 VQSEGPAVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADI
a986	VQSEGPAVVNIQAAPAPRTQNGSSNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADI 70 80 90 100 110 120
m986.pep	130 140 150 160 170 180 GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLLNDKREYTAKLIGSDVQSDVALLKIDA 130 140 150 160 170 180
m986.pep	190 200 210 220 230 240 TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTDV
a986	
m986.pep	250 260 270 280 290 300 INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ 250 260 270 280 290 300
m986.pep	310 320 330 340 350 360 LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL 310 320 330 340 350 360
m986.pep	370 380 390 400 410 420 PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES
	370 380 390 400 410 420
m986.pep	430 440 450 460 470 480 AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN
	430 440 450 460 470 480
m986.pep	490 500 VPLLIMRRGNTLFIALNLQX !!!!!!!!!!!!!!! VPLLIMRRGNTLFIALNLQX
	490 500

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2973>: g987.seq

¹ ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG

```
51 TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTTA
     ATACTTCCAA ACCTGTCCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
      CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCCACGA
      AGCCTTTGCC GCCCGCGCC CCCTTATCGA ATCTGCCGAA CACAGCCTCG
      ATTTGCAATA CTACATTTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
     AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
      ggacgacaAC AACAcgcgcg gcttggacga tctcctGCTC GCCCTCGACA
 351
     GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtcgt CCTACGCAAA
 451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
 501 GCACAACAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
 551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
 601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
     CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
      TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
      GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
      GCCCCTCTAC CAAAAAATAC AGACGGACG CATCGACTGG CAGAGCGTCC
      AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
      CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
     AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
     CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacq qCAAACGCAT
1251 CTTCATCGGC TCATTCAACC TCGACCCCCG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 AccetCGCCG AtacCACAC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG
```

#### This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```
987.pep

1 MKTRSLISLL CLLLCSCSSW LPPLEERTES RHFNTSKPVL LDNILQIRHT
51 PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHDPATRK TYPNEPEAKL WKRIAAKILS
501 LLPIEGLL*
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2975>:

```
m987.seq
         ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG
      51 TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
     101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
     151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
     201 AGCCTTTGCC GCCCGCGCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
     251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
     301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
     351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
     401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
     451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
         GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
         GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
         GATTTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
         CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
     701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
     751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
     801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
     851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
```

901	CGCAAACCGC	CGATTGCCGG	GCGGCTGCAA	GACGCGCTCA	AACAGCCCGA
951	AAAAAGCGTC	TATCTGGTTT	CACCCTATTT	CGTTCCCACA	AAATCCGGCA
1001	CAGACGCACT	GGCAAAACTG	GTGCAGGACG	GCATAGACGT	TACCGTTCTG
1051	ACCAACTCGC	TGCAGGCGAC	CGACGTTGCC	GCCGTCCATT	CCGGCTATGT
1101	CAAATACCGA	AAACCGCTGC	TCAAAGCCGG	CATCAAACTC	TACGAGCTGC
1151	AACCCAACCA	TGCCGTCCCC	GCCACAAAAG	ACAAAGGCCT	GACCGGCAGC
1201	TCCGTAACCA	GCCTGCACGC	CAAAACCTTC	ATTGTGGACG	GCAAACGCAT
1251	CTTCATCGGT	TCGTTCAACC	TCGACCCCCG	TTCCGCGCGT	CTCAACACCG
1301	AAATGGGCGT	TGTTATCGAA	AGCCCCAAAA	TCGCAGAACA	GATGGAGCGC
1351	ACCCTTGCCG	ATACCACACC	CGCCTACGCC	TACCGCGTTA	CCCTCGACAG
1401	GCACAACCGC	CTGCAATGGC	ACGATCCCGC	CACCCGAAAA	ACCTACCCGA
1451	ACGAACCCGA	AGCCAAACTT	TGGAAACGCA	TCGCCGCAAA	AATCCTATCC
1501	CTGCTGCCCA	TAGAAGGTTT	ATTATAG		

#### This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

m987.pep					
1	MKTRSLISLL	CLLLCSCSSW	LPPLEERTES	RHFNTSKPVR	LDNILQIRHT
51	PHTNGLSDIY	LLNDPHEAFA	ARAALIESAE	HSLDLQYYIW	RNDISGRLLF
101	NLVYLAAERG	VRVRLLLDDN	NTRGLDDLLL	ALDSHPNIEV	RLFNPFVLRK
151	WRALGYLTDF	PRLNRRMHNK	SFTADNRATI	LGGRNIGDEY	FKVGEDTVFA
201	DLDILATGSV	VGEVSHDFDR	YWASHSAHNA	TRIIRSGDIG	KGLQALGYND
251	ETSRHALLRY	RETVEQSPLY	QKIQTGCIDW	QSVRTRLISD	DPAKGLDRDR
301	RKPPIAGRLQ	DALKQPEKSV	YLVSPYFVPT	KSGTDALAKL	VQDGIDVTVL
351	TNSLQATDVA	AVHSGYVKYR	KPLLKAGIKL	YELQPNHAVP	ATKDKGLTGS
401	SVTSLHAKTF	IVDGKRIFIG	SFNLDPRSAR	LNTEMGVVIE	SPKIAEQMER
451	TLADTTPAYA	YRVTLDRHNR	LOWHDPATRK	TYPNEPEAKL	WKRIAAKILS
501	LLPIEGLL*				

## Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987	97.8% identity in 508 aa overlap
-007	10 20 30 40 50 60 MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY
m987.pep	
g987	MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIY
<b>3</b>	10 20 30 40 50 60
	70 80 90 100 110 120
m987.pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLLDDN
-007	
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDN 70 80 90 100 110 120
	70 80 90 100 110 120
	130 140 150 160 170 180
m987.pep	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
g987	NTRGLDDLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
	130 140 150 160 170 180
•	100 200 210 200 220
m987.pep	190 200 210 220 230 240 LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG
mad/.pep	
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
950,	190 200 210 220 230 240
	250 260 270 280 290 300
m987.pep	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR
_	
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR
	250 260 270 280 290 300
	310 320 330 340 350 360
m987.pep	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA
	THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY O

						111111
g987	RKPPIAGRLQDAL	QPEKSVYLV:	SPYFVPTKSGT	DALAKLVQDG	IDVTVLTNS	LQATDVA
-	310	320	330	340	350	360
	370	380	390	400	410	420
m987.pep	AVHSGYVKYRKPLI	KAGIKLYEL	QPNHAVPATKI	KGLTGSSVTS	LHAKTFIVDO	GKRIFIG
		111111111	1   1   1   1   1   1   1		111111111	111111
g987	AVHSGYVKYRKPLI	KAGIKLYEL	QPNHAVPATKE	KGLTGSSVTS	LHAKTFIVDO	GKRIFIG
_	370	380	390	400	410	420
	430	440	450	460	470	480
m987.pep	SFNLDPRSARLNTE	MGVVIESPK	[AEQMERTLAI	TTPAYAYRVT	LDRHNRLQWI	HDPATRK
				111 111111	11:111111	
g987	SFNLDPRSARLNTE	MGVVIESPK	[AEQMERTLAD	TTPEYAYRVT	LDKHNRLQW	IDPATRK
	430	440	450	460	470	480
		•				
	490	500	509			
m987.pep	TYPNEPEAKLWKRI	AAKILSLLP1	EGLLX			
		111111111				
g987	TYPNEPEAKLWKRI	AAKILSLLPI	EGLLX			
-	490	500				

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2977>:

```
a987.seq
         ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG
      51
         TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
     101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
     151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
     201 AGCCTTTGCC GCCCGCGCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
     251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCCG ACTGCTGTTC
         AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
         GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTC GCCCTCGACA
         GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
         TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCGCCTCA ACCGCCGCAT
         GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
    551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
     601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
     651 CTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
    701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
    751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
    801 GCCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
    851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
    901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
    951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
   1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
   1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
   1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACTC TACGAGCTGC
   1151
         AACCCAACCA TGCCGTCCCT GCCACAAAG ACAAAGGCCT GACCGGCAGC
         TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
         CTTCATCGGC TCATTCAACC TCGACCCCCG TTCCGCACGG CTCAATACTG
   1251
   1301 AAATGGGCGT TGTTATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
   1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
   1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
   1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
   1501 CTGCTGCCCA TAGAAAGTTT ATTATAG
```

### This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

, beb					
1	MKTRSLISLL	CLLLCSCSSW	LPPLEERTES	RHFNTSKPVR	LDNILQIRHT
51	PHTNGLSDIY	LLNDPHEAFA	ARAALIESAE	HSLDLQYYIW	RNDISGRLLF
101	NLVYLAAERG	VRVRLLLDDN	${\tt NTRGLDDLLL}$	ALDSHPNIEV	RLFNPFVLRK
151	WRALGYLTDF	PRLNRRMHNK	SFTADNRATI	LGGRNIGDEY	FKVGEDTVFA
201	DLDILATGSV	VGEVSHDFDR	YWASHSAHNA	TRIIRSGNIG	KGLQALGYND
251	ETSRHALLRY	RETVEQSPLY	QKIQTGRIDW	QSVQTRLISD	DPAKGLDRDR
301	RKPPIAGRLQ	DALKQPEKSV	YLVSPYFVPT	KSGTDALAKL	VQDGIDVTVL

351 401 451 501	TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER TLADTSPEYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAAKILS LLPIESLL*
m987/a987	98.8% identity in 508 aa overlap
m987.pep	10 20 30 40 50 60  MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY
m987.pep	70 80 90 100 110 120 LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAAERGVRVRLLLDDN
m987.pep a987	130 140 150 160 170 180 NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
m987.pep a987	190 200 210 220 230 240 LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG
m987.pep a987	250 260 270 280 290 300 KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR
m987.pep a987	310 320 330 340 350 360 RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA
m987.pep	370 380 390 400 410 420 AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
m987.pep a987	430 440 450 460 470 480  SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRLQWHDPATRK
m987.pep a987	490 500 509 TYPNEPEAKLWKRIAAKILSLLPIEGLLX

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2979>: g988.seq

51	AAGTCGTGAA			TTTGCCCAGT	CGGgaATGGA
101	TAATCGAATT	GTTGGAGCGC	AAAGGTGTGC	CTTCAAAAAT	CGAATCGCTT
151	GCACGCGAGC	TGTCGATTAC	GGAAGacgag	tATGTCTTTT	TTGAACGCCG
201	TCTGAaggCG	atgGCGCGGG	AcggtCAGGT	TTTAATCAAC	CGCCgaggcg
251	CagtTTGCGc	gGCggacaag	ctgGATTTGG	TCAAATGccg	Cgtcgaggcg
301	catAAgGAcg	gtttcggctt	cgcCGTGCCG	CTCATGCCGA	TGGACGAAGG
351	GGATTTCGTT	TTATACGAAC	GCCAgatgcg	tggTGtcatG	CAcggcgaca
401	ccgttACCGT	CCGTCCTGCg	ggtatggaCC	GCAGGGGccg	ccgcGAAggg
451	acqtttctGG	ATATTGTCGA	ACGCGCGCAA	AGCAAAGTTG	TCGGCCGTTT
501	CTATATGGAT	AGGGGCGTGG	CGATTTTGGA	GCCGGAAGAC	AAGCGTCTGA
551	ACCAAAGCAT	CGTGTTGGAA	CCGGACGGCG	TGGCGCGTTT	CAAACCCGAA
601	TCCGGTCAGG	TTATCGTCGG	CAAAATTGAG	GTTTATCCCG	AGCAAAACCG
651	GCCTGCAGTG	GCAAAAATCA	TTGAAGTTTT	GGGCGATTAT	GCCGACAGCG
701	GGATGGAAAt	cqAAATTGCC	GTGCGCAAGC	ATCATTTGCC	GCAccgaTTC
751	AGTGAagcgt	gtGcCAAATC	CGcqaaAAAA	ATtcccgacc	ATGTACGCAA
801	AAGCGATTTG	AAAGGCCGCG	TCGATTTGTG	CGACCTTCCT	TTGGTAACGA
851	TAGACGGCGA	AACGGCGCGC	GATTTCGACG	ACGCGGTGTT	TGCCGAAAAA
901	GTCGGACGCA	ATTACCGCCT	GGTCGTGGCG	ATTGCGGATG	TCAGCCATTA
951	TGTCCGCCCT	GACGATGCGA	TTGATGCAGA	TGCTCAAGAA	CGCAGTACCA
1001	GCGTGTATTT	CCCGCGCCGT	ATGATTCCGA	TGCTGCCGGA	AAACCTGTCC
1051	AACGGCATCT	GCTCGCTCAA	TCCCGATGTC	GAGCGTTTGT	GTATGGTGTG
	CGATATGGTC	GTTACCTATG	CGGGCAATAT	CAAAGAATAC	CGCTTCTATC
1101	CCGCCGTGAT	GCGCTCTCAT	GCCCGCCTGA	CCTACAACCA	AGTTTGGAAA
1151			GAATCCGCAC	AAAGCCCAAA	TCGACACGCT
1201	TGGCTTTCAG	ACGGCATCGG	TGCAGAAAAA	ACGTCTGGCG	CGCGGGGCGG
1251	TTACAAGCTG	TTTAAAATTT	= '		
1301	TGGAGTTTGA	AAGCGTCGAA	ACCCAGATGA	TTTTCGACGA	CAACGGCAAA
1351	ATCGAAAAAA	TTGTCCCCGT	CGTCCGCAAC	gatGCCCACA	AGCTGATTGA
1401	AGAATGTATG	CTGGCGGCGA	ATGTTTGCGC	GGCGGATTTT	CTGTTGAAAA
1451	ACAAACATAC	GGCTTTGTTC	CGCAACCATT	TGGGCCCCAC	GCCCGAAAAA
1501	CTCGCCACCC	TGCGCGAGCA	GCTCGGTCTG	TTGGGGCTTC	AACTTGGCGG
1551	CGGCGACAAC	CCGTCGCCGA	AAGACTATGC	CGCGCTTGCC	GAACAATTCA
1601	AAGGCAGGCC	GGATGCCGAA	TTGCTGCAAG	TCATGATGTT	GCGCTCCATG
1651	CAGCAGGCGG	TTTACGAACC	GCATTGCGAA	GGGCATTTCG	GTTTGGCTTA
1701	TGAAGCATAC	GCCCACTTTA	CCTCGCCCAT	CCGCCGCTAT	CCCGACCTGA
1751	CCGTCCACCG	TGCCATCAAA	GCCGTATTGA	ACCGGAAAAC	CTACACGCCA
1801	AACAAAAGCT	GGCAGGCTTT	GGGCGTGCAT	ACTTCGTTTT	GCGAACGCCG
1851	TGCCGACGAT	GCTGGCCGCG	ATGTGGAAAA	CTGGCTGAAA	ACTTATTATA
1901	TGCGCGATAA	GGTCGGTGAA	ATATTTGAAG	${\tt GcaaaatCtc}$	ccggggtgtg
1951	gcaaaTtttg	gaATATTTGT	CACTTTGGAC	GATATccata	tcgacggtct
2001	ggtacaTATC	AGCGatttgg	gcgaAGATTA	TTTCaacttc	cgcccgAAA
2051	TCATGGCAAT	CGAAGGCGAA	CGCAGCGGCA	TCCGTTTCAA	TATGGGGGAC
2101	AGGGTTGCCG	TCCGGGTCGC	GCGTGCCGAT	TTGGATGATG	GAAAAATCGA
2151	CTTTGTCCTA	ATTGCCGGAG	AAAGCGGCAG	GCGGCGGAAG	GTCAAATTAT
2201	CCGCATCTGC	CAAACCGGCA	GGGGCGGCGG	GGAAAGGGAA	ATCGAAAACC
2251	ACCGCCGAGA	AAAAAACAGC	CCGATGCGGC	AAAGTAAGGG	GAAGGGGCGT
2301	GCCTGCCGTT	GCCGAATCGG	GGAAAAAGGC	AAAGAAACCG	GTTCCGATTA
2351		ACGGAAAGGC			·
2001	11001 OFFICE				

### This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIESL ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA HKDGFGFAVP LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG 151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE 201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK 251 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS 301 351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK 401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK 451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK 501 LATLREQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM 551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP 601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYYMRDKVGE IFEGKISRGV 651 ANFGIFVTLD DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD 701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT TAEKKTARCG KVRGRGVPAV AESGKKAKKP VPIKVKKRKG KS* 751

WO 99/57280

1399

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2981>:

m988.seq (partial) ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA 51 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA 101 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG 151 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC 251 AGTGAAGCGT GTGCCAAAGC TGCGAAAAAA ATTCCCGTCC ATGTACGCAA 301 AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA 351 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA 401 GTCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCGGATG TCAGCCATTA 451 501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT 551 AACGGCATTT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG 601 651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC 701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA TGGATTTCAG ACGCCATCGA CCATCCGTAC AAAGCCCAAA TCGACACCCT 751 851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA ATCGAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCCACA AGCTGATTGA 901 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTC CTGTTGAAAA 951 ACAAGCATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA 1001 1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG 1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA 1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA 1201 1251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA CCGTACACCG CGCCATCAAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA 1301 AAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG 1351 TGCCGACGAC GCCAGCCGCG ACGTGGAAAA CTGGCTGAAA ACCTATTATA 1401 TGCGCGATAA GGTCGGCGAA GTATTCGAAG GTAAAATCTC CGGCATGACC 1451 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT 1501 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA 1551 1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCAACAT GGGGGACAGG GTTGCCGTCC GGGTCGCCCG TGCCGATTTG GATGACGGAA AAATCGATTT 1651 TGTCCTGATT GCCGGGGGA GCGGCAGGGG GCGGAAAGTT AAATCATCCG 1701 CGTCTGCCAA ACCGCCAGGG ACGGCGGGGA AAGGGAAGCC GAAAACCGCC 1751

1801	GCCGAGAAAA	AAACAGCCCG	AGGCGGCAAA	GTAAGGGGAA	GGGGCGCGTC
1851	TGCCGCCGCA	GAATCGAGGA	AAAAGGCAAA	GAAACCGGTT	CCGATTAAGG
1901	TAAAAAAAACG	GAAAGGCAAA	TCATAA		

### This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

•					
m988.pep	(partial)				
1	TVLDIVERAQ	SKVVGRFYMD	RGVAILEPED	KRLNQSIVLE	PDGVARFKPE
51	SGQVIVGEIE	VYPEQNRPAV	AKIIEVLGDY	ADSGMEIEIA	VRKHHLPHQF
101	SEACAKAAKK	IPVHVRKSDL	KGRVDLRDLP	LVTIDGETAR	DFDDAVFAEK
151	VGRNYRLVVA	IADVSHYVRP	DDVIDADAQE	RSTSVYFPRR	VIPMLPENLS
201	NGICSLNPDV	ERLCMVCDMV	VTYAGNIKEY	RFYPAVMRSH	ARLTYNQVWK
251	WISDGIDHPY	KAQIDTLYKL	FKILQKKRFE	RGAVEFESVE	TQMIFDDNGK
301	IEKIVPVVRN	DAHKLIEECM	LAANVCAADF	LLKNKHTALF	RNHLGPTPEK
351	LATLREQLGL	LGLQLGGGDN	PSPKDYAALV	EQFKGRPDAE	LLQVMMLRSM
401	QQAVYEPHCD	GHFGLAYEAY	AHFTSPIRRY	PDLTVHRAIK	AVLNQQTYTP
451	KKSWQALGVH	TSFCERRADD	ASRDVENWLK	TYYMRDKVGE	VFEGKISGMT
501	SFGIFVTLDG	IHIDGLVHIS	DLGEDYFNFR	PEIMAIEGER	SGIRFNMGDR
551	VAVRVARADL	DDGKIDFVLI	AGGSGRGRKV	KSSASAKPAG	TAGKGKPKTA
601	AEKKTARGGK	VRGRGASAAA	ESRKKAKKPV	PIKVKKRKGK	S*

# Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

_			
		10	20 30
m988.pep			SKVVGRFYMDRGVAILEPED
g988	LYERQMRGVMHGDTVTVRPAG	MDRRGRREGTFLDIVERAQ 150 160	
	130 140	130 100	170 180
	40 50	60 70	80 90
m988.pep	KRLNQSIVLEPDGVARFKPES	GQVIVGEIEVYPEQNRPAV	AKIIEVLGDYADSGMEIEIA
g988	KRLNQSIVLEPDGVARFKPES		
	190 200	210 220	230 240
	100 110	120 130	140 150
m988.pep	VRKHHLPHQFSEACAKAAKKI		
• •	11111111:111111:1111		FILLIALITATION
g988	VRKHHLPHRFSEACAKSAKKI		
	250 260	270 280	290 300
	160 170	180 190	200 210
m988.pep	VGRNYRLVVAIADVSHYVRPDI		
ms co. Pop			
g988	VGRNYRLVVAIADVSHYVRPD	~	MIPMLPENLSNGICSLNPDV
	310 320	330 340	350 360
	220 230	240 250	260 270
m988.pep	ERLCMVCDMVVTYAGNIKEYR		
mooo.pcp			
g988	ERLCMVCDMVVTYAGNIKEYR		
	370 380	390 400	410 420
	280 290	200 210	200 220
m988.pep	FKILQKKRFERGAVEFESVET	300 310	
mooo.pep			
g988	FKILQKKRLARGAVEFESVET		
•	430 440	450 460	470 480
	340 350	360 370	380 390
m988.pep	LLKNKHTALFRNHLGPTPEKLA		
q988	LLKNKHTALFRNHLGPTPEKL		
J			III III III XI NGKEDHE

		490	500	510	520	530	540
		400	410	420	430	440	450
m988.pep	LLQVMM:	LRSMQQAVYE	PHCDGHFGLA	YEAYAHFTSP:	IRRYPDLTVH	RAIKAVLNQQʻ	TYTP
	11111	11111111	111:11111			11111111::	1111
g988	LLQVMM					RAIKAVLNRK'	
		550	560	570	580	590	600
		460	470	480	400	F 0.0	T 0 0
-000	VVCWAN				490	500 S-GMTSFGIF	509
m988.pep	VV2MÖW			MPKITIMED	.vGEvrEGK1.	5-GM15FG1F	V 1 L D
q988	NKSWOAI			ı I I I I I I I I I I VWI KTYYMRDI	KVGETFEGKT:	SRGVANFGIF	ת.זי <i>חיו</i> .
9500	tittoo.	610	620	630	640	650	660
•							000
	510	520	530	540	550	560	569
m988.pep	GIHIDG	LVHISDLGED	YFNFRPEIMA:	EGERSGIRF	MGDRVAVRV	ARADLDDGKI	DFVL
	11111					1111111111	HIII
g988	DIHIDGI					ARADLDDGKI	DFVL
		670	680	690	700	710	720
		<b>5</b> 00	500				
	570	580	590	600	610	620	629
m988.pep		RGRKVKSSASA	AKPAGTAGKGI 			ASAAAESRKKA	AKKP
~000	TACRECI	ו ווון וון				:  :        /PAVAESGKK/	
g988	TAGESGI	730	740	750	760	770	780
		730	740	750	700	770	780
	630	640					
m988.pep	VPIKVK						
	111111						
g988	VPIKVK	KRKGKSX					
<b>3</b>		790					

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2983>:

```
a988.seq
         ATGAATAAAA ATATTAAATC TTTAAATTTA CGGGAAAAAG ACCCGTTTTT
         AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGGAATGGA
         TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
         GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
    151
         TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
        CGGTTTGCGC GGCGGACAAA TTGGATTTGG TCAAATGCCG TGTCAAGGCG
    251
         CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
    301
    351
         TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
         TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCCG CCGCGAAGGG
         ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
    451
    501
         CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
    551
         ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
    601
         TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
         GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
    651
         GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
    701
    751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
    801 AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
         TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
    901 ATCGGACGCA ATTACCGTCT GGTCGTGGCG ATTGCCGATG TCAGCCATTA
    951
        TGTCCGCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
   1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTTGCCGGA AAACCTGTCC
   CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
   1101
         CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
   1151
         TGGCTTTCAG GCGGCATCGA GCATCCGTTC AAAACCCAAA TCGACACGCT
         TTACAAACTC TTCAAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
   1251
         TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
   1351
         ATTGAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCCACA AGCTGATTGA
   1401
         AGAATGTATG TTGGCGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
   1451
         ACAAGCATAC CGCATTGTTC CGCAACCATT TGGGGCCCAC GCCCGAAAAA
         CTCGCCGCCT TGCGCGAGCA GCTCGGTCTG TTGGGGGCTTC AACTTGGCGG
   1501
   1551
         CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA
```

a988

1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG

1601	AAGGCAGGCC GGATGCCG				
1651	CAACAGGCGG TTTACGAA	CC GCATTGCGAC	GGACACTTTG	GTCTTGCCTA	
1701	CGAAGCATAC GCCCACTT	CA CCTCGCCCAT	CCGCCGCTAT	CCCGACCTGA	
1751	CCGTACACCG CGCCATCA	AA GCCGTGTTGA	ATCAGCAAAC	CTACACGCCA	
1801	AAAAAAAGCT GGCAGGCT	TT GGGCGTGCAT	ACCTCGTTCT	GTGAGCGCCG	
1851	TGCCGACGAC GCCAGCCG	CG ACGTGGAAAA	CTGGCTGAAA	ACCTATTATA	
1901	TGCGCGATAA GGTCGGCG	ΔΔ GΤΔΤΤΓGΑΑG	GTAAAATCTC	CGGCATGACC	
	AGTTTTGGTA TCTTTGTA				
1951	GCATATCAGC GATTTGGG				
2001					
2051	TGGCAATCGA AGGCGAAC	GC AGCGGCATCC	GTTTCAACAT	GGGGACAGG	
2101	GTTGCCGTCC GGGTCGCC	CG TGCCGATTTG	GATGACGGAA	AAATCGATTT	
2151	TGTCCTGATT GCCGGGGG				
2201	CGTCTGCCAA ACCGGCAG				
2251	GCCGAGAAAA AAACAGCC	CG AGGCGGCAAA	GTAAGGGGAA	GGGGCGCGTC	
2301	TGCCGCCGCA GAATCGAG				
2351	TAAAAAAACG GAAAGGCA				
2551	THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O				
erat '		CEO I	D 2004, ODI	7.000 00.	
This correspond	ls to the amino acid sec	quence <seq i<="" td=""><td>D 2984; OKI</td><td>1 988.a&gt;:</td><td></td></seq>	D 2984; OKI	1 988.a>:	
a988.pep					
i	MNKNIKSLNL REKDPFLS	RE KORYEHPLPS	REWIIELLER	KGVPSKIEAL	
- 51	VRELSIKEEE YEFFERRL	KA MARDGOVI.TN	RRGAVCAADK	LDLVKCRVKA	
101	HKDRFGFAVP LTPAKDGD				
151	TVLDIVERAQ SKVVGRFX				
201	SGQVIVGEIE VYPEQNRP				
251	SEACAKAAKK IPDHVRKS				
301	IGRNYRLVVA IADVSHYV	RP DDAIDTDAQE	RSTSVYFPRR	VIPMLPENLS	
351	NGICSLNPHV ERLCVVCD	MV ITYAGNIKEY	RFYPAVMRSH	ARLTYNQVWK	
401	WLSGGIEHPF KTQIDTLY	KL FKILOKKRFE	RGAVEFDSIE	TOMLFDDNGK	
451	IEKIVPVVRN DAHKLIEE				
501	LAALREOLGL LGLQLGGG				
	QQAVYEPHCD GHFGLAYE				
551					
601	KKSWQALGVH TSFCERRA				
651	SFGIFVTLDG IHIDGLVH				
201	VAVRVARADL DDGKIDFV	T.T AGGSGRGRKV	KSSASAKPAG	TAGKGKPKTA	
701	AWAKAWADT DDGWIDLA	TI MOODOMONIN			
701 751	AEKKTARGGK VRGRGASA				
751	AEKKTARGGK VRGRGASA	AA ESRKKAKKPV	PIKVKKRKGK		
	AEKKTARGGK VRGRGASA	AA ESRKKAKKPV	PIKVKKRKGK		
751	AEKKTARGGK VRGRGASA	AA ESRKKAKKPV	PIKVKKRKGK lap	S*	Λ
751 m988/a988	AEKKTARGGK VRGRGASA	AA ESRKKAKKPV	PIKVKKRKGK lap 10	20 3	0
751	AEKKTARGGK VRGRGASA	AA ESRKKAKKPV	PIKVKKRKGK lap 10 TVLDIVERAQS	S*  20 3  EKVVGRFYMDRGVAILEPE	D
751 m988/a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i	AA ESRKKAKKPV n 641 aa over	PIKVKKRKGK lap 10 TVLDIVERAQS	S*  20 3 SKVVGRFYMDRGVAILEPE	D I
751 m988/a988	AEKKTARGGK VRGRGASA 97.0% identity i	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE	PIKVKKRKGK lap 10 TVLDIVERAQS           GTVLDIVERAQS	S*  20 3 SKVVGRFYMDRGVAILEPE	D I D
751 m988/a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i	AA ESRKKAKKPV n 641 aa over	PIKVKKRKGK lap 10 TVLDIVERAQS           GTVLDIVERAQS	S*  20 3 SKVVGRFYMDRGVAILEPE	D I D
751 m988/a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE	PIKVKKRKGK lap 10 TVLDIVERAQS           GTVLDIVERAQS	S*  20 3 SKVVGRFYMDRGVAILEPE	D I D
751 m988/a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i LYERQMRGIMHGDIVT 130	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE	PIKVKKRKGK  lap  10  TVLDIVERAQS            GTVLDIVERAQS 0 160	S*  20 3 SKVVGRFYMDRGVAILEPE	D I D O
751 m988/a988 m988.pep a988	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130 40	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6	PIKVKKRKGK  lap  10  TVLDIVERAQS           GTVLDIVERAQS 0 160 0 70	S*  20 3 SKVVGRFYMDRGVAILEPE                 SKVVGRFXMDRGVAILEPE 170 18	D I D O
751 m988/a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI	PIKVKKRKGK  lap  10  TVLDIVERAQS            GTVLDIVERAQS 0 160 0 70  EVYPEQNRPAVA	S*  20 3 SKVVGRFYMDRGVAILEPE                 SKVVGRFXMDRGVAILEPE 170 18  80 9 AKIIEVLGDYADSGMEIEI	D I D O O A
751 m988/a988 m988.pep a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI	PIKVKKRKGK  lap  10  TVLDIVERAQS            GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVE	S*  20 3  SKVVGRFYMDRGVAILEPE                    SKVVGRFXMDRGVAILEPE  170 18  80 9  AKIIEVLGDYADSGMEIEI	D I D O O A I
751 m988/a988 m988.pep a988	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI	PIKVKKRKGK  lap  10  TVLDIVERAQS            GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVE           EVYPEQNRPAVE	20 3 SKVVGRFYMDRGVAILEPE	D I D O O A I A
751 m988/a988 m988.pep a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI	PIKVKKRKGK  lap  10  TVLDIVERAQS            GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVE           EVYPEQNRPAVE	S*  20 3  SKVVGRFYMDRGVAILEPE                    SKVVGRFXMDRGVAILEPE  170 18  80 9  AKIIEVLGDYADSGMEIEI	D I D O O A I A
751 m988/a988 m988.pep a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI             FKPESGQVIVGEI 200 21	PIKVKKRKGK  lap  10  TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVE           EVYPEQNRPAVE 0 220	20 3 SKVVGRFYMDRGVAILEPE                   SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI	D I D O O A I A O
751 m988/a988 m988.pep a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21	PIKVKKRKGK  lap  10  TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVA            EVYPEQNRPAVA 0 220  0 130	20 3 SKVVGRFYMDRGVAILEPE SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI SKIIEVLGDYADSGMEIEI AKIIEVLGDYADSGMEIEI 230 24	D I D 0 0 A I A 0 0
751 m988/a988 m988.pep a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21	PIKVKKRKGK  lap  10  TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVA            EVYPEQNRPAVA 0 220  0 130	20 3 SKVVGRFYMDRGVAILEPE                   SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI	D I D 0 0 A I A 0 0
751 m988/a988 m988.pep a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD	PIKVKKRKGK  lap  10  TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVA            EVYPEQNRPAVA 0 220  0 130  LKGRVDLRDLPI	20 3 SKVVGRFYMDRGVAILEPE	DIDO OAIAO OK
751 m988/a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR                   KRLNQSIVLEPDGVAR 190  100  VRKHHLPHQFSEACAK	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI               FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD	PIKVKKRKGK  lap  10  TVLDIVERAQS            GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVE            EVYPEQNRPAVE 0 220  0 130  LKGRVDLRDLPI	20 3 SKVVGRFYMDRGVAILEPE                  SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI                    AKIIEVLGDYADSGMEIEI 230 24 140 15 LVTIDGETARDFDDAVFAE	D   D 0 0 A   A 0 0 K
751 m988/a988 m988.pep a988 m988.pep	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR                  KRLNQSIVLEPDGVAR 190  100  VRKHHLPHQFSEACAK	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD	PIKVKKRKGK  lap  10  TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVE            EVYPEQNRPAVE 0 220  0 130  LKGRVDLRDLPI	20 3 SKVVGRFYMDRGVAILEPE                  SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI                   AKIIEVLGDYADSGMEIEI 230 24 140 15 LVTIDGETARDFDDAVFAE	DIDO OAIAO OK!K
751 m988/a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR                   KRLNQSIVLEPDGVAR 190  100  VRKHHLPHQFSEACAK	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI               FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD	PIKVKKRKGK  lap  10  TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70  EVYPEQNRPAVE            EVYPEQNRPAVE 0 220  0 130  LKGRVDLRDLPI	20 3 SKVVGRFYMDRGVAILEPE                  SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI                    AKIIEVLGDYADSGMEIEI 230 24 140 15 LVTIDGETARDFDDAVFAE	DIDO OAIAO OK!K
751 m988/a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD             AAKKIPDHVRKSD 260 27	PIKVKKRKGK  lap  10 TVLDIVERAQS            GTVLDIVERAQS 0 160  0 70 EVYPEQNRPAVE            EVYPEQNRPAVE 0 220  0 130 LKGRVDLRDLPI            LKGRVDLRDLPI 0 280	20 3 SKVVGRFYMDRGVAILEPE                   SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI	DIDO OAIAO OKIKO
751 m988/a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA 97.0% identity i  LYERQMRGIMHGDIVT 130  40  KRLNQSIVLEPDGVAR	AA ESRKKAKKPV n 641 aa over  VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD             AAKKIPDHVRKSD 260 27	PIKVKKRKGK  lap  10 TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70 EVYPEQNRPAVE             EVYPEQNRPAVE 0 220  0 130 LKGRVDLRDLPI            LKGRVDLRDLPI 0 280  0 190	20 3 SKVVGRFYMDRGVAILEPE                   SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI                    AKIIEVLGDYADSGMEIEI 230 24 140 15 LVTIDGETARDFDDAVFAE                   LVTIDGETARDFDDAVFAE 290 30	D   D 0 0 0 A   A 0 0 K   K 0 0
751 m988/a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA  97.0% identity i  LYERQMRGIMHGDIVT  130  40  KRLNQSIVLEPDGVAR                    KRLNQSIVLEPDGVAR  190  100  VRKHHLPHQFSEACAK                     VRKHHLPHQFSEACAK  250  160  VGRNYRLVVAIADVSH	AA ESRKKAKKPV n 641 aa over  VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD              AAKKIPDHVRKSD 260 27 170 18 YVRPDDVIDADAQ	PIKVKKRKGK  lap  10 TVLDIVERAQS            GTVLDIVERAQS 0 160  0 70 EVYPEQNRPAVE            EVYPEQNRPAVE 0 220  0 130 LKGRVDLRDLPI            LKGRVDLRDLPI            0 280  0 190 ERSTSVYFPRAVE	20 3 SKVVGRFYMDRGVAILEPE SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI 230 24 LVTIDGETARDFDDAVFAE 290 30 ZVIPMLPENLSNGICSLNPD	D   D 0 0 0 A   A 0 0 K   K 0 0 V
751 m988/a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA  97.0% identity i  LYERQMRGIMHGDIVT  130  40  KRLNQSIVLEPDGVAR                       KRLNQSIVLEPDGVAR  190  100  VRKHHLPHQFSEACAK                        VRKHHLPHQFSEACAK  250  160  VGRNYRLVVAIADVSH :	AA ESRKKAKKPV n 641 aa over  VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD              AAKKIPDHVRKSD 260 27 170 18 YVRPDDVIDADAQ	PIKVKKRKGK  lap  10 TVLDIVERAQS            GTVLDIVERAQS 0 160 0 70 EVYPEQNRPAVA             EVYPEQNRPAVA 0 220 0 130 LKGRVDLRDLPI            LKGRVDLRDLPI            CSSTSVYFPRRV	20 3 SKVVGRFYMDRGVAILEPE                  SKVVGRFXMDRGVAILEPE                  SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI                          AKIIEVLGDYADSGMEIEI 230 24 140 15 LVTIDGETARDFDDAVFAE                           LVTIDGETARDFDDAVFAE 290 30  200 21 VIPMLPENLSNGICSLNPD	DIDO OAIAO OKIKO OVI
751 m988/a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA  97.0% identity i  LYERQMRGIMHGDIVT  130  40  KRLNQSIVLEPDGVAR                       KRLNQSIVLEPDGVAR  190  100  VRKHHLPHQFSEACAK                        VRKHHLPHQFSEACAK  250  160  VGRNYRLVVAIADVSH :	AA ESRKKAKKPV n 641 aa over  VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD              AAKKIPDHVRKSD 260 27 170 18 YVRPDDVIDADAQ	PIKVKKRKGK  lap  10 TVLDIVERAQS            GTVLDIVERAQS 0 160 0 70 EVYPEQNRPAVA             EVYPEQNRPAVA 0 220 0 130 LKGRVDLRDLPI            LKGRVDLRDLPI            CSSTSVYFPRRV	20 3 SKVVGRFYMDRGVAILEPE SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI 230 24 LVTIDGETARDFDDAVFAE 290 30 ZVIPMLPENLSNGICSLNPD	DIDO OAIAO OKIKO OVI
751 m988/a988 m988.pep a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA  97.0% identity i  LYERQMRGIMHGDIVT  130  40  KRLNQSIVLEPDGVAR                       KRLNQSIVLEPDGVAR  190  100  VRKHHLPHQFSEACAK                        VRKHHLPHQFSEACAK  250  160  VGRNYRLVVAIADVSH :	AA ESRKKAKKPV n 641 aa over  VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD              AAKKIPDHVRKSD 260 27 170 18 YVRPDDVIDADAQ	PIKVKKRKGK  lap  10 TVLDIVERAQS            GTVLDIVERAQS 0 160 0 70 EVYPEQNRPAVE             EVYPEQNRPAVE 0 220 0 130 LKGRVDLRDLPI            LKGRVDLRDLPI            CSSTSVYFPRRE	20 3 SKVVGRFYMDRGVAILEPE                  SKVVGRFXMDRGVAILEPE                  SKVVGRFXMDRGVAILEPE 170 18 80 9 AKIIEVLGDYADSGMEIEI                          AKIIEVLGDYADSGMEIEI 230 24 140 15 LVTIDGETARDFDDAVFAE                           LVTIDGETARDFDDAVFAE 290 30  200 21 VIPMLPENLSNGICSLNPD	DIDO OAIAO OK!KO OV!V
751 m988/a988 m988.pep a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA  97.0% identity i  LYERQMRGIMHGDIVT  130  40  KRLNQSIVLEPDGVAR                     KRLNQSIVLEPDGVAR  190  100  VRKHHLPHQFSEACAK                     VRKHHLPHQFSEACAK  250  160  VGRNYRLVVAIADVSH  :	AA ESRKKAKKPV  n 641 aa over  VRPAGMDGRGRRE 140 15  50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21  110 12 AAKKIPVHVRKSD              AAKKIPDHVRKSD 260 27  170 18 YVRPDDVIDADAQ               YVRPDDAIDTDAQ	PIKVKKRKGK  lap  10 TVLDIVERAQS            GTVLDIVERAQS 0 160 0 70 EVYPEQNRPAVE             EVYPEQNRPAVE 0 220 0 130 LKGRVDLRDLPI            LKGRVDLRDLPI            CSSTSVYFPRRE	20 3 SKVVGRFYMDRGVAILEPE	DIDO OAIAO OK!KO OV!V
751 m988/a988 m988.pep a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA  97.0% identity i  LYERQMRGIMHGDIVT  130  40  KRLNQSIVLEPDGVAR                      KRLNQSIVLEPDGVAR  190  100  VRKHHLPHQFSEACAK                      VRKHHLPHQFSEACAK  250  160  VGRNYRLVVAIADVSH  :                  IGRNYRLVVAIADVSH  310	AA ESRKKAKKPV n 641 aa over  VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD              AAKKIPDHVRKSD 260 27 170 18 YVRPDDVIDADAQ       :      YVRPDDAIDTDAQ 320 33	PIKVKKRKGK  lap  10 TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70 EVYPEQNRPAVE             EVYPEQNRPAVE 0 220  0 130 LKGRVDLRDLPI            LKGRVDLRDLPI            ERSTSVYFPRRE 0 340	20 3 SKVVGRFYMDRGVAILEPE	DIDO 0AIAO 0K!KO 0V!VO
751 m988/a988 m988.pep a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA  97.0% identity i  LYERQMRGIMHGDIVT  130  40  KRLNQSIVLEPDGVAR                      KRLNQSIVLEPDGVAR  190  100  VRKHHLPHQFSEACAK                      VRKHHLPHQFSEACAK  250  160  VGRNYRLVVAIADVSH  :                  IGRNYRLVVAIADVSH  310	AA ESRKKAKKPV  n 641 aa over  VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI               FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD               AAKKIPDHVRKSD 260 27 170 18 YVRPDDVIDADAQ       :      YVRPDDAIDTDAQ 320 33	PIKVKKRKGK  lap  10 TVLDIVERAQS             GTVLDIVERAQS 0 160 0 70 EVYPEQNRPAVA             EVYPEQNRPAVA 0 220 0 130 LKGRVDLRDLPI            LKGRVDLRDLPI            ERSTSVYFPRRV 1           ERSTSVYFPRRV 0 340 0 250	20 3 SKVVGRFYMDRGVAILEPE	DIDO OAIAO OKIKO OVIVO O
751 m988/a988 m988.pep a988 m988.pep a988 m988.pep a988	AEKKTARGGK VRGRGASA  97.0% identity i  LYERQMRGIMHGDIVT  130  40  KRLNQSIVLEPDGVAR                      KRLNQSIVLEPDGVAR  190  100  VRKHHLPHQFSEACAK                      VRKHHLPHQFSEACAK  250  160  VGRNYRLVVAIADVSH  :                  IGRNYRLVVAIADVSH  310  220  ERLCMVCDMVVTYAGN	AA ESRKKAKKPV n 641 aa over  VRPAGMDGRGRRE 140 15 50 6 FKPESGQVIVGEI              FKPESGQVIVGEI 200 21 110 12 AAKKIPVHVRKSD              AAKKIPDHVRKSD 260 27 170 18 YVRPDDVIDADAQ               YVRPDDAIDTDAQ 320 33 230 24 IKEYRFYPAVMRS	PIKVKKRKGK  lap  10 TVLDIVERAQS             GTVLDIVERAQS 0 160  0 70 EVYPEQNRPAVE             EVYPEQNRPAVE 0 220  0 130 LKGRVDLRDLPI            LKGRVDLRDLPI            ERSTSVYFPRN 1          ERSTSVYFPRN 0 340  0 250 HARLTYNQVWKE	20 3 SKVVGRFYMDRGVAILEPE	DIDO OAIAO OKIKO OVIVO OL

ERLCVVCDMVITYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSGGIEHPFKTQIDTLYKL

			•				
	37	0	380	390	400	410	420
m988.pep	28 FKILOKKRF	•	290 SVETQMIFDD	300 NGKIEKIVPV	310 VRNDAHKLIE	320 ECMLAANVCA	330 ADF
mood.pop						1111111111	
a988	FKILQKKRF 43	ERGAVEFD	SIETQMLFDD 440	NGKIEKIVPV 450	VRNDAHKLIE 460	ECMLAANVCA 470	ADF 480
	34		350	360	370	380	390
m988 pep	LLKNKHTAL	FRNHLGPT	PEKLATLREC	PGTPGTÖTGG	GUNPSPKDYF	ALVEQFKGRE	DAE
-000		FRMHLGPT	PEKTAATREC	TGLLELLI MGLGLGLG	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	:        ALAGQFKGRP	DAE
a988	49		500	510	520	530	540
	40	Λ	410	420	430	440	450
m988.pep						AIKAVLNQQT	
mado.pep						11111111	
a988						AIKAVLNQQT	
	55	0	560	570	580	590	600
	46	0	470	480	490	500	510
m988.pep	KKSWQALGV	HTSFCERR	ADDASRDVEN	WLKTYYMRDK	VGEVFEGKIS	GMTSFGIFVT	LDG
						111111111	
a988						GMTSFGIFVT	
	61	0	620	630	640	650	660
	52	0	530	540	550	560	570
m988.pep						ADLDDGKIDF	
a988	IHIDGLVHI 67		NERPEIMALE	GERSGIRENM 690	IGDRVAVRVAR 700	ADLDDGKIDF 710	720
	67	U	660	690	700	710	120
	58		590	600	610	620	630
m988.pep						AAAESRKKAK	
						111111111	
a988	AGGSGRGRK 73		PAGTAGKGKF 740	750	760	AAAESRKKAK 770	780
	73	J	, 40	. 50			
	64	_					
m988.pep	PIKVKKRKG						
a988							
a 200	79						
		-					

# The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2985>: 9989.seq

989.seq					
1	ATGACCCCTT	TCACACTGAA	AAAAACCGTC	CTGCTGCTCG	GCACTGCCTT
51	TGCCGCCGCA	TCTGTCCACG	CATCCGGCTA	CCACTTCGGC	ACACAGTCGG
101	TCAACGCGCA	AAGCACGGCA	AATGCCGCCG	ACGCGTCGAC	CATCTTCTAC
151	AATCCCGCCG	GCCTGACCAA	ACTCGACAGC	AGCCAGATTT	CCGTCAACGC
201	CAACATCGTG	CTGCCCAGCA	TTCATTATGA	AGCAGATTCC	GCCACCGACT
251	TTACCGGGCT	TCCCGTCCAA	GGTTCTAAAA	ACGGCAAAAT	CACCAAAACC
301	ACGGTCGCAC	CCCACATTTA	CGGCGCATAC	AAAGTCAACG	ACAATCTGAC
351	CGTGGGCTTG	GGCGTGTACG	TCCCCTTCGG	CTCTGCCACC	GAATACGAAA
401	AAGATTCCGT	GTTGCGCCAC	AACATCAACA	AACTCGGTCT	GACCAGCATC
451	GCCGTCGAAC	CTGTCGCCGC	GTGGAAACTC	AACGAACGCC	ATTCCTTCGG
501	CGCAGGCATC	ATCGCCCAAC	ATAATTCCGC	CGAACTGCGC	AAATATGCCG
551	ACTGAGGAAT	CCCAAAAAAA	GCGCAAATGC	TGCAAGCAAC	ACCTTCTAAT
601	CCTACTGCCG	CTGCTCAAAT	CAAGGCCGAC	GGACACGCCG	ATGTCAAAGG
651	CAGCGATTGG	GGCGTCGGCT	ACCAACTGGC	GTGGATGTGG	GACATCAACG
701	ACCGCGCGCG	CGTGGGCGTG	AACTACCGTT	CCAAAGTTTC	ACACACGCTC
751	AAAGGCGATG	CCGAATGGGC	GGCAGACGGC	GCGGCGGCGA	AACAACAGTG
801	GAATGACAAT	ATGCTCACAC	CGCTCGGTTA	CACGGCGAAT	GAAAAAGCCA
851	GTGTCAAAAT	CGTAACGCCT	GAGTCTTTGT	CCGTACACGG	CATGTACAAA

WO 99/57280

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1404
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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACTTGGA CGCGCCACAG
 951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA
```

### This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```
g989.pep
         MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
         NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
     101 TVAPHIYGAY KVNDNLTVGL GVYVPFGSAT EYEKDSVLRH NINKLGLTSI
     151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
     201 PTAAAQIKAD GHADVKGSDW GVGYQLAWMW DINDRARVGV NYRSKVSHTL
     251 KGDAEWAADG AAAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMYK
         VSDKADLFGD VTWTRHSRFN KAELFFEKEK NIANGKKSDR TTITPNWRNT
         YKVGLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
         KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
```

IGLQYTYKFK * 451

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2987>:

```
m989.seq
         ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
      1
         TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
      51
    101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
    151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
    201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
    251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTC GAAAAGCGGC
    301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
         CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
     401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
     451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
     501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
     551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
     601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAGGC
     651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
     701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACTAC
     751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
     801 CGGCGCGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
     851 ACACGGCGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
     901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCGGCGA
     951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
    1001 AAAAAGAAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
    1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
    1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
          TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
          TGGTTCTCCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
          TGCCGCCTAC ACCCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
          AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
          AAAAACCACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
    1351
    1401
```

### This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```
MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEAADA
 1
    STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
    GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNGVA EAAKIQADGH ADVKGSDWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMYKVSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT
```

a989.seq

351	PNWRNTYKVG	FGGSYQISEP	LQLRAGIAFD	KSPVRNADYR	MNSLPDGNRI
					Dercycevor

401 WFSAGMKYHI GKNHVVDAAY THIHINDTSY RTAKASGNDV DSKGASSARF

451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results: Homology with a predicted ORF from *N. gonorrhoeae* 

	g989/m989	90.0% identity in 468 aa overlap
	g989.pep m989	10 20 30 40 50  MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAADASTIFYNPAGL    :
	g989.pep m989	60 70 80 90 100 110  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN                              TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN  70 80 90 100 110 120
	g989.pep m989	120 130 140 150 160 170 LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN
	g989.pep	180 190 200 210 220 230 SAELRKYADXGIPKKAQMLQATPSNPTAAAQIKADGHADVKGSDWGVGYQLAWMWDI
	g989.pep	240 250 260 270 280 290  NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES
	g989.pep	300 310 320 330 340 350 LSVHGMYKVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKSDRTTITPNWRNTYK
	g989.pep	360 370 380 390 400 410 VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDA   :
	g989.pep	420 430 440 450 460 AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX
The f	following pa	artial DNA sequence was identified in N. meningitidis <seq 2989="" id="">:</seq>

ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT

51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG

101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA

151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA

201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG

251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTC GAAAAGCGGC

301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT

301	AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT	
351	CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG	
401	CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC	
451	GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA	
501	ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC	
551	TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA	
601	GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA	
651	CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA	
701	TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAACTA CCGTTCCAAA	
751	GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT	
801	GGCGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC	
851	CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA	
901	CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC	
951	TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAACTGGTT TTTGAAAAAG	
1001	AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC	
1051	TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCTTATC AAATCAGCGA	
1101	ACCGCTGCAA CTGCGCGCG GCATCGCTTT TGACAAATCG CCCGTCCGCA	
1151	ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC	
1201	TCCGCCGGCA TGAAATACCA TATCGGCAAA AACCACGTCG TCGATGCCGC	
1251	CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA	
1301	GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAAC	
1351	CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA	
1551		
This corresponds	s to the amino acid sequence <seq 2990;="" 989.a="" id="" orf="">:</seq>	
	to the annio acid soquence bby 15 2550, ord 505.2	
a989.pep	MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA	
1	MTPSALKKTV LLLGTAFAAA SAQASGIHIG IQSVNAQSIA NAAAACAADA	
51	STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG	
101	KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL	
151	GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK	
201	ETPPNPTKAA QIKADGHADV KGSDWGFGYQ LAWMWDINDR ARVGVNYRSK	
251	VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV	
301	HGMYKVSDKA DLFGDVTWTR HSRFDKAELV FEKEKTIVNG KSDRTTITPN	
	WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF	
351	MKMIIVAGEG GOIOTOREDO DIGAGLACIDAS LAMMEDIAM DELEGIACIA	
351 401	SACMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN	
401	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN	
	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*	
401 451	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*	
401	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN	
401 451	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap	
401 451 m989/a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60	
401 451	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989	### SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*    93.1% identity in 467 aa overlap	
401 451 m989/a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989	### SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN  ###################################	
401 451 m989/a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989	### SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN  ###################################	
401 451 m989/a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989 m989.pep	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989 m989.pep	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989 m989.pep	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989 m989.pep	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60 MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	
401 451 m989/a989 m989.pep a989 m989.pep a989 m989.pep a989	SAGMKYHIGK NHVVDAAYTH IHINDTSYRT AKASGNDVDS KGASSARFKN HADIIGLQYT YKFK*  93.1% identity in 467 aa overlap  10 20 30 40 50 60  MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL	

	240	250	260	270	280	290	
	300	310	320	330	340	350	359
m989.pep	LSVHGM	YKVSDKADLE	GDVTWTRHSR	FDKAELVFEF	(EKTVVKGKSD         :   :	RTTITPNWF	RNTYKV
a989	LSVHGM	YKVSDKADLF	GDVTWTRHSR	FDKAELVFE	(EKTIVNGKSD	RTTITPNWE	RNTYKV
4303	300 .	310	320	330	340	350	
	360	370	380	390	400	410	419
m989.pep		QISEPLQLRA	GIAFDKSPVR	NADYRMNSLE	PDGNRIWFSAG	MKYHIGKNH	AADVVF
	[1][][	1111111111		111111111	1		
a989					PDGNRIWFSAG		AAGVVI
	360	370	380	390	400	410	
	420	430	440	450	460		
m989.pep	YTHIHI	NDTSYRTAKA	SGNDVDSKGA	SSARFKNHAI	OIIGLQYTYKF	'KX	
	111111	11111111	11111111111				
a989	YTHIHĪ				DIIGLQYTYKF	KX	
	420	430	440	450	460		

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2991>:

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m990.seq
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      1
         CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
     101 ATTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
    151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
    201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
    251 TAAAGCAGGC GGTTAAAAGT CAATTACAGG ATTTATACAA AACAAGACCG
     301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
     351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCC GATTTAATTA
     401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
     451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
     501 CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
     551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
     601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
         CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCCTGTTC GGCTACGACG
         TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
         CAATCCGGCG TGGTTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
          CGGGCGCAAA CTGATTGCGG CAAAAACGGC GGATTCCGGT TCGTTTGCGT
          TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
          GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
          AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
     951
          TGCGTGCCGC CGACAGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
    1001
          CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTCGCATC AAAATATACG
    1051
          GGGCGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
    1101
    1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCGTGATG
         GGCGGCAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
    1201
    1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
    1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
    1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
    1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
    1451 CGGAAGGCAT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
    1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGCGGCTTTA CCGACAGCGA
         GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
    1551
         GCATTCGGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
    1601
          CCTTTTGCCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
    1651
          AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
    1701
          GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
    1751
          TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
    1801
          GCTGTTTTGA
    1851
```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>: m990.pep

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1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGKNYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
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### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2993>:

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a990.seq
         ATGTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
         CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
    101 ATTTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
    151 GAAATCAATA TCCAAGGTAA AAACTACAAT AGCGGCATAC TCGCCGTCGA
    201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
     251 TAAAGGATGC GGTTAAGAAG CAATTACAGG ATTTATACAA AACAAGACCC
     301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGAACA
     351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
     401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
     451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
         CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
     501 CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
         ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
     651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCCTGTTC GGCTACGACG
     701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
     751 CAATCCGGCG TGGTTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
     801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCGT
     851 TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
     901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
     951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTCGGGC
    1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
    1051 CAAAAATTGT GGCTGCGCTT CATCGGCGGC CGGTCGCATC AAAATATACG
    1101 GGGCGGCGC GCTGCGGACG GGCGGCGCAA AGGCGTGCAA ATCGGCGGCG
    1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
    1201 GGCGGCAGGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
    1251 AGGCAGTTAT TTGCATGGTT ATGGCGGGGG TGTTTATGCT GCGTGGCATC
    1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
    1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
    1401 AACCAAAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
    1451 CGGAAGGCGT TGTCGGAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
    1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGCGGCTTTA CCGACAGCGA
    1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
    1601 GCATTCGGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
    1651 CCTTTTGCCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
    1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
    1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
          TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
    1801
    1851 GCTGTTTTGA
```

### This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

corresponds to the amino acid sequence \SEQ 1D 2554, Old 556.25.						
a990.pep					DOMESTICAN	
1	MFRAQLGSNT	RSTKIGDDAD	FSFSDKPKPG	TSHYFSSGKT	DÖM22F1G1D	
51	EINIQGKNYN	SGILAVDNMP	VVKKYITDTY	GDNLKDAVKK	QLQDLYKTRP	
101	EAWEENKKRT	EEAYIEQLGP	KFSILKQKNP	DLINKLVEDS	VLTPHSNTSQ	
151	TSLNNIFNKK	LHVKIENKSH	VAGQVLELTK	MTLKDSLWEP	RRHSDIHMLE	
201	TSDNARIRLN	TKDEKLTVHK	AYQGGADFLF	GYDVRESDKP	ALTFEEKVSG	
251	OSGVVLERRP	ENLKTLDGRK	LIAAEKADSN	SFAFKQNYRQ	GLYELLLKQC	
301	EGGFCLGVQR	LAIPEAEAVL	YAQQAYAANT	LFGLRAADRG	DDVYAADPSR	
351	OKLWLRFIGG	RSHQNIRGGA	AADGRRKGVQ	IGGEVFVRQN	EGSRLAIGVM	

### 1409 `

401 451 501 551 601	GGRAGQHASV NGKGGAAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG YGKRTDGDKE AALSLKWLF*
m990/a990	96.0% identity in 619 aa overlap
m990.pep	10 20 30 40 50 60  MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN
m990.pep a990	70 80 90 100 110 120 SGILAVDNMPVVKKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT
m990.pep	130 140 150 160 170 180 KFSTLKQTMPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK !!!
m990.pep	190 200 210 220 230 240 MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP
m990.pep	250 260 270 280 290 300 ALTFEDKVSGQSGVVLERRPENLKTLDGRKLIAAKTADSGSFAFKQNYRQGLYELLLKQC      :
m990.pep	310 320 330 340 350 360 EGGFCLGVQRLAIPEAEAVLYAQQAYAANTLFGLRAADRGDDVYAADPSRQKLWLRFIGG
m990.pep a990	370 380 390 400 410 420 RSHQNIRGGAAADGWRKGVQIGGEVFVRQNEGSRLAIGVMGGRAGQHASVNGKGGAAGSD
m990.pep	430 440 450 460 470 480 LYGYGGGVYAAWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN  :
m990.pep	490 500 510 520 530 540 ALVAEGIVGKGNNVRFYLQPQAQFTYLGVNGGFTDSEGTAVGLLGSGQWQSRAGIRAKTR      :
m990.per a990	550 560 570 580 590 600  FALRNGVNLQPFAAFNVLHRSKSFGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG

```
600
                                                                   590
                                                       580
                                            570
                                 560
                      550
                      610
              YGKRTDGDKEAALSLKWLFX
m990.pep
              111111111111111111111111
              YGKRTDGDKEAALSLKWLFX
a990
                                  620
                      610
```

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 2995>:

```
ATGTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
    GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGCGCGTTG GGTTATACGG
 1
101 GATATGACAG TGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GGCACTGCAG GGGACGTGGG TTTCGACGCG CCCGTTCGCC GACGGGCATC
    GGCGAAATCC GGCCACAGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGATACCCT TCACGTCATC GACGGCGACG GCGCGAAACA TAAAATTCGG
301 ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTTC
    GCGCGACAAC CTGCGCGCGG CGGCGGAGGG TAGGAAAGTC AGTGTACGTG
401 TGTTTGAAAC CGACCGCTAT CAGCGCGAAG TGGCGCAGGT ATCCGCCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATTA
    TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GGCGGATTTT GCCGACTATG
    CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCCGTG GGCGTACCGC CGGGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATTCCGTGGG CGAATGGTTG GGCATTTGGT
701
```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```
MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYDSEAV RTAVAVLDVL
a992.pep
         GTAGDVGFDA PVRRRASAKS GHSYTGTVSK VYDGDTLHVI DGDGAKHKIR
       1
     101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
         KTDLNLMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQA ERERKGLWKA
```

201 KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2997>:

```
ATGTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
m992.seq
         GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGTGCGTTG GGTTATACGG
         GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
      51
    151 GGCGCGGCAG GGGACGCGGG TTCCGACGCG CCCGCCCGCC GCCGAGCATC
     201 GGCGAAATCC GGCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
         GCGACACCCT TCACGTTATC GACGGCGACG GCGCGAAACA CAAAATCCGG
     301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
     351 GCGCGACAAC CTGCGCGCGG CGGCGGAAGG CAGGAAAGTC AGCGTGCGCG
     401 TGTTCGATAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGGC
         AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATTA
     501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GGCGGATTTT GCCGATTATG
     451
     551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
     601 AAAAATCCGC AAGCGCCGTG GGCGTACCGC CGAGCAGGCA GGAGCGGCGG
          GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTTGGT
     701 AA
```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```
MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL
m992.pep
         GAAGDAGSDA PARRASAKS GHRYTGTVSK VYDGDTLHVI DGDGAKHKIR
      51
         MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFDTDRY QREVAQVSVG
         KTDLNLMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQA ERERKGLWKA
     101
     201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from N. gonorrhoeae

	10	20	30	40	50	60
m992.pep	MFRRHRHLKNMQI	KKIMKWLPVAL	SLLGALGYTO	GYGSEAVRTAV	AVLDVLGAA	GDAGSDA
	1111111111111111	11111111111	1111111111	[] [] [] [] [] []	111111111	11:1-11
q992	MFRRHRHLKNMQI	KKIMKWLPVAL	SLLGALGYTO	SYDSEAVRTAV	/AVLDVLGTA	GDVGFDA
9	10	20	30	40	50	60
	70	80.	90	100	110	120
m992.pep	PARRRASAKSGH	RYTGTVSKVYDG	DTLHVIDGDO	SAKHKIRMAYI	DAPEMKQAY	
	1:1111111111	1111111111111	1111111111	[		
q992	PVRRRASAKSGHS	YTGTVSKVYDO	DTLHVIDGDO	GAKHKIRMAY)	DAPEMKQAY	STRSRDN
9552	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVF	RVFDTDRYQREV	AQVSVGKTDI	LNLMQVQDGAA	AWHYKSYAKE	QQDKADF
	31111111111111	111:111:111		[[[[]]]		
q992	LRAAAEGRKVSVF	RVFETDRYQREV	AQVSAGKTDI	LNLMQVQDGAA	WHYKSYAKE	QQDKADF
9332	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAER	RKGLWKAKNPO	)APWAYRRAGI	RSGGGNKDWMI	DAVGEWLGIW	X
most.pep			11111111		:	I
q992	ADYADAQIQAERI	RKGLWKAKNPO	APWAYRRAGI	RSGGGNKDWMI	OSVGEWLGIW:	X
9552	190	200	210	220	230	

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 2999>:

1992.seq					
1	ATGTTCAGAC	GGCATCGGCA	TTTGAAAAAT	ATGCAGATTA	AAAAAATCAT
51	GAAATGGCTT	CCCGTCGCCT	TGTCGCTTTT	GGGTGCGTTG	GGTTATACGG
101		CGAGGCGGTG			
151	GGCGCGGCAG	GGGACGCGGG	TTCCGACGCG	CCCGCCCGCC	GCCGAGCATC
201	GGCGAAATCC	GGCCACCGCT	ACACAGGCAC	GGTGTCCAAA	GTCTATGACG
251	GCGACACCCT	TCACGTTATC	GACGGCGACG	GCGCGAAACA	CAAAATCCGG
301	ATGGCGTATA	TCGACGCGCC	GGAGATGAAA	CAGGCTTACG	GCACGCGTTC
351	GCGCGACAAC	CTGCGCGCGG	CGGCGGAAGG	CAGGAAAGTC	AGCGTCCGCG
401	TGTTCGACAC	CGACCGCTAC	CAGCGCGAAG	TGGCGCAGGT	TTCTGTCGGC
451	AAAACCGATT		GCAGGTGCAG		
501	TAAAAGTTAT	GCTAAAGAAC	AGCAGGATAA	GGCGGATTTT	GCCGATTATG
551		AATTCAGGCG	GAAAGGGAAC	GCAAAGGATT	GTGGAAAGCT
601		AAGCGCCGTG		CGGGCAGGCA	GGAGCGGCGG
651		GATTGGATGG		CGAATGGTTG	GGCATTTGGT
701	AA	GIIII DGIII CO			•
701	AA				

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

- MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL 51 GAAGDAGSDA PARRRASAKS GHRYTGTVSK VYDGDTLHVI DGDGAKHKIR 101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFDTDRY QREVAQVSVG 151 KTDLNLMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQA ERERKGLWKA 201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from N. meningitidis

a992/m992	100.0% identity	in 233 a	a overlap			
	10	20	30	40	50	60
a992.pep	MFRRHRHLKNMQIK	KIMKWLPVA	LSLLGALGYTG	YGSEAVRTA	VAVLDVLGAAG	DAGSDA
F-F	111111111111111111111111111111111111111	1111111111	11111111111	11111111	1111111111	
m992	MFRRHRHLKNMQIK	KIMKWLPVA	LSLLGALGYTG	YGSEAVRTA	VAVLDVLGAAC	
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRY	TGTVSKVYD	GDTLHVIDGDG	AKHKIRMAY:		
• •	[ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [ [	111111111	111111111111	11111111		
m992	PARRRASAKSGHRY	TGTVSKVYD	GDTLHVIDGDG	AKHKIRMAY:	IDAPEMKQAYO	STRSRDN
	70	80	90	100	110	120
	130	140	150	160	170	180
	130	140	130	100	1,0	100

PCT/US99/09346 WO 99/57280

```
1412
```

```
LRAAAEGRKVSVRVFDTDRYQREVAQVSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF
a992.pep
         {\tt LRAAAEGRKVSVRVFDTDRYQREVAQVSVGKTDLNLMQVQDGAAWHYKSYAKEQQDKADF}
m992
               130
                      140
                              150
                                     160
                                             170
                              210
                                     220
                      200
               190
         ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX
a992.pep
         ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX
m992
                              210
                                     220
                      200
```

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 3001>:
g993.seq
```

```
CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
 1
     CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGGAAA
 51
     TTACCGGGCA GTATCTGCAC TATATTGCCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGTCTGC TTGCCTACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGGA CGCGCTGCCG CGTGCGGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
     TTCATCGCCC TGTTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GGCGCGATGT GTTCTAA
```

#### This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>: q993.pep

- LKVVLGSFQG PLDLLLYLIR KQNIDVLDIP MVEITGQYLH YIAQMEAYQF 1
- DLAAEYLLMA AMLIEIKSRL LLPRTEAVED EEADPRAELV RRLLAYEQMK 51 LAAOGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA 101
- 151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHALFNP EQGAAYVIVN
- 201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 3003>: m993.seq

```
TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
      TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCCG ATGGTGAAGA
 51
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
.201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCCTGC TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGGA CGCGCTGCCC CGAGCCGGAC GGGATTTCGC
      GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCGTCAAC
601 TTCATCGCAC TGTTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
 651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
 701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GGCGCGATGT GTTCTAA
```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>: m993.pep

- LKVVLGSFQG PLDLLLYLIR KQNIDVLDIP MVKITEQYLH YIAQIETYQF
- 51 DLAAEYLLMA AMLIEIKSRL LLPRTETVED EEADPRAELV RRLLAYEQMK 101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
- KHTRSHEVIK ETISVRAQMT AILRRLNGHG ICRFHDLFNP KQGAAYVVVN
- FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from N. gonorrhoeae

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from N. gonorrhoeae

```
m993/q993
          93.1% identity in 248 aa overlap
                        20
          LKVVLGSFQGPLDLLLYLIRKQNIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA
m993.pep
          g993
          LKVVLGSFQGPLDLLLYLIRKQNIDVLDIPMVEITGQYLHYIAQMEAYQFDLAAEYLLMA
                10
                        20
                                30
                                        40
                                                50
                70
                        80
                                90
                                       100
                                               110
                                                       120
          AMLIEIKSRLLLPRTETVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY
m993.pep
          AMLIEIKSRLLLPRTEAVEDEEADPRAELVRRLLAYEQMKLAAQGLDALPRAGRDFAWAY
q993
                70
                        80
                                90
                                       100
               130
                       140
                               150
                                       160
                                               170
m993.pep
          LPLEIAVEAKLPEVYITDLTQAWLGILSRAKHTRSHEVIKETISVRAQMTAILRRLNGHG
          LPLEIAAETKLPEVYIADLMQAWLGILSRAKHTRSHEVIQETLSVRAQMTAILRRLNEHG
a993
                       140
                               150
                                       160
                                               170
               190
                       200
                               210
                                       220
                                               230
                                                       240
          ICRFHDLFNPKQGAAYVVVNFIALLELAKEGLVRIVQEDGFGEIRISLNHEGAHSDGISG
m993.pep
          ICRFHALFNPEQGAAYVIVNFIALLELAKEGLVGIVQEDGFGEIRISLNHEGAHSDGIFG
q993
               190
                       200
                               210
                                       220
               249
m993.pep
          TRGGRDVFX
          1111111111
          TRGGRDVFX
q993
```

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 3005>:

```
a993.seq
         CTGAAAGTCG TATTGAGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
         CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGAAGA
      51
     101
         TTACCGAACA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
         GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
    151
    201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
    251
         ACCCGCGTGC CGAGTTGGTG CGCCGCCTGC TGGCTTACGA GCAGATGAAG
    301 CTGGCGGCAC AAGGGTTGGA TGCGCTTCCT CGTGCGGGCC GGGATTTCGC
         ATGGGCATAC CTGCCACTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
    401
         TCTATATTAC CGACTTGACG CAGGCGTGGC TGAGTATTTT GTCTCGGGCA
    451
         ANACATACGC GCAGCCACGA AGTTATCAAA GAAACCATCT CCGTGCGCGC
         GCAAATGACG GCAATCCTGC GCCGTTTGAA CAAACACGGG ATATGCAGGT
    501
    551
         TTCACGACCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GGTCGTCAAC
    601
         TTCATCGCAC TGTTGGAGCT TGCCAAAGAA GGTTTGGTCG GAATCGTACA
    651 GGAAGTCGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
    701 ATTCAGACGG CATTTCCGGC ACACGGGGCG GGCGCGATGT GTTCTAA
```

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>: a993.pep

```
1 LKVVLSSFQG PLDLLLYLIR KQNIDVLDIP MVKITEQYLH YIAQIETYQF
51 DLAAEYLLMA AMLIEIKSRL LLPRTETVED EEADPRAELV RRLLAYEQMK
```

- 101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
- 151 KHTRSHEVIK ETISVRAQMT AILRRLNKHG ICRFHDLFNP EQGAAY<u>VVVN</u> 201 FIALLELAKE GLVGIVQEVG FGEIRISLNH EGAHSDGISG TRGGRDVF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from N. meningitidis

	10	20	30	40	50	60
	70	80	90	100	110	120
a993.pep	AMLIEIKSRLLLP	RTETVEDEEAD	PRAELVRRL	LAYEQMKLAA(	)GLDALPRAGE	RDFAWAY
					:	
m993	AMLIEIKSRLLLP			-		
	70	80	90	100	110	120
	• • • •		150	* 60	170	
	130	140	150	160	170	180
a993.pep	LPLEIAVEAKLPE	VYITDLTQAWL	SILSRAKHTI	RSHEVIKETIS	VRAQMTAILF	RRLNKHG
		11111111111				111 11
m993	LPLEIAVEAKLPE'	VYITDLTQAWL	GILSRAKHTI	RSHEVIKETIS	VRAQMTAILF	RRLNGHG
	130	140	150	160	170	180
	190	200	210	220	230	240
a993.pep	ICRFHDLFNPEQGA	<b>AAYVVVNFIAL</b>	LELAKEGLVO	GIVQEVGFGEI	RISLNHEGAH	ISDGISG
	[]]]]]]]]]]			1111 1111	1111111111	111111
m993	ICRFHDLFNPKQG2	AAYVVVNFIAL	LELAKEGLVE	RIVQEDGFGEI	RISLNHEGAH	ISDGISG
	190	200	21 Ö	220	230	240
	249					
a993.pep	TRGGRDVFX					
	11111111					
m993	TRGGRDVFX					

The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 3007>: g996.seq

```
ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGCGCGTTGC TTCTTACCGC
51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTCACCT TCGGCTACGG AGCAAACCCC
151 GGCGAATCCT ACCCCGCGCA ACTGCAAAAAA CTGACGGGTT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCGCAAAGT TCCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAAA CATTCCCGCC GTCCTCGTCG
401 GCGTGCCGCA CATCACACTG GGCGCTTGT TCGGGCATTT GAGCGACCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CGCCTGGGCG GAAATTTTGG GCAATAATAA TCTGAAATCC GACCAAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTCG CCGAAAATTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA
```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>: g996.pep

- 1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
- 51 GESYPAQLQK LTGWNIVNGG VSGDTSAQAL SRLPALLARK PKLVIVGIGG
- 101 NDFLRKVPEE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
- 151 PLYEDLSEEY GIPLFGGAWA EILGNNNLKS DQIHANGKGY RKFAENLNQF
- 201 LRKHGFR*

### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 3009>:

```
ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGCGCGTTGC TGCTTACCGC

51 CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA

101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCT

151 GGCGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT

201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCCTGC

251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC

301 AACGACTTTC TGCGCAAAGT TCCCAAGGAG CAGACCCGGC CCAATATCGC

351 GAAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCCGGC GTCCTCGTCG

401 GCGTGCCGCA CATCACACTG GGTGCGTTGT TCGGCGATCAT

451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG

501 CGCCTGGGGCG GAAATTTTGG GCGATATATAA TCTGAAATCC GACCAAATCC

551 ACGCCAACGG CAAAGGCTAT CGGAAATTTT GAATCAATTT

601 TTGAGAAAAC AGGGGTTTAG ATAA
```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>: m996.pep

- 1 MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
- 51 GESYPAQLQK LTGWNIVNGG VSGDTSAQAL SRLPALLARK PKLVIVGIGG

```
1415
```

- 101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
- PLYEDLSEEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF

LRKQGFR 201

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from N. gonorrhoeae

```
98.1% identity in 207 aa overlap
m996/q996
                         20
                                 30
                                         40
                                                 50
          MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK
m996.pep
          MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK
g996
                 10
                         20
                                 30
                                         40
                         80
                                        100
                 70
          LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
m996.pep
          LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPEEQTRANIAKII
g996
                                 90
                                        100
                                                110
                         80
                130
                        140
                                150
                                        160
                                                170
          ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEEYGIPLFGGAWAEILGDNNLKS
m996.pep
          ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEEYGIPLFGGAWAEILGNNNLKS
g996
                        140
                                150
                                        160
                                                170
                                                         180
                130
                190
                        200
          DQIHANGKGYRKFAEDLNQFLRKQGFR
m996.pep
          111111111111111111111111111111
          DQIHANGKGYRKFAENLNQFLRKHGFRX
q996
                        200
                190
```

The following partial DNA sequence was identified in N. meningitidis <SEO ID 3011>: a996.seq

```
ATGAACAGAA GAACCTTCCT CCTCGGCGCA GGCGCGTTGC TCCTTACCGC
    CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
 51
101 CCGTACTTGC CTTGGGCGAT TCGCTTACCT TCGGCTACGG CGCAAACCCC
    GGCGAATCCT ACCCCGCGCA ACTGCAAAAA CTGACGGGTT GGAATATTGT
151
201 CAACGGCGGC GTATCGGGCG ATACATCCGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCGCAAAGT TCCCAAGGAG CAGACCCGCG CCAATATCGC
    GAAAATCATC GAAACCGTGC AGAAGGAAAA CATCCCCGCC GTCCTCGTCG
401 GCGTGCCGCA CATTACCTTG GGCGCGTTGT TCGGGCATTT GAGCGATCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG
    CGCGTGGGCG GAAATTTTGG GCGATAATAA TCTGAAATCC GACCAAATCC
501
551 ACGCCAACGG CAAAGGCTAT CGGAAATTTG CCGAAGATTT GAATCAATTT
    TTGAGAAAAC AGGGGTTTAG ATAA
```

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>: a996.pep

- MNRRTFLLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
- GESYPAQLQK LTGWNIVNGG VSGDTSAQAL SRLPALLARK PKLVIVGIGG 51
- 101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
- 151 PLYEDLSEEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. meningitidis

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from N. meningitidis

```
100.0% identity in 207 aa overlap
a996/m996
                                                      40
             {\tt MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPAQLQK}
a996.pep
```

```
MNRRTFLLGAGALLLTACGRKSARTHAKI PEGSTVLALGDSLTFGYGANPGESYPAQLQK
m996
                      20
               10
                             90
                                    100
                                           110
                      80
         LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
a996.pep
         LTGWNIVNGGVSGDTSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
m996
               70
                      80
                             90
                                    100
                                           110
                                           170
                                                  180
                                    160
              130
                     140
                             150
         ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEEYGIPLFGGAWAEILGDNNLKS
a996.pep
         ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEEYGIPLFGGAWAEILGDNNLKS
m996
              130
                             150
                                    160
                     200
              190
         DOIHANGKGYRKFAEDLNQFLRKQGFRX
a996.pep
         DQIHANGKGYRKFAEDLNQFLRKQGFR
m996
              190
                     200
```

```
The following partial DNA sequence was identified in N. gonorrhoeae <SEQ ID 3013>:
         (partial)
q997.seq
```

```
ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
     CTGGGCCGGC TTGTCCGCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
     CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
101
     GGAAATACCG ACGGTTTCGG TTTTTTGGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCAGACC
     CCCGTGCCGC CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
251
     TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
301
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACTGCTTG
    CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
    ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
451
     GCAGTTTTGG CAGCCCTTGG TCTGGGGCGC GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
     CGTCGCCGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
651
     GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
     CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGCc CGCCCCGCTG ACcGGCATtg CCGAcggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGGCAGGC tccggactgc CcccaaAacg
     aagTCTCCGC cGTCAttagc GTTTCCGAcc GCGtcggcgC Gtttgcaaac
1001
1051 cga...
```

#### This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>: g997.pep

```
MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
    GNTDGFGFLD NGQHILLGAY RGVLRLMKTI GSDPRAAFLR VPLHWHMHGG
    LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPDT
101
    TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVLT
201 KKSGSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
    LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
251
    AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
```

#### The following partial DNA sequence was identified in N. meningitidis <SEQ ID 3015>: m997.seq

```
ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
    CTGGGCAGGA CTGTCCGCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
51
    CCCTGTTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
101
    GGAAATACCG ACGGTTTCGG TTTTTTGGAC AACGGGCAGC ACATTTTGCT
151
    CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCGGATC
    CCCGTGCCGC CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
251
    TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCGCTGCATA TTTTGGGCGG
301
    CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAACTGCTTG
351
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
    ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
451
    GCAGTTTTGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAA
```

```
CCGCAAGCCT GCGCGTGTTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
 551
     AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
     CGTCGCCGAA CCCGCCTTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
 651
     GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
     CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
 751
     CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
 801
     CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
 851
     GCCGAACCCG TCCGCCTGCC CGCCCCGCTG ACCGGCCTTG CCGACGGCAC
 901
     GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
 951
     TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1001
     GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1051
     GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1101
     CAGCCGATGC CCCGCCGCCG GACTTGTCGT GGTTGCACCG GCACCGCATC
1151
     TTCCCCGCCG GCGACTACCT CCACCCGGAC TACCCCGCCA CGCTCGAAGC
1201
     CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1251
     GCGATGCCGT CTGA
1301
```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

m997.pep

MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA GNTDGFGFLD NGQHILLGAY RGVLRLMKTI GSDPRAAFLR VPLHWHMHGG 51 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPDT 101 TVAOWLKORN VPRAAVMOFW OPLVWGALNT PLETASLRVL CNVLSDGVLT 151 KKSGSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY 251 AEPVRLPAPL TGLADGTVQW LLCRGRLGLP ENEVSAVISV SDRVGAFANR 301 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from N. gonorrhoeae

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from N. gonorrhoeae

g997/m997 96.0% identity in 351 aa overlap 40 30 MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGFLD g997.pep MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGFLD m997 20 30 90 100 110 120 NGQHILLGAYRGVLRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL g997.pep NGQHILLGAYRGVLRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL m997 70 80 90 100 110 120 130 140 150 160 170 ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT g997.pep ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT m997 160 170 130 140 150 220 230 240 200 210 190 g997.pep PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRVC PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC m997 190 200 210 220 250 260 270 280 290 RLNTLPDGKVLVNGEAFDAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY q997.pep RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY m997 250 260 270 280 290 300 320 330 340 AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFANR q997.pep m997 AEPVRLPAPLTGLADGTVQWLLCRGRL-GLPENEVSAVISVSDRVGAFANRAWADKAHAD 310 320 330 340 350

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 3017>: a997.800

```
ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
  51 CTGGGCCGGC TTGTCCGCCG CCGTTACCTT GGCGCGCAC GCCGACGTTA
 101 CCCTGTTTGA AGCCGGCCGG CAGGCGGCG GCAGGGCGCG CGCACTGGCC
 151
     GGAAATACCG ACGGTTTCGG TTTTTTGGAC AACGGGCAGC ATATTTTACT
 201 CGGCGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCAGACC
 251 CCCATGCCGC CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
     TTGCAGTTCC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
 301
     CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACTGCTTG
 351
 401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
 451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
 501
     GCAGTTTTGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAA
 551 CCGCAAGCCT GCGCGTGTTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
 601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
 651
     CGTCGCCGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
 701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
     CTCGTCAACG GCGAACCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
 801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
     CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
 851
901 GCCGAACCCG TCCGCTTGCC TGCCCCGCTG ACCGGACTTG CCGACGGCAC
     GGTGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
951
1001
     TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051
     GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101
     GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCCG GATTTGTCGT GGTTGCACCG GCACCGCATC
     TTCCCCGCCG GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1201
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>: a997.pep

```
1 MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51 GNTDGFGFLD NGQHILLGAY RGVLRLMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPDT
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVLT
201 KKSGSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTVQW LLCRGRLGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

#### Homology with a predicted ORF from N. meningitidis

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from N. meningitidis

a997/m997	98.2% identity in 437 aa overlap
	10 20 30 40 50 60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARALAGNTDGFGFLD
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGFLD
	10 20 30 40 50 60
	70 80 90 100 110 120
a997.pep	NGQHILLGAYRGVLRLMKTIGSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL
m997	NGQHILLGAYRGVLRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL
	70 80 90 100 110 120
	130 140 150 160 170 180
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMOFWOPLVWGALNT
	130 140 150 160 170 180
	190 200 210 220 230 240
a997.pep	PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC

WO 99/57280 PCT/US99/09346

1419

```
PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLORLGADIRLETRVC
m997
                                          220
                 190
                                 210
                                                  230
                         260
                 250
                                 270
                                         280
                                                  290
                                                          300
           {\tt RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY}
a997.pep
           RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
m997
                250
                         260
                                 270
                                         280
                                                  290
                                                          300
                310
                         320
                                 330
                                         340
                                                  350
                                                          360
          AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
a997.pep
           AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
m997
                         320
                                 330
                370
                         380
                                 390
                                         400
                                                  410
          KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVQ
a997.pep
           KRILPHLGEPEAVRVITEKRATTAADAPPPDLSWLHRHRIFPAGDYLHPDYPATLEAAVO
m997
                370
                         380
                                 390
                                         400
                                                  410
                                                          420
                430
a997.pep
          SGFASAEACLQSLSDAVX
          13111111111111111111
m997
          SGFASAEACLQSLSDAVX
                430
```

g999.seq Not found yet g999.pep Not found yet

The following partial DNA sequence was identified in N. meningitidis <SEQ ID 3019>: m999.seq

```
ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
 51
    AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
    GTATCCAGGC TGCTGATTGT ACCGCCCCAA TGGACATCAC AGTTGAACAA
101
    TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
151
    AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
201
    TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
251
301
    ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
    ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
351
    TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
    CAACTTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
451
501
    AGCAACAGCG CAAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551
    TTTTTGAAAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA
```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>: m999.pep

```
1 MNMKKLISAI CVSIVLSACN QQSKTAQAEE PVQSIQAADC TAPMDITVEQ
51 YLINLEQAFK TQNVSTKIHN KNIVKTDCGY DLTLVMDFGA IALKLDEQQK
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTTT DKLGESEAGK
151 QLFTALTEVV KESNQTGATA QKDVPADGIL YSVVFEKETN TIAIIGRKQP
```

a999.seq Not found yet a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

#### **CLAIMS**

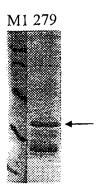
- 1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
- 2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
  - 3. A protein having 50% or greater homology to a protein according to claim 1.
- 4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
  - 5. An antibody which binds to a protein according to any one of claims 1 to 3.
- 6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
- 7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
- 8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
- 9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
- 10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
- 11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
- 12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
- 13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
  - 14. A composition according to claim 11 for use as a pharmaceutical.
- 15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

- 16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.
- 17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.
- 18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

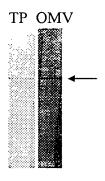
### 279 (10.5 kDa)

Fig. 2

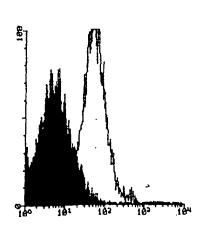
A) PURIFICATION



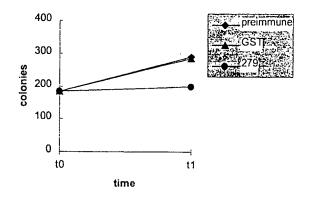
**B)WESTERN BLOT** 



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

#### 279

The predicted gene 279 was cloned in pGex vector and expressed in E. coli. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, N. meningitidis total protein extract; OMV, N. meningitidis outer membrane vescicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the N. meningitidis immunoreactive band (B).

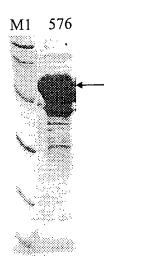
2/30

PCT/US99/09346

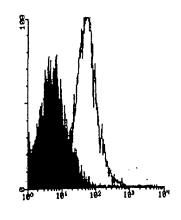
Fig. 3

576 (27.8 kDa)

A) PURIFICATION



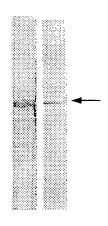
C) FACS



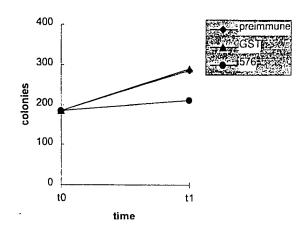
#### E) ELISA assay: positive

#### B) WESTERN BLOT

TP OMV



#### D) BACTERICIDAL ASSAY



#### 576

The predicted gene 576 was cloned in pGex vector and expressed in E. coli. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, N. meningitidis total protein extract; OMV, N. meningitidis outer membrane vescicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the N. meningitidis immunoreactive band (B).

Fig. 4

TP

519 (33 kDa)

#### A) PURIFICATION

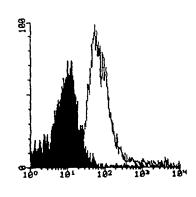
M1 519

**OMV** 

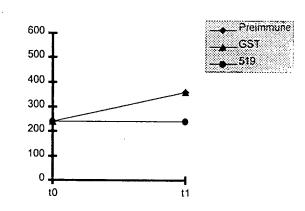
### B) WESTERN BLOT



#### C) FACS



#### D) BACTERICIDAL ASSAY



#### E) ELISA assay: positive

#### 519

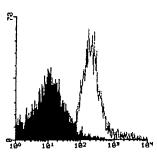
The predicted gene 519 was cloned in pET vector and expressed in E. coli. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, N. meningitidis total protein extract; OMV, N. meningitidis outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the N. meningitidis immunoreactive band (B).

### 121 (40 kDa)

### A) PURIFICATION

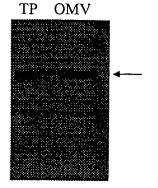
M1 121

### C) FACS

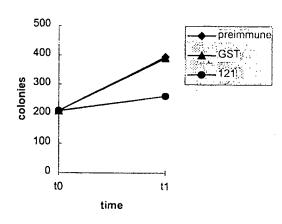


E) ELISA assay: positive

### B) WESTERN BLOT



#### D) BACTERICIDAL ASSAY



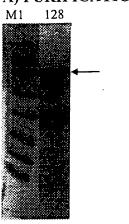
#### 121

The predicted gene 121 was cloned in pET vector and expressed in E. coli. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, N. meningitidis total protein extract; OMV, N. meningitidis outer membrane vescicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the N. meningitidis immunoreactive band (B).

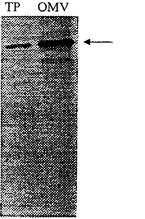
### 128 (101 kDa)

Fig. 6

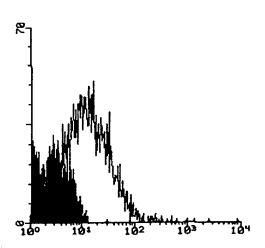
A) PURIFICATION



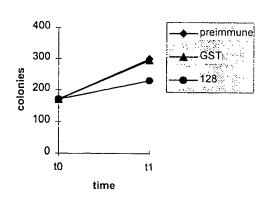
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

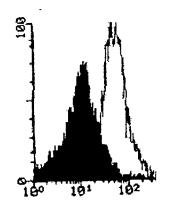
#### 128

The predicted gene 128 was cloned in pET vector and expressed in E. coli. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, N. meningitidis total protein extract; OMV, N. meningitidis outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the N. meningitidis immunoreactive band (B).

A) PURIFICATION

M1 206

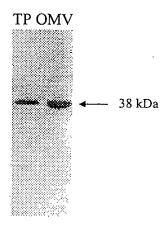
C) FACS



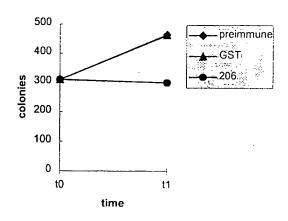
E) ELISA assay: positive

Fig. 7

#### B) WESTERN BLOT



#### D) BACTERICIDAL ASSAY



#### 206

The predicted gene 206 was cloned in pET vector and expressed in E. coli. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in E. coli without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from E. coli expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, N. meningitidis total protein extract; OMV, N. meningitidis outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the N. meningitidis immunoreactive band (B).

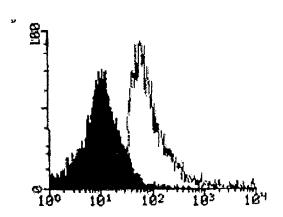
287 (78 kDa)

Fig. 8

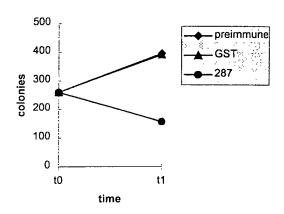
A) PURIFICATION



B) FACS



C) BACTERICIDAL ASSAY



D) ELISA assay: positive

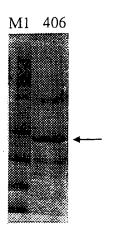
287

The predicted gene 287 was cloned in pGex vector and expressed in E. coli. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

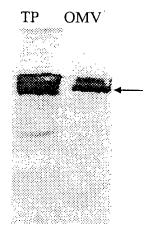
406 (33 kDa)

Fig. 9

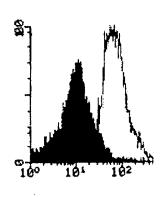
A) PURIFICATION



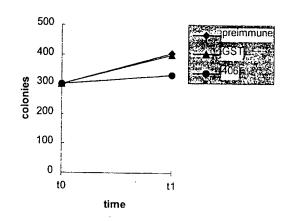
B) WESTERN BLOT



C) FACS



D) BACTERICIDAL ASSAY



E) ELISA assay: positive

#### 406

The predicted gene 406 was cloned in pET vector and expressed in E. coli. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, N. meningitidis total protein extract; OMV, N. meningitidis outer membrane vescicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the N. meningitidis immunoreactive band (B).

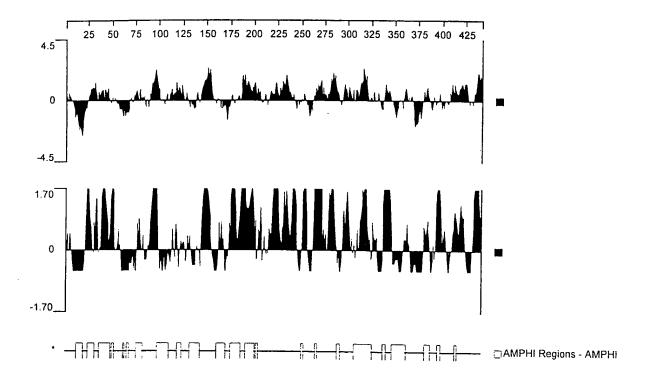


Fig. 10

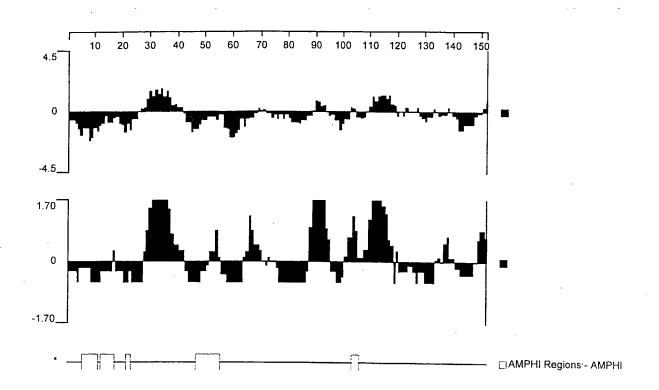


Fig. 11

11/30 **576-1** 

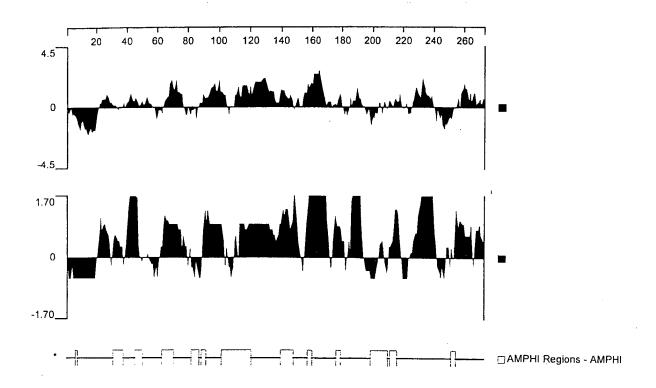


Fig. 12

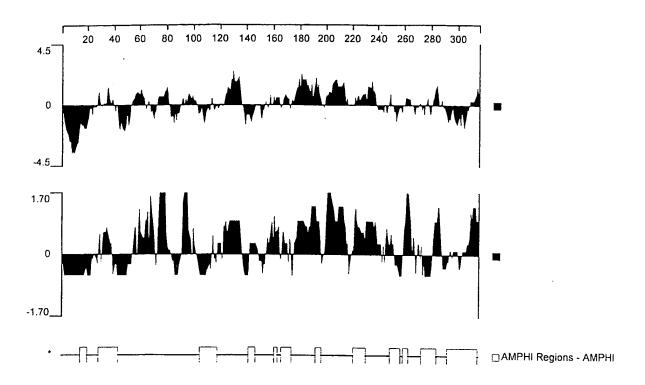


Fig. 13

13/30 **121-1** 

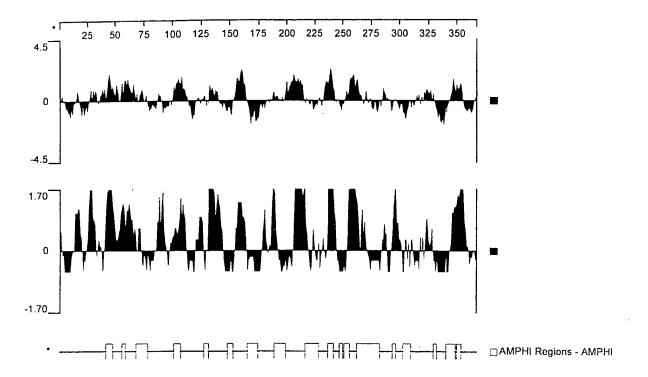


Fig. 14

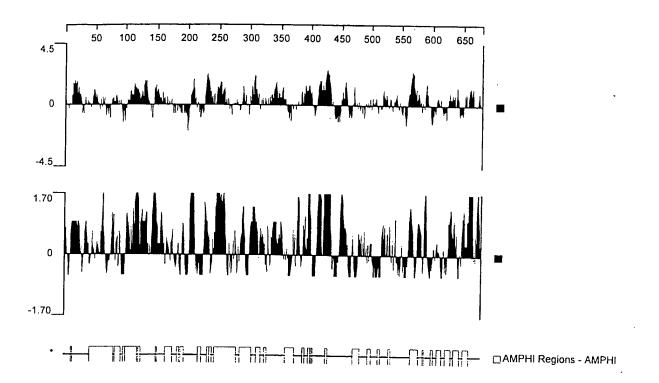


Fig. 15

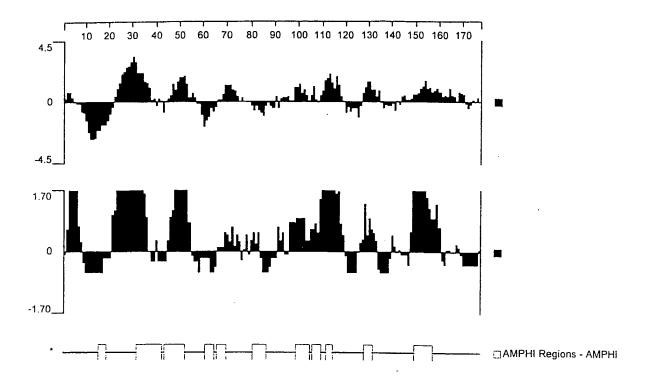


Fig. 16

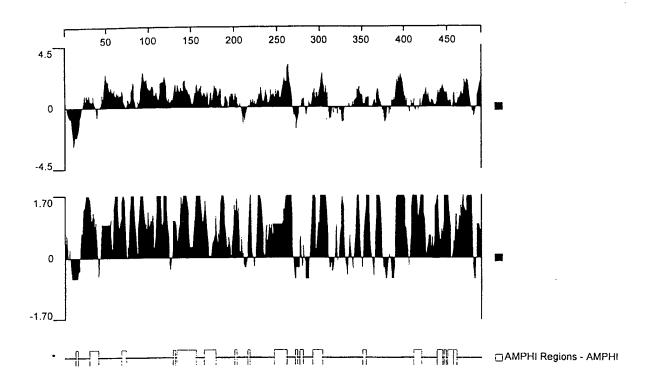


Fig. 17

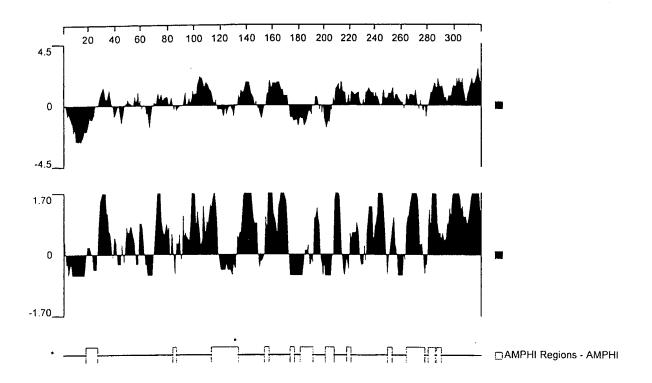


Fig. 18

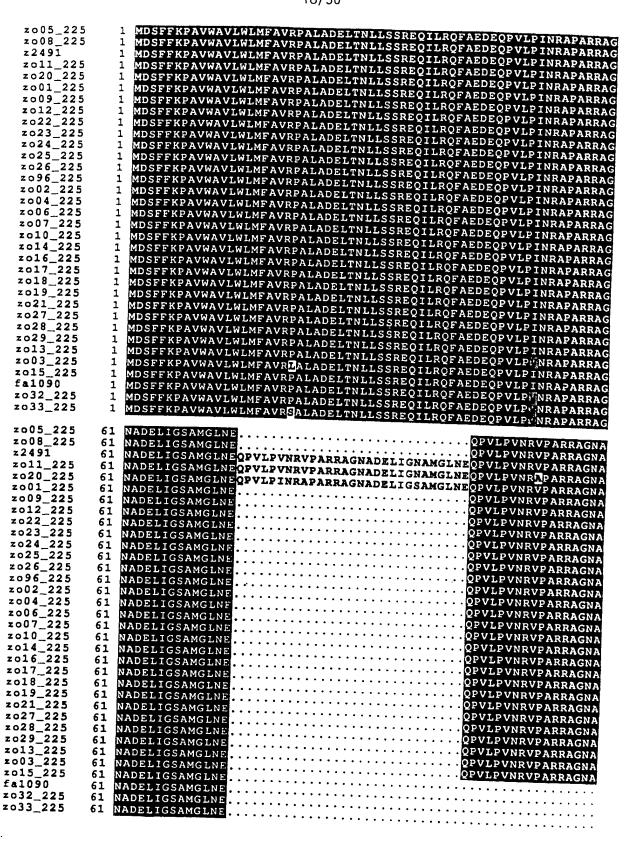


Fig. 19A

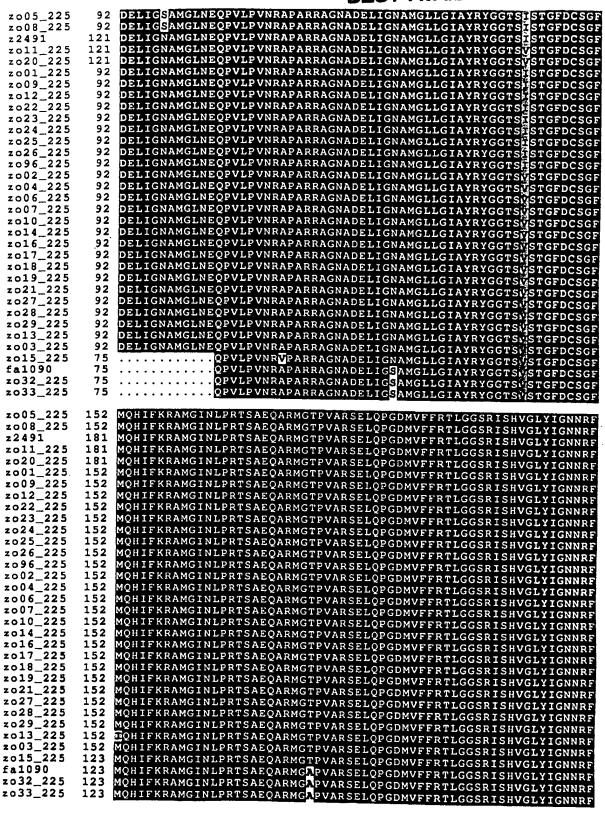


Fig. 19B

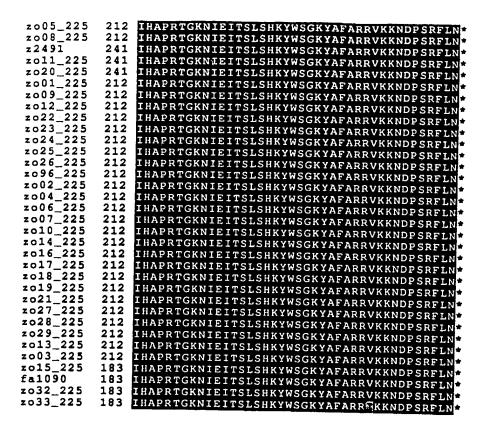


Fig. 19C

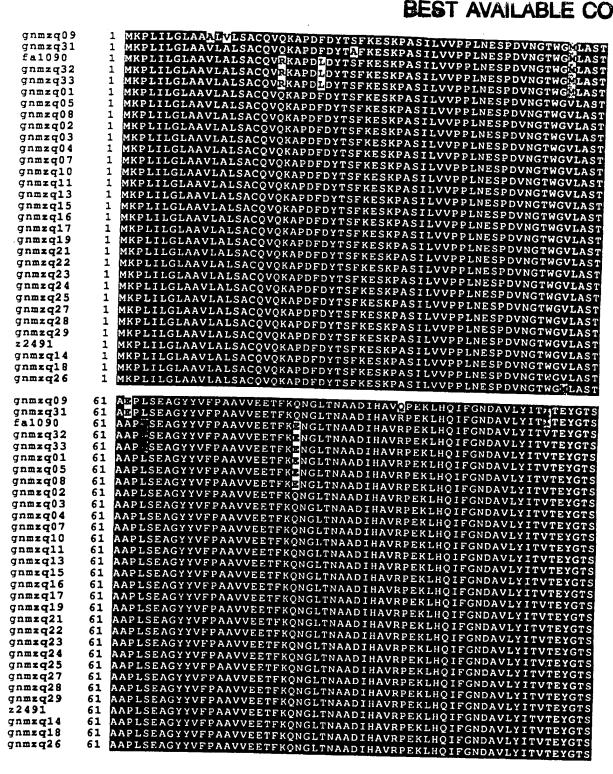


Fig. 20A

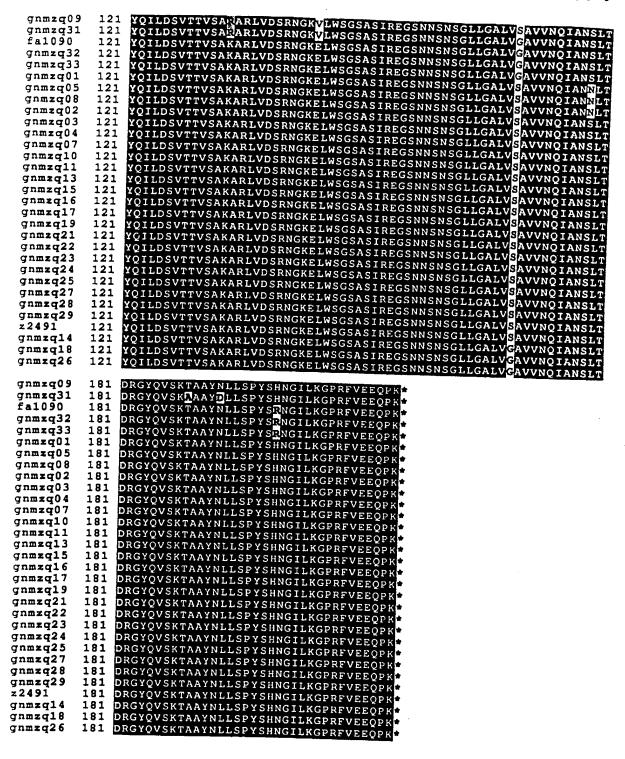
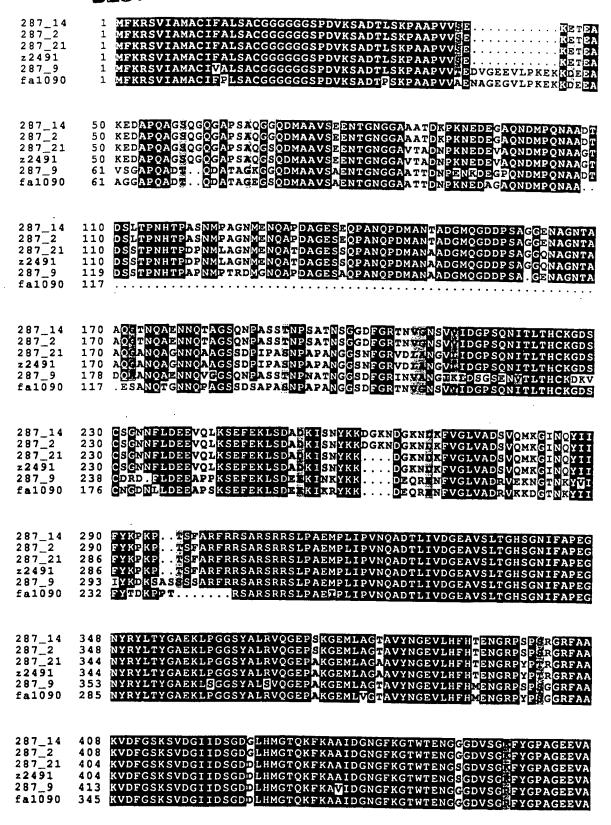


Fig. 20B

WO 99/57280 PCT/US99/09346



287_14	468	GKYSYRPTDAEKGGFGVFAGKKEOD
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287_21	464	GKYSYRPTDAEKGGFGVFAGKKEOD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEOD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEOD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKIND*

FIG. 21B

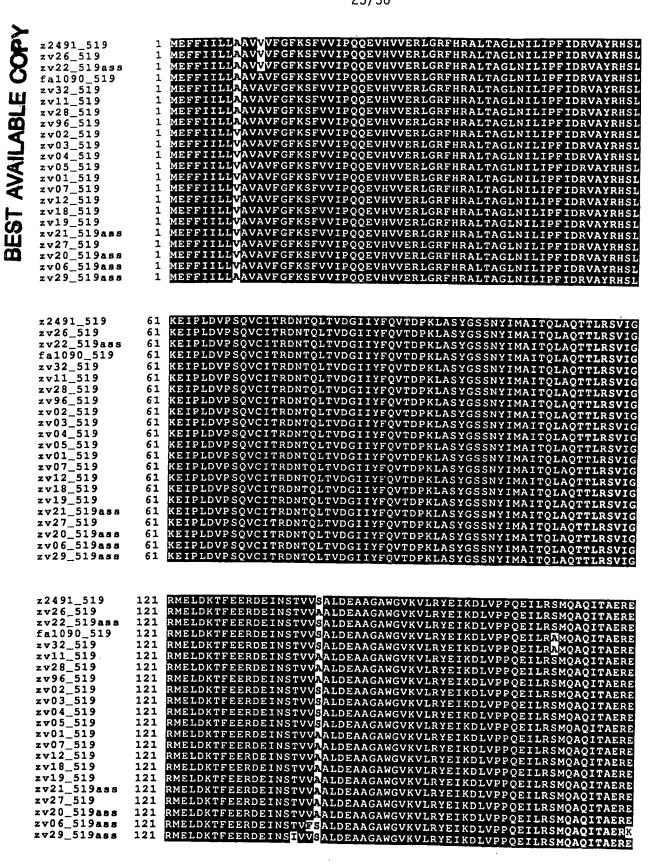


FIG. 22A

zv07_519 zv12_519 zv18_519 zv19_519 zv21_519ass

zv27_519 zv20_519ass zv06_519ass zv29_519ass

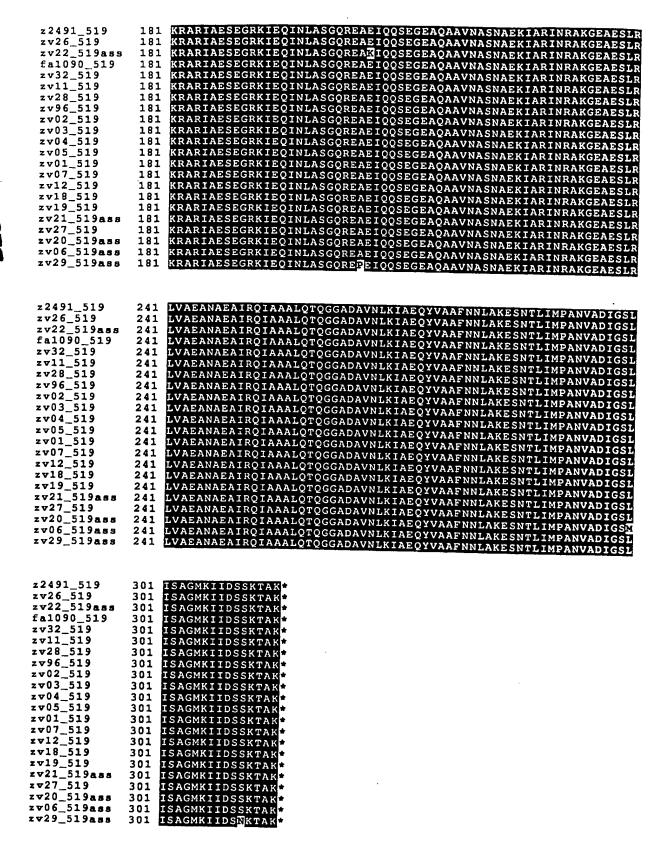


Fig. 22B

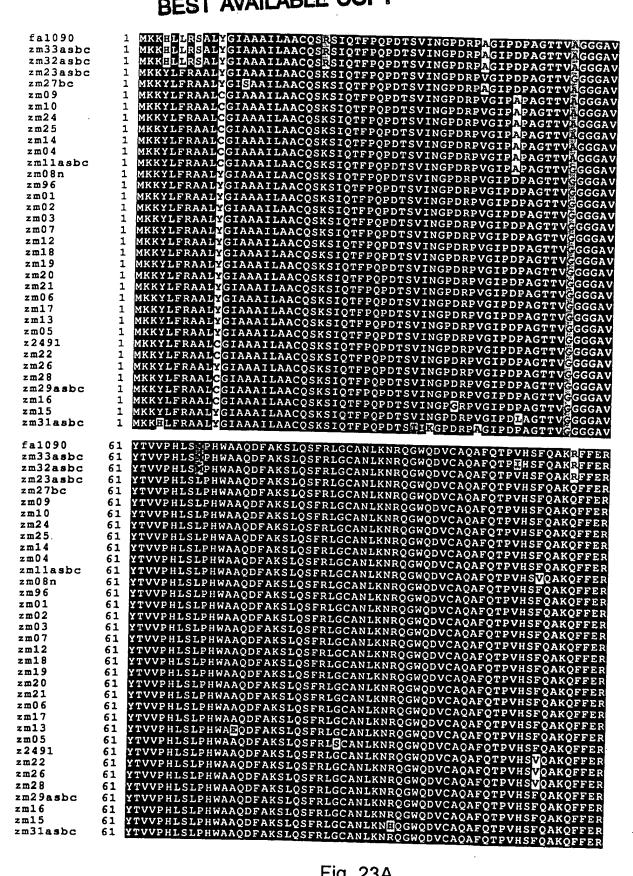


Fig. 23A

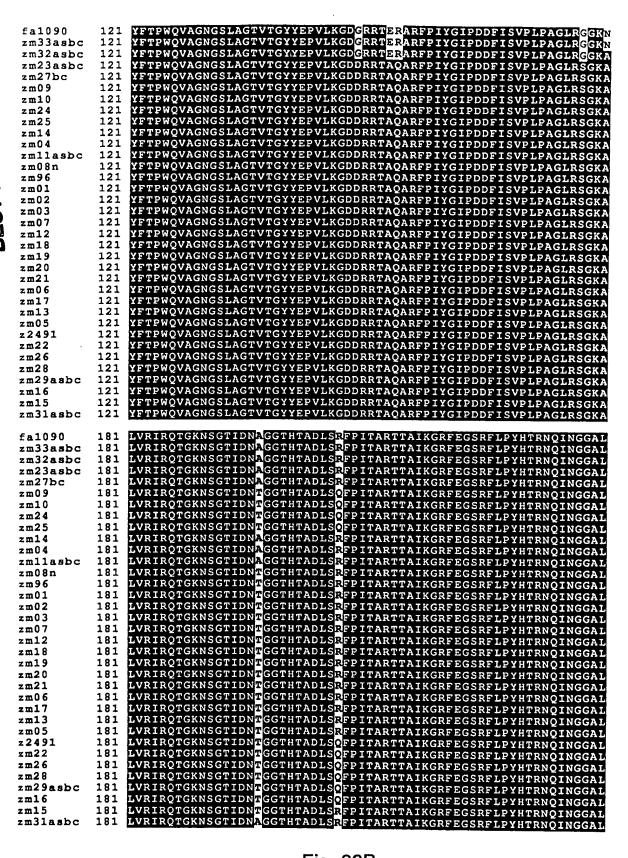


Fig. 23B

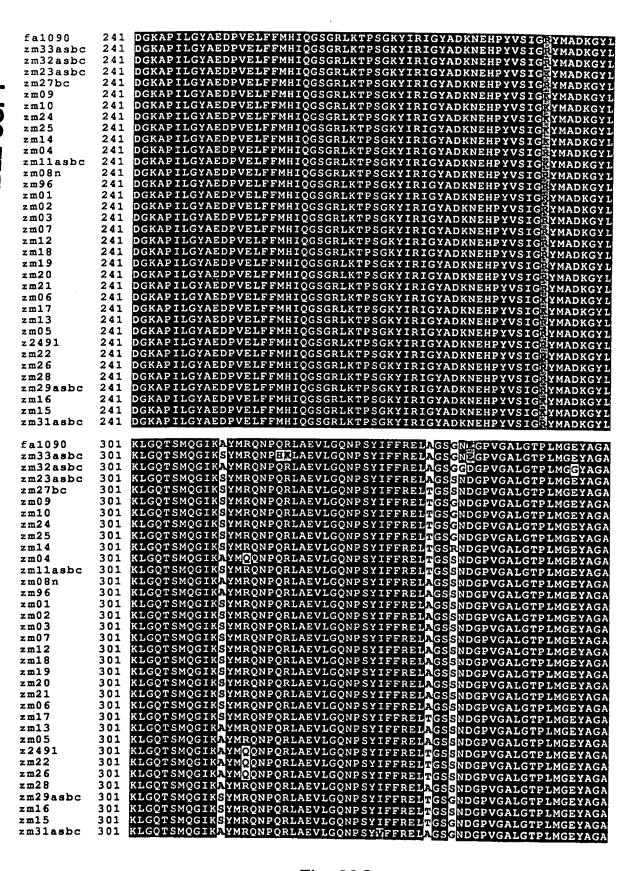


Fig. 23C

zm31aabc

```
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       zm33asbc
       zm32asbc
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       zm23asbc
                                                              361
       zm27bc
                                                              361
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      zm24
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Fig. 23D